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> O <
O | O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq99var" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "kml07.key":
seq99 (AA) ID seq99 AA preliminary pattern
1 followed by
2 cf
2 q or a
2 w or l
2 any character
2 x or k or a
2 any character
2 m or l
2 x or k
2 kvr

Selected files:
File : hu.pep

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact Indirect file
Find non-matching hits only No Sequence or key file
Report key used Yes List of hits
Note position of hit Yes Hit display
Display full annotations Yes Name and annotations
Sequence context 50

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

-----
1 match found in sequence:
tthul ; TOIG of: tthul check: 8418 from: 1 to: 711
(from "hu.pep")
TOIG of: tthul check: 8418 from: 1 to: 711

Pl:TFHUL - lactotransferrin precursor [validated] - human
N:Alternate names: lactoferrin
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169;
A31000; S74119; A03261; A38029
R:Cho, Y.
Submitted to the EMBL Data Library, March 1994
A:Reference number: G06820
A:Accession: G01394
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-711 <CHO>
A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237
R:Rey, M.W.; Woloshuk, S.L.; deSoet, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A:Reference number: S11228; MUID:90384839; PMID:2402455
A:Accession: S11228
A:Molecule type: mRNA
A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>
A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416
R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A:Title: Differential molecular mechanism of the estrogen action that regulates
lactoferrin gene in human and mouse.
A:Reference number: A45401; MUID:93125571; PMID:1480183
A:Accession: A45401
A:Molecule type: DNA
A:Residues: 1-15 <TEN>
A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312
A:Experimental source: placenta
A:Note: sequence extracted from NCBI backbone (NCBIP:122202)
R:Powell, M.J.; Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A:Title: Nucleotide sequence of human lactoferrin cDNA.
A:Reference number: S10324; MUID:90326549; PMID:2374734
A:Accession: S10324
A:Molecule type: mRNA
A:Residues: 3-711 <POW>
A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412
R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A:Reference number: S15853; MUID:91264786; PMID:2049066
A:Accession: S15853
A>Status: nucleic acid sequence not shown; not compared with conceptual
translation
A:Molecule type: mRNA
A:Residues: 20-31 <ST1>
A:Accession: S20841
A:Molecule type: protein
A:Residues: 20-28, 'X', 30-31 <ST2>
R:Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A:Title: Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis.
A:Reference number: S07160; MUID:88001031; PMID:3477300
A:Accession: S07160
A:Molecule type: mRNA
A:Residues: 436-487, 'A', 489-711 <RAD>
A:Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855
R:Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal
leukocytes, leukemic cells, and breast cancer.
A:Reference number: A61169; MUID:91235214; PMID:1674448
A:Accession: A61169
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 3-701, 'SWKPVN' <PAN>
A:Experimental source: normal breast tissue
R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.;
Spij, G.; Montreuil, J.; Jolles, P.
Eur. J. Biochem. 145, 659-666, 1984
A:Title: Human lactotransferrin: amino acid sequence and structural comparisons
with other transferrins.
A:Reference number: A31000; MUID:85076667; PMID:6510420
A:Accession: A31000
A:Molecule type: protein
A:Residues:
20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-409, '
N', 411, 'SVLMDSEGGFLAR', 412-531, 'E', 533-694, 'R', 696-711 <MET>
A:Note: this is the final paper in a series
R:Houen, G.; Hoegdall, E.V.; Barkholt, V.; Nørskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A:Title: Lactoferrin: similarity to diamine oxidase and purification by
aminoethyl affinity chromatography.
A:Reference number: S74119; MUID:97054624; PMID:8898921
A:Accession: S74119
A:Molecule type: protein
A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOH>
A:Experimental source: neutrophil granulocytes
C:Genetics:
A:Gene: GDB:LTf

```

A/Cross-references: GDB:119368; OMIM:150210  
 A:Map position: 3q21-3q23  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein; iron binding; milk  
 F1-19/Domain: signal sequence #status predicted <Sig>  
 F120-711/Product: lactotransferrin #status experimental <MAT>  
 F121-356/Domain: transferrin repeat homology <TRH1>  
 F1360-699/Domain: transferrin repeat homology <TRH2>  
 F129-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds:  
 #status experimental  
 F1257,498/binding site: carbohydrate (Asn) (covalent) #status experimental  
 F1368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide  
 bonds: #status predicted

TFHUL Length: 711 January 24, 2003 09:39 Type: P Check: 8418 ..  
 Found using 'seq99' (kam107.key)

1 MKLVFLVLLFLGALGLCLAGRRRSVOMCAVSQPEATKCFQWQRMKRVGPPVSCIKRD  
 39  
 50

61 SPIQICQIAENRADAVTLDDGGFIYEAGLAPYKLRPVAAE  
 39

1 match found in sequence:  
 trfhuman ; Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin  
 (from "hu.pep")  
 TOIG of: trf\_human check: 8418 from: 1 to: 711

-----  
 ID TREL\_HUMAN STANDARD; PRT; 711 AA.  
 AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9HLZ3; Q96KZ4;  
 AC Q96KZ5;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;  
 Lactoferrin B; Lactoferrin C]  
 OS LTP OR LF.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=90384839; PubMed=2402455;  
 RA Rey M.W., Moloshuk S.L., de Boer H.A., Pieper F.R.;  
 ET "Complete nucleotide sequence of human mammary gland lactoferrin.";  
 RL Nucleic Acids Res. 18:5288-5288(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Cho Y.Y.;  
 RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC Connely O.M.;  
 RA Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Liang Q., Jimenez-Flores R., Richardson T.;  
 RT "Molecular cloning and sequence analysis of human lactoferrin.";  
 RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RA Wei X., Han J., Rado T.A.;  
 RT "Human neutrophil lactoferrin coding and 5' flanking region DNA  
 sequences.";  
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.

[6]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Mammary Gland;  
 RA Cheng H., Chen X., Huan L.;  
 RT "cDNA cloning and sequence analysis of human lactoferrin.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 3-711 FROM N.A.  
 RC TISSUE=Mammary Gland;  
 RX MEDLINE=90326549; PubMed=2374734;  
 RA Powell M.J., Ogden J.E.;  
 RT "Nucleotide sequence of human lactoferrin cDNA.";  
 RL Nucleic Acids Res. 18:4013-4013(1990).  
 RN [9]  
 RP SEQUENCE OF 20-711.  
 RX MEDLINE=85076667; PubMed=6510420;  
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
 LeGrand D., Spik G., Montreuil J., Jolles P.;  
 RT "Human lactotransferrin: amino acid sequence and structural  
 comparisons with other transferrins.";  
 RL Eur. J. Biochem. 145:659-666(1984).  
 RN [10]  
 RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
 RX MEDLINE=82046817; PubMed=6794640;  
 RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
 Jolles P.;  
 RT "The present state of the human lactotransferrin sequence. Study and  
 alignment of the cyanogen bromide fragments and characterization of  
 N- and C-terminal domains";  
 RL Biochim. Biophys. Acta 670:243-254(1981).  
 RN [11]  
 RP SEQUENCE OF 609-711.  
 RX MEDLINE=82262043; PubMed=7049727;  
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
 Jolles P.;  
 RT "An 88 amino acid long C-terminal sequence of human  
 lactotransferrin";  
 RL FEBS Lett. 142:107-110(1982).  
 RN [12]  
 RP SEQUENCE OF 436-711 FROM N.A.  
 RX MEDLINE=88001031; PubMed=3477300;  
 RA Rado T.A., Wei X., Benz E.J. Jr.;  
 RT "Isolation of lactoferrin cDNA from a human myeloid library and  
 expression of mRNA during normal and leukemic myelopoiesis.";  
 RL Blood 70:989-993(1987).  
 RN [13]  
 RP SEQUENCE OF 237-711 FROM N.A.  
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
 Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
 Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
 Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
 Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
 Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
 Sagripanti J.L.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
 RX MEDLINE=90064528; PubMed=2585506;  
 RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
 RT "Structure of human lactoferrin: crystallographic structure analysis  
 and refinement at 2.8-A resolution.";  
 RL J. Mol. Biol. 209:711-734(1989).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RA Haridas M., Anderson B.F., Baker E.N.;  
 RT "Structure of human diferric lactoferrin refined at 2.2-A  
 resolution.";  
 RL Acta Crystallogr. D 51:629-646(1995).



[16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
BA Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
binding properties and crystal structure of the histidine-  
253-->methionine mutant.";  
RL Biochemistry 36:341-346(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347; Jameson G.B., Baker E.N.;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in Aspergillus  
awamori.";  
RL Acta Crystallogr. D 55:403-407(1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
and analysis of ligand-induced conformational change.";  
RL Acta Crystallogr. D 54:1319-1335(1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1169293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioïd antagonist peptides derived  
from human lactoferrin.";  
RL Agric. Biol. Chem. 54:1803-1810(1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
RA Qumsiyeh M.B., Lin P.-Y., Bassi S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaranickavel G., Munier F., Schorderet D.F.,  
RA El Matti L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejtmancik J.P., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RL Mol. Vision 4:31-32(1998).  
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
OF AN ANION, USUALLY BICARBONATE.  
CC -!- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST  
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
-----  
CC EMBL; X53961; CRA37914.1; -  
CC EMBL; U07643; AAB60324.1; -  
CC EMBL; M93150; AAA36159.1; -  
CC EMBL; M83202; AAA59511.1; -  
CC EMBL; M83205; AAA58656.1; -  
CC EMBL; M18642; AAA86665.1; -  
CC EMBL; AF332168; AAG48753.1; -  
CC EMBL; BC015822; AAH15822.1; -  
CC EMBL; BC015823; AAH15823.1; -  
CC EMBL; M73700; AAA59479.1; -  
CC EMBL; X52941; CRA37116.1; -  
CC EMBL; U95626; AAB57795.1; -

PIR; S11228; TFHUL.  
PDB; 1LCF; 31-AUG-94.  
PDB; 1LCT; 31-OCT-93.  
PDB; 1LFG; 31-JUL-94.  
PDB; 1LPH; 31-OCT-93.  
PDB; 1LFI; 31-OCT-93.  
PDB; 1LGS; 31-AUG-94.  
PDB; 1LGC; 31-AUG-94.  
PDB; 1BKA; 08-NOV-96.  
PDB; 1DSN; 08-MAR-96.  
PDB; 1HSE; 12-MAR-97.  
PDB; 1VFD; 21-APR-97.  
PDB; 1VFE; 01-APR-97.  
PDB; 1BOL; 18-NOV-98.  
PDB; 1CB6; 12-MAR-99.  
GlycoSuiteDB; P02788; -  
DR Genew; HGNC:6720; LTF.  
DR MIM; 150210; -  
DR MIM; 245480; -  
DR InterPro; IPR001156; Transferrin.  
DR Pfam; PF00405; transferrin; 2.  
DR PRINTS; PR00422; TRANSFERRIN.  
DR SMART; SM00094; TR\_FER; 2.  
DR PROSITE; PS00205; TRANSFERRIN\_1; 2.  
DR PROSITE; PS00206; TRANSFERRIN\_2; 2.  
DR PROSITE; PS00207; TRANSFERRIN\_3; 2.  
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
KW Signal; Polymorphism; 3D-structure.  
FT SIGNAL 1 19  
FT CHAIN 20 711 LACTOFERRIN.  
FT PEPTIDE 339 344 LACTOFERROXIN A.  
FT PEPTIDE 544 548 LACTOFERROXIN B.  
FT PEPTIDE 681 687 LACTOFERROXIN C.  
FT REPEAT 20 364 1.  
FT REPEAT 365 711 2.  
FT DISULFID 29 65  
FT DISULFID 39 56  
FT DISULFID 135 218  
FT DISULFID 177 193  
FT DISULFID 190 201  
FT DISULFID 251 265  
FT DISULFID 368 400  
FT DISULFID 378 391  
FT DISULFID 425 706  
FT DISULFID 447 669  
FT DISULFID 479 554  
FT DISULFID 503 637  
FT DISULFID 513 527  
FT DISULFID 524 537  
FT DISULFID 595 609  
FT DISULFID 647 652  
FT METAL 80  
FT METAL 112 112 IRON 1.  
FT METAL 212 212 IRON 1.  
FT METAL 273 273 IRON 1.  
FT METAL 415 415 IRON 2.  
FT METAL 455 455 IRON 2.  
FT METAL 548 548 IRON 2.  
FT METAL 617 617 IRON 2.  
FT BINDING 141 141 ANION (POTENTIAL).  
FT BINDING 485 485 ANION (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. ).  
FT CARBOHYD 498 498 N-LINKED (GLCNAC. ).  
FT VARIANT 30 30 A -> T.  
FT VARIANT 48 48 /FTID=VAR\_013504.  
FT VARIANT 149 149 K -> R (IN DBSNP:1126478).  
FT VARIANT 423 423 I -> T (IN DBSNP:1126479).  
FT VARIANT 423 423 G -> C (IN DBSNP:1042055).  
FT VARIANT 580 580 /FTID=VAR\_013507.  
FT VARIANT 580 580 E -> D (IN DBSNP:2073495).  
FT /FTID=VAR\_013508.



Number of sequence hits: 2  
Number of separate matches: 2  
Number of sequence hits saved: 0

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:37:21 ; Search time 21.0698 Seconds  
(without alignments)  
56.918 Million cell updates/sec

Title: US-09-743-107b-101

Perfect score: 51

Sequence: 1 GPPVSCIKR 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	16	AA87905	Human lactoferrin
2	51	100.0	22	AAV6886	Amino acid sequenc
3	51	100.0	21	AAV78004	Human lactoferrin
4	51	100.0	23	AAV78005	Human lactoferrin
5	51	100.0	25	AAV69353	Human lactoferrin
6	51	100.0	15	AAV88217	Amino acid sequenc
7	51	100.0	25	AAW24267	Antifungal peptide
8	51	100.0	25	AAW24268	Antifungal peptide
9	51	100.0	25	AAV07252	Lactoferrin peptid
10	51	100.0	25	AAV83109	Synthetic lactofer

11	51	100.0	25	21	AAV85010	Human lactoferrin
12	51	100.0	25	21	AAV78002	Human lactoferrin
13	51	100.0	25	21	AAV78003	Human lactoferrin
14	51	100.0	28	16	AAV87907	Human lactoferrin
15	51	100.0	29	21	AAV57320	Human lactoferrin
16	51	100.0	29	21	AAV78100	Human lactoferrin
17	51	100.0	36	14	AAV44846	Lactoferrin-relate
18	51	100.0	36	17	AAV10517	Lactoferrin-derive
19	51	100.0	36	17	AAV10521	Lactoferrin-derive
20	51	100.0	36	17	AAV91857	Lactoferrin-derive
21	51	100.0	36	17	AAV90811	Lactoferrin-derive
22	51	100.0	36	17	AAV87626	Lactoferrin-derive
23	51	100.0	36	18	AAV24269	Antifungal peptide
24	51	100.0	36	18	AAV24271	Antifungal peptide
25	51	100.0	36	20	AAV07253	Lactoferrin peptid
26	51	100.0	47	15	AAV48535	Lactoferrin-derive
27	51	100.0	47	15	AAV57467	Lactoferrin-derive
28	51	100.0	47	16	AAV84704	Bovine lactoferrin
29	51	100.0	47	16	AAV80269	Anti-parasitic lac
30	51	100.0	47	17	AAV10519	Lactoferrin-derive
31	51	100.0	47	18	AAV26155	Lactoferrin-derive
32	51	100.0	47	18	AAV24270	Antifungal peptide
33	51	100.0	47	18	AAV14041	Anti-parasitic pep
34	51	100.0	47	19	AAV70315	Thrombus formation
35	51	100.0	47	19	AAV70316	Thrombus formation
36	51	100.0	47	19	AAV53230	Lactoferrin hydrol
37	51	100.0	47	19	AAV41295	Apoptosis inducer
38	51	100.0	47	20	AAV07254	Lactoferrin peptid
39	51	100.0	47	21	AAV56544	Peptide SEQ ID NO:
40	51	100.0	48	20	AAV93883	Bifidobacterium bi
41	51	100.0	49	20	AAV93882	Bifidobacterium bi
42	51	100.0	49	20	AAV93884	Bifidobacterium bi
43	51	100.0	50	16	AAV82027	Human lactoferrin
44	51	100.0	51	21	AAV22817	Human lactoferrin
45	51	100.0	51	21	AAV22822	Lactoferrin 6 kD v

#### ALIGNMENTS

RESULT 1  
AA87905  
ID AA87905 standard; peptide; 16 AA.  
XX AA87905;  
XX  
DT 01-MAR-1996 (first entry)  
XX  
DE Human lactoferrin (25-40).  
XX  
KW antiviral; lactoferrin;  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "optionally this site is acetylated or  
FT preceded by a peptide"  
FT Modified-site 16 /note= "optionally this site may be in amide form  
or followed by a peptide"

JP07069915-A.

14-MAR-1995.

02-SEP-1993; 93JP-0240284.

02-SEP-1993; 93JP-0240284.

(SNOW ) SNOW BRAND MILK PROD CO LTD.

WFI; 1995-144726/19.

XX Inhibitor against viral infection and proliferation - contains  
 PT peptide having sequence from lactoferrin  
 XX  
 PS Claim 1; Page 2; 10pp; Japanese.  
 XX  
 CC The sequence is one of six peptides disclosed as having inhibitory  
 CC effect against viral infection. The peptides are derived from  
 CC lactoferrin. Their activity is demonstrated against cytomegalovirus.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 51; DB 16; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.033;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPPVSCIKR 9  
 DB 8 GPPVSCIKR 16  
 RESULT 2  
 AAY68866  
 ID AAY68866 standard; Peptide; 22 AA.  
 XX  
 AC AAY68866;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of human lactoferrin derived from PRL100.  
 XX  
 KW Human; lactoferrin; mass production; antibacterial.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 2 /note= "encoded by GC"  
 FT Misc-difference 19 /note= "encoded by GC"  
 FT  
 XX WO200004132-A1.  
 PN  
 PD 27-JAN-2000.  
 XX  
 PF 14-JUL-1999; 99WO-KR00373.  
 XX  
 PR 15-JUL-1998; 98KR-0029351.  
 PR 13-JUL-1999; 99KR-0029042.  
 XX  
 PA (SAMY-) SAMYANG GENEX CORP.  
 XX  
 PI Sung CK, Joo IS, Woo MS, Kim SK, Lee JH, Lee KS, Kim YH;  
 PI Hong SS, Lee H;  
 XX  
 XX WPI; 2000-182411/16.  
 DR N-PSDB; AAZ60706.  
 XX  
 PT Lactoferrin polypeptides used as e.g. bactericides or growth promoters,  
 PT are mass produced from genetically engineered micro-organisms -  
 XX  
 PS Example 2; Page 8; 24pp; English.  
 XX  
 CC The present sequence is encoded by a fragment of the lactoferrin gene  
 CC derived from plasmid PRL100. The nucleotide sequence acts as a template  
 CC for PCR. The peptide fragment contains the disulphide cysteine bond.  
 CC The amplified fragment was cloned, and used in the method of the  
 CC invention. The specification describes a method for the mass production  
 CC and culture of lactoferrin polypeptides from micro-organisms. The  
 CC method uses plasmid vectors to transform yeast cells that are resistant  
 CC to lactoferrin polypeptides. As the micro-organism is resistant to the  
 CC antibacterial peptide produced, the number of contaminating organisms  
 CC is reduced whilst maintaining high polypeptide production rates. The

CC micro-organism is useful in the mass production of lactoferrin  
 CC polypeptides. The micro-organism can also be used to produce other  
 CC antibacterial peptides that are difficult to mass produce due to their  
 CC ability to slow down the growth of, or even kill, host cells.  
 XX  
 SQ Sequence 22 AA;  
 Query Match 100.0%; Score 51; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.045;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPPVSCIKR 9  
 DB 14 GPPVSCIKR 22  
 RESULT 3  
 AAY78004  
 ID AAY78004 standard; Peptide; 23 AA.  
 XX  
 AC AAY78004;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:4.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO200001730-A1.  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SB01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 5; Page 57-58; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 23 AA;



PN JP07274970-A.  
 XX 24-OCT-1995.  
 XX 01-APR-1994; 94JP-0085244.  
 XX 01-APR-1994; 94JP-0085244.  
 XX (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1995-399338/51.  
 XX Recombinant vector contg. lactoferrisin gene - used to prepare an  
 PT antibacterial peptide  
 XX Claim 6; Page 11; 18pp; Japanese.  
 XX A recombinant vector in which a DNA sequence encoding at least the  
 CC generic lactoferrisin antibacterial peptide AAR88216 (specific  
 CC examples of which are given in AAR84083-85) is inserted, pref.  
 CC downstream of the vector's regulatory sequence, is claimed. Pref.  
 CC examples of amino acid sequences contg. the above peptide are  
 CC given in AAR8217/18. The regulatory sequence is the tac promoter  
 CC from shuttle vector pGEX2, the GAL1 promoter from vector pKOM2 or  
 CC Rous Sarcoma Virus long terminal repeat from vector pRSVNot.  
 XX  
 XX Sequence 25 AA;  
 SQ  
 Query Match 100.0%; Score 51; DB 16; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPPVSCIKR 9  
 DB 15 GPPVSCIKR 23  
 RESULT 7  
 AAW24267  
 ID AAW24267 standard; peptide; 25 AA.  
 XX AAW24267;  
 XX 15-OCT-1997 (first entry)  
 XX Antifungal peptide #3, derived from lactoferrin.  
 XX Lactoferrin; hydrolysis; antifungal agent; hydrolysate; food;  
 KW azole-type anti-fungal compound; dermatophytosis; dermatomycosis.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 3..20  
 FT  
 XX JP09165342-A.  
 XX 24-JUN-1997.  
 XX 14-DEC-1995; 95JP-0347405.  
 XX 14-DEC-1995; 95JP-0347405.  
 XX (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1997-381279/35.  
 XX Antifungal agents containing azole(s) and lactoferrin hydrolysate -  
 PT for treatment of dermatophytosis and dermatomycosis  
 XX Disulfide-bond 3..20  
 XX JP09165342-A.  
 XX 24-JUN-1997.  
 XX 14-DEC-1995; 95JP-0347405.  
 XX 14-DEC-1995; 95JP-0347405.  
 XX (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1997-381279/35.  
 XX Antifungal agents containing azole(s) and lactoferrin hydrolysate -  
 PT for treatment of dermatophytosis and dermatomycosis  
 XX Claim 4; Page 8; 10pp; Japanese.  
 XX The sequences given in AAW24265-72 are peptides which are derived from

CC lactoferrin by hydrolysis. These peptides may be used in the antifungal  
 CC agents of the invention which also contain as the active component an  
 CC azole-type anti-fungal compound. The antifungal agents are used for  
 CC treatment of dermatophytosis and dermatomycosis. The antifungal agents  
 CC of this invention show the same as or higher effect at one quarter to  
 CC one sixteenth the dose of known antifungal compounds, so the dose of  
 CC these compounds having adverse reactions can be reduced. Lactoferrin  
 CC hydrolysates have no toxicity since they have been used as a part  
 CC of food.  
 XX  
 XX Sequence 25 AA;  
 SQ  
 Query Match 100.0%; Score 51; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPPVSCIKR 9  
 DB 15 GPPVSCIKR 23  
 RESULT 8  
 AAW24268  
 ID AAW24268 standard; peptide; 25 AA.  
 XX AAW24268;  
 XX 15-OCT-1997 (first entry)  
 XX Antifungal peptide #4, derived from lactoferrin.  
 XX Lactoferrin; hydrolysis; antifungal agent; hydrolysate; food;  
 KW azole-type anti-fungal compound; dermatophytosis; dermatomycosis.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 3..20  
 FT  
 XX JP09165342-A.  
 XX 24-JUN-1997.  
 XX 14-DEC-1995; 95JP-0347405.  
 XX 14-DEC-1995; 95JP-0347405.  
 XX (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1997-381279/35.  
 XX Antifungal agents containing azole(s) and lactoferrin hydrolysate -  
 PT for treatment of dermatophytosis and dermatomycosis  
 XX Claim 4; Page 9; 10pp; Japanese.  
 XX The sequences given in AAW24265-72 are peptides which are derived from  
 CC lactoferrin by hydrolysis. These peptides may be used in the antifungal  
 CC agents of the invention which also contain as the active component an  
 CC azole-type anti-fungal compound. The antifungal agents are used for  
 CC treatment of dermatophytosis and dermatomycosis. The antifungal agents  
 CC of this invention show the same as or higher effect at one quarter to  
 CC one sixteenth the dose of known antifungal compounds, so the dose of  
 CC these compounds having adverse reactions can be reduced. Lactoferrin  
 CC hydrolysates have no toxicity since they have been used as a part  
 CC of food.  
 XX  
 XX Sequence 25 AA;  
 SQ  
 Query Match 100.0%; Score 51; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9  
 Db 15 GPPVSCIQR 23

## RESULT 9

AAV07252  
 ID AAV07252 standard; peptide; 25 AA.

XX AC AAV07252;  
 XX 06-JUL-1999 (first entry)

XX Lactoferrin peptide #2.

XX Lactoferrin; hydrolysate; quinolone; bactericidal; antibacterial; drug.  
 XX Unidentified.

XX Key Location/Qualifiers  
 FT Disulfide-bond 3..20 /note= "optional"  
 FT

XX JPI1092375-A.

XX 06-APR-1999.

XX 25-SEP-1997; 97JP-0278113.

XX 25-SEP-1997; 97JP-0278113.

XX (MORG ) MORINAGA MILK IND CO LTD.

XX WPI; 1999-283486/24.

XX New anti-bactericide - for enhancing bactericidal ability of new  
 PT quinolone anti-bactericide

XX Claim 4; Page 7; 10pp; Japanese.

XX This sequence represents a peptide derived from a lactoferrin hydrolysate  
 CC which is used with a novel quinolone bactericidal compound to generate an  
 CC antibacterial composition. Addition of the lactoferrin hydrolysate, or  
 CC peptides from it, can reduce the dosage of quinolone drugs required in  
 CC the composition.

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 51; DB 20; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9  
 Db 15 GPPVSCIQR 23

## RESULT 10

AAV83109  
 ID AAV83109 standard; peptide; 25 AA.

XX AC AAV83109;  
 XX 24-JUL-2000 (first entry)

XX Synthetic lactoferrin fragment.  
 XX Lactoferrin; antimicrobial; cytostatic; infection; tumour;  
 XX sterilisation; wound healing; spermicide; human.

XX Synthetic.  
 OS Homo sapiens.

XX Svendsen JS, Rekaldal O, Sveinbjornsson B, Vorland L;  
 XX

PN WO200012541-A2.

XX 09-MAR-2000.

XX 31-AUG-1999; 99WO-GB02850.

XX 28-AUG-1998; 98GB-0018938.

XX (ALPH-) ALPHARMA AS.  
 XX (GARD/) GARDNER R.

XX Svendsen JS, Rekaldal O, Sveinbjornsson B, Vorland L;  
 XX WPI; 2000-270793/23.

XX Cytotoxic peptides useful as medicament for treating tumors and  
 PT bacterial infections, comprises one or more non-genetic bulky and  
 PT lipophilic amino acids

XX Example 1; Figure 1; 114pp; English.

XX Cytotoxic 7-25 mer lactoferrin peptides which comprise three or more  
 CC cationic residues and have one or more non-genetic bulky and  
 CC lipophilic amino acids have cytostatic and antimicrobial activity.  
 CC The peptides are useful as medicament for treating bacterial  
 CC infections and tumours. They are also useful for sterilising  
 CC agents for materials susceptible to microbial contamination. They may  
 CC also be used as promoters of wound healing and spermicides. The small  
 CC size of the peptides gives them an increased half life and allows  
 CC efficient biodelivery. The peptides can be administered without need  
 CC for an injection, such as by inhalation or by absorption across the  
 CC blood capillaries of the nasal passages. This synthetic lactoferrin  
 CC peptide corresponds to amino acids 18-42 of human lactoferrin.

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 51; DB 21; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9  
 Db 15 GPPVSCIQR 23

## RESULT 11

AAV85010  
 ID AAV85010 standard; peptide; 25 AA.

XX AC AAV85010;  
 XX 20-JUN-2000 (first entry)

XX Human lactoferricin peptide LFH (18-42) amino acid sequence.  
 XX Lactoferrin; lactoferricin; antibacterial; bacterial infection;  
 XX bacterial growth; solid tumour; treatment; human.

XX Homo sapiens.

XX WO200012542-A2.

XX 09-MAR-2000.

XX 31-AUG-1999; 99WO-GB02851.

XX 28-AUG-1998; 98GB-0018938.

XX (ALPH-) ALPHARMA AS.  
 XX (GARD/) GARDNER R.

XX Svendsen JS, Rekaldal O, Sveinbjornsson B, Vorland L;  
 XX



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DR WPI; 2000-256582/22.
XX
XX Modified cytotoxic lactoferrin peptide useful for preparing
PT pharmaceutical composition against bacterial infections and tumours and
PT for inhibiting bacterial growth -
XX
XX Example 1; Fig 1; 112pp; English.
XX
XX This sequence represents a human lactoferricin peptide. Lactoferrin is a
CC weak iron transporter which also shows weak antibacterial effect.
CC Lactoferricin B (LFB) is a peptide produced when bovine lactoferrin is
CC digested with pepsin. LFB is more active than lactoferrin. The two
CC tryptophan residues at positions 6 and 8 in LFB 17-31 cannot be
CC substituted with alanine without loss of antibacterial activity. The
CC invention relates to a modified cytotoxic lactoferrin peptide of 7-25
CC amino acids in length with three cationic residues and one or more extra
CC bulky and lipophilic amino acids, than its native peptide. The invention
CC also relates to the esters, amides, salts and cyclic derivatives of the
CC modified peptide. The modified lactoferrin peptides of the invention are
CC useful for treating bacterial infections and tumours, for preparing
CC medicaments and for inhibiting bacterial growth. LFB and its fragments
CC are useful for manufacturing medicaments for treating solid tumours. The
CC modified peptides have a very small size, which is suitable for
CC biodelivery. Due to the smaller size, the circulating half-life of the
CC peptide is increased as they are less vulnerable to endopeptidases. The
CC observed cytolytic effect of the modified lactoferrin peptides in tumours
CC is not species specific and they have greater utility in treating human
CC tumours.
XX
XX Sequence 25 AA;
SQ
Query Match 100.0%; Score 51; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
DB 15 GPPVSCIKR 23
|||||
|||||

RESULT 12
AAY78002
ID AAY78002 standard; Peptide; 25 AA.
XX
XX AAY78002;
AC
XX
XX 25-APR-2000 (first entry)
DT
XX
XX Human lactoferrin derived peptide SEQ ID NO:2.
DE
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
FN
XX
XX 13-JAN-2000.
PD
XX
XX 06-JUL-1999; 99WO-SE01230.
PF
XX
XX 06-JUL-1998; 98SE-0002441.
PR
XX
XX 17-JUL-1998; 98SE-0002562.
PR
XX
XX 29-DEC-1998; 98SE-0004614.
PR
XX
XX (ASCI-) A+ SCI INVEST AB.
PA
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumours and for use in infant formula food -
XX
XX Claim 4; Page 57; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC

```

CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 25 AA;

Query Match 100.0%; Score 51; DB 21; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.051; 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

QY 1 GPPVSCIKR 9  
 DB 17 GPPVSCIKR 25

#### RESULT 14

AAR87907  
 ID AAR87907 standard; peptide; 28 AA.

XX AAR87907;

DT 01-MAR-1996 (first entry)

XX Human lactoferrin (25-52).

XX antiviral; lactoferrin;

OS Synthetic.

XX Key Location/Qualifiers  
 FH Disulfide-bond 13..22

FT /note= "optionally this bond may be reduced"

XX JP07069915-A.

XX 14-MAR-1995.

XX 02-SEP-1993; 93JP-0240284.

XX 02-SEP-1993; 93JP-0240284.

XX (SNOW ) SNOW BRAND MILK PROD CO LTD.

XX WPI; 1995-144726/19.

XX Inhibitor against viral infection and proliferation - contains  
 PT peptide having sequence from lactoferrin

XX Claim 3; Page 2; 10pp; Japanese.

XX The sequence is one of six peptides disclosed as having inhibitory  
 CC effect against viral infection. The peptides are derived from  
 CC lactoferrin. Their activity is demonstrated against cytomegalovirus.

XX Sequence 28 AA;

Query Match 100.0%; Score 51; DB 16; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9

Db 8 GPPVSCIKR 16

#### RESULT 15

AAV57320  
 ID AAV57320 standard; peptide; 29 AA.

XX AAV57320;

DT 13-JUN-2000 (first entry)

XX Human lactoferrin partial peptide sequence.

XX Lactoferrin; anti-microbial; adhesive; coating material; clothing;  
 KW waste water treatment; leather; fiber; human.

XX Homo sapiens.

XX JP2000045182-A.

XX 15-FEB-2000.

XX 23-JUL-1998; 98JP-0207751.

XX 23-JUL-1998; 98JP-0207751.

XX (PEPU-) PEPUCHIDO SCI YG.

XX (FUJI-) FUJII KAIHATSU KENKYUSHO YG.

XX (MARU-) MARUJU KK.

XX WPI; 2000-306598/27.

XX Antimicrobial fiber for bandage, gauze, sheet and fiber goods comprises  
 PT anti-microbial component fixed to fiber by water soluble resin -

XX Disclosure; Page 4; 10pp; Japanese.

XX The invention provides water soluble resin-based fixing agent which  
 CC dissociates the anionic polymer component in water, fixes cationic anti-  
 CC microbial component into a fiber to form anti-microbial fiber. Cow or  
 CC human lactoferrin peptides may be used as the anti-microbial component  
 CC in the anti-microbial fiber of the invention. The agent is useful as  
 CC adhesive, coating material, waste water treatment and in fixing  
 CC antimicrobial component to a fiber to form antimicrobial fiber useful as  
 CC a bandage, gauze, sheet, clothing others or leathers, and fiber goods.  
 CC The antimicrobial activity is measured against E. coli, S. aureus,  
 CC methicillin-resistant S. aureus and P. aeruginosa. The antimicrobial  
 CC fiber formed has excellent antimicrobial activity and wash durability.  
 CC The leather used has excellent antimicrobial processing agent. Fixing of  
 CC lactoferrin to the fiber is reliable. The present sequence represents a  
 CC human lactoferrin partial peptide fragment.

SQ Sequence 29 AA;

Query Match 100.0%; Score 51; DB 21; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 0.059; 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

QY 1 GPPVSCIKR 9

DB 21 GPPVSCIKR 29

Search completed: February 21, 2003, 07:56:46  
 Job time : 22.0698 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:50:40 ; Search time 6.69767 Seconds  
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39.537 Million cell updates/sec

Title: US-09-743-107B-101  
Perfect score: 51  
Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	22	4	US-09-508-734-4
2	51	100.0	25	1	US-07-755-161A-10
3	51	100.0	25	1	US-07-891-174-10
4	51	100.0	25	1	US-08-204-487-7
5	51	100.0	29	4	US-09-508-734-8
6	51	100.0	36	1	US-07-755-161A-8
7	51	100.0	36	1	US-07-891-174-8
8	51	100.0	36	1	US-08-356-771-30
9	51	100.0	36	1	US-08-381-984-29
10	51	100.0	47	2	US-08-464-182A-6
11	51	100.0	47	2	US-08-406-271-6
12	51	100.0	50	2	US-08-693-274A-7
13	51	100.0	54	2	US-08-464-182A-2
14	51	100.0	54	2	US-08-406-271-2
15	51	100.0	694	3	US-08-724-586-2
16	51	100.0	694	4	US-09-421-632-2
17	51	100.0	694	4	US-09-332-190-2
18	51	100.0	705	2	US-08-655-640-2
19	51	100.0	708	2	US-08-655-640-4
20	51	100.0	709	1	US-08-154-019-2
21	51	100.0	709	1	US-08-461-333-2
22	51	100.0	709	3	US-08-464-167-2
23	51	100.0	709	3	US-09-158-313-2
24	51	100.0	709	4	US-08-476-798-2
25	51	100.0	711	1	US-08-145-681-2
26	51	100.0	711	1	US-08-250-308-2
27	51	100.0	711	1	US-08-154-019-4

28	51	100.0	711	1	US-08-461-333-4	Sequence 4, Appli
29	51	100.0	711	1	US-08-453-703-2	Sequence 2, Appli
30	51	100.0	711	1	US-08-456-106-2	Sequence 2, Appli
31	51	100.0	711	3	US-08-484-167-4	Sequence 4, Appli
32	51	100.0	711	3	US-09-158-313-4	Sequence 4, Appli
33	51	100.0	711	3	US-08-456-108-2	Sequence 2, Appli
34	51	100.0	711	4	US-08-476-798-4	Sequence 4, Appli
35	51	100.0	711	4	US-09-265-577-2	Sequence 2, Appli
36	51	100.0	711	5	PCT-US93-03614-3	Sequence 2, Appli
37	49	96.1	52	4	US-09-017-043A-3	Sequence 3, Appli
38	49	96.1	53	2	US-08-454-182A-5	Sequence 5, Appli
39	49	96.1	53	2	US-08-406-271-5	Sequence 5, Appli
40	45	88.2	24	4	US-09-508-734-6	Sequence 6, Appli
41	44	86.3	48	2	US-08-693-274A-10	Sequence 10, Appli
42	44	86.3	50	4	US-09-017-043A-5	Sequence 5, Appli
43	44	86.3	52	2	US-08-464-182A-17	Sequence 17, Appli
44	44	86.3	52	2	US-08-406-271-17	Sequence 17, Appli
45	41	80.4	20	1	US-07-755-161A-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-508-734-4  
; Sequence 4, Application US/09508734  
; Patent No. 6423509  
; GENERAL INFORMATION:  
; APPLICANT: Samyang Genex Corporation  
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
; FILE REFERENCE: PA/SYG/00139  
; CURRENT APPLICATION NUMBER: US/09/508,734  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: PCT/KR99/00373  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: KR1998-29351  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-508-734-4

Query Match 100.0%; Score 51; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9

DB 14 GPPVSCIKR 22

## RESULT 2

US-07-755-161A-10  
; Sequence 10, Application US/07755161A  
; Patent No. 5304633  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,161A  
FILING DATE: 19910905  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 4  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 21"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 21  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 4"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 100.0%; Score 51; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPPVSCIKR 9  
DB 16 GPPVSCIKR 24  
RESULT 3  
US-07-891-174-10  
; Sequence 10, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:

NAME/KEY: modified site  
LOCATION: 4  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 21"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 21  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 4"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-10

Query Match 100.0%; Score 51; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 16 GPPVSCIQR 24

RESULT 4  
US-08-204-487-7

Sequence 7, Application US/08204487  
Patent No. 5565425  
GENERAL INFORMATION:  
APPLICANT: YAMAMOTO, NAOKI  
APPLICANT: NAKASHIMA, HIDEKI  
APPLICANT: MOSUCHI, WATARU  
APPLICANT: TANAKA, SHIGEKI  
APPLICANT: DOSAKO, SHUN-ICHI  
APPLICANT: KAWASAKI, YOSHIHIRO  
APPLICANT: UCHIDA, TOSHIKI  
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
ADDRESSEE: THIBEAULT  
STREET: 53 STATE STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,487  
FILING DATE: 02-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, PAULA A.  
REGISTRATION NUMBER: 32,503  
REFERENCE/DOCKET NUMBER: FUN-019  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..25  
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE  
OTHER INFORMATION: (18-48)"  
US-08-204-487-7

Query Match 100.0%; Score 51; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 15 GPPVSCIQR 23

RESULT 5

US-09-508-734-8  
Sequence 8, Application US/09508734  
Patent No. 6423509  
GENERAL INFORMATION:  
APPLICANT: Samyang Genex Corporation  
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
FILE REFERENCE: PA/SYG/00139  
CURRENT APPLICATION NUMBER: US/09/508,734  
CURRENT FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: PCT/KR99/00373  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: KR1998-29351  
PRIOR FILING DATE: 1998-07-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Kopatentin 1.71  
SEQ ID NO 8  
LENGTH: 29  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-508-734-8

Query Match 100.0%; Score 51; DB 4; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 20 GPPVSCIQR 28

RESULT 6

US-07-755-161A-8  
Sequence 8, Application US/07755161A  
Patent No. 5304633  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptides and an  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,161A  
FILING DATE: 19910905  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL LINE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 9  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 9 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 26"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 26  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 26 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 9"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 35  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 35 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 10 of SEQ ID NO. 9"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:

ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-755-161A-8  
Query Match 100.0%; Score 51; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred.No. 0.017;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 1 GPPVSCIKR 9  
Db 21 GPPVSCIKR 29  
RESULT 7  
US-07-891-174-8  
Sequence 8, Application US/07891174  
Patent No. 5317084  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptides and an  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/891,174  
FILING DATE: 29-MAY-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/755,161  
FILING DATE: 05-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:

ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 9  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 9 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 26"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 26  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 26 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 9"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 35  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 35 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 10 of SEQ ID NO. 9"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-8

Query Match 100.0%; Score 51; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
Db 21 GPPVSCIKR 29

RESULT 8  
US-08-256-771-30  
Sequence 30, Application US/08256771  
Patent No. 5656591  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues at positions 9 and  
OTHER INFORMATION: 26 are linked by disulfide bond, and Cys residue at position 1;  
OTHER INFORMATION: by disulfide bond to Cys residue at position 10 of SEQ ID NO.  
US-08-256-771-30

Query Match 100.0%; Score 51; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
Db 21 GPPVSCIKR 29

RESULT 9  
US-08-381-984-29  
Sequence 29, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850

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; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 9
; OTHER INFORMATION: and 26 are linked by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at position 35
; OTHER INFORMATION: is linked by disulfide linkage with the cysteine residue at P
; OTHER INFORMATION: SEQ ID NO. 5804555 32"
; US-08-381-984-29
;
; Query Match 100.0%; Score 51; DB 1; Length 36;
; Best Local Similarity 100.0%; Pred. No. 0.017;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GPPVSCIKR 9
; Db 21 GPPVSCIKR 29
;
; RESULT 10
; US-08-464-182A-6
; Sequence 6, Application US/08464182A
; Patent No. 5849885
; GENERAL INFORMATION:
; APPLICANT: Nuijens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,182A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,271
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

```

```

; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-004920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..47
; OTHER INFORMATION: /note= "Lactoferricin H"
; US-08-464-182A-6
;
; Query Match 100.0%; Score 51; DB 2; Length 47;
; Best Local Similarity 100.0%; Pred. No. 0.021;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GPPVSCIKR 9
; Db 32 GPPVSCIKR 40
;
; RESULT 11
; US-08-406-271-6
; Sequence 6, Application US/08406271
; Patent No. 5919913
; GENERAL INFORMATION:
; APPLICANT: Nuyens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,271
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-004910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..47

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OTHER INFORMATION: /note= "Lactoferricin H"

US-08-406-271-6

Query Match 100.0%; Score 51; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 32 GPPVSCIQR 40

## RESULT 12

US-08-693-274A-7

; Sequence 7, Application US/08693274A  
; Patent No. 5861491  
; GENERAL INFORMATION:  
; APPLICANT: Nuijens, Jan H.  
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/693,274A  
; FILING DATE: 16-OCT-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/464,182  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,271  
; FILING DATE: 09-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/00583  
; FILING DATE: 16-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/198,321  
; FILING DATE: 16-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 016994-0049300S  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..50  
; OTHER INFORMATION: /note= "HLP cDNA GPE N-terminus"

US-08-693-274A-7

Query Match 100.0%; Score 51; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 32 GPPVSCIQR 40

Qy 1 GPPVSCIQR 9  
Db 32 GPPVSCIQR 40

## RESULT 13

US-08-464-182A-2

; Sequence 2, Application US/08464182A  
; Patent No. 5849885  
; GENERAL INFORMATION:  
; APPLICANT: Nuijens, Jan H.  
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,182A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,271  
; FILING DATE: 09-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/198,321  
; FILING DATE: 16-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 016994-0049200S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 326-2400  
; TELEFAX: (650) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..54  
; OTHER INFORMATION: /note= "HLP cDNA of GPE"

US-08-464-182A-2

Query Match 100.0%; Score 51; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 32 GPPVSCIQR 40

## RESULT 14

US-08-406-271-2

; Sequence 2, Application US/08406271  
; Patent No. 5919913  
; GENERAL INFORMATION:  
; APPLICANT: Nuyens, Jan H.  
; APPLICANT: Van Veen, Harry H.

Qy 1 GPPVSCIQR 9  
Db 32 GPPVSCIQR 40

;; TITLE OF INVENTION: Isolation of Lactoferrin from Milk  
;; NUMBER OF SEQUENCES: 28  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
;; STREET: One Market Plaza, Steuart Street Tower, 20th  
;; CITY: San Francisco  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94105  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/406,271  
;; FILING DATE: 09-MAR-1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/198,321  
;; FILING DATE: 16-FEB-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 016994-004910  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 326-2400  
;; TELEFAX: (415) 326-2422  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 54 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..54  
;; OTHER INFORMATION: /note= "HLF cdna of GPE"  
US-08-406-271-2

Query Match 100.0%; Score 51; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9  
|||  
Db 32 GPPVSCIQR 40

RESULT 15  
US-08-724-586-2  
;; Sequence 2, Application US/08724586  
;; Patent No. 6066469  
;; GENERAL INFORMATION:  
;; APPLICANT: Kruzel, Marian L.  
;; APPLICANT: Kurecki, Tomasz  
;; APPLICANT: Gollnick, Paul D.  
;; APPLICANT: Doyle, Darrell J.  
;; TITLE OF INVENTION: Cloning, Expression, and Uses of Human  
;; NUMBER OF SEQUENCES: 8  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jacobson, Price, Holman & Stern  
;; STREET: 400 Seventh St. N.W.  
;; CITY: Washington D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20004  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/724,586  
;; FILING DATE: 30-SEPT-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/238,445  
;; FILING DATE: 05-MAY-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Player, William E.  
;; REGISTRATION NUMBER: 31,409  
;; REFERENCE/DOCKET NUMBER: 10505/P58185C  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 638-6666  
;; TELEFAX: (202) 393-5350  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 694 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-724-586-2

Query Match 100.0%; Score 51; DB 3; Length 694;  
Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9  
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Db 34 GPPVSCIQR 42

Search completed: February 21, 2003, 08:04:28  
Job time : 6.69767 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 08:08:15 ; Search time 5.16279 Seconds  
(without alignments)  
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Title: US-09-743-107B-101

Perfect score: 51

Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	25	9	US-09-798-869-20
2	51	100.0	694	9	US-10-023-096-2
3	44	86.3	25	9	US-09-798-869-22
4	39	76.5	191	9	US-09-989-442-145
5	39	76.5	1924	9	US-09-866-557A-2
6	36	70.6	64	10	US-09-917-340-87
7	36	70.6	64	10	US-09-917-340-88
8	36	70.6	164	9	US-09-854-133-203
9	36	70.6	164	10	US-09-738-973-203
10	35	68.6	162	10	US-09-977-034-24
11	35	68.6	240	10	US-09-925-297-810
12	34	66.7	156	10	US-09-764-870-402
13	33	64.7	33	10	US-09-864-761-45683
14	33	64.7	64	10	US-09-917-340-85
15	33	64.7	75	10	US-09-764-878-165
16	33	64.7	179	9	US-09-924-340-36
17	33	64.7	179	9	US-09-992-600A-36
18	33	64.7	197	9	US-09-905-558C-2
19	33	64.7	231	10	US-09-925-302-474

20	64.7	234	9	US-09-941-831-23	Sequence 23, Appl
21	64.7	234	10	US-09-764-877-1775	Sequence 1775, Ap
22	64.7	26926	9	US-09-759-508B-2	Sequence 2, Appli
23	62.7	143	10	US-09-864-761-37379	Sequence 37379, A
24	61	51	10	US-09-864-761-44156	Sequence 44156, A
25	61	65	10	US-09-864-761-35016	Sequence 35016, A
26	61	90	10	US-09-925-300-1777	Sequence 1777, Ap
27	61	121	9	US-09-974-879-143	Sequence 143, App
28	61	138	9	US-09-738-626-3842	Sequence 3842, Ap
29	61	144	10	US-09-864-761-37049	Sequence 37049, A
30	61	240	10	US-09-864-761-47947	Sequence 47947, A
31	61	278	10	US-09-925-301-1245	Sequence 1245, Ap
32	61	381	9	US-09-808-602-6	Sequence 6, Appli
33	61	381	9	US-09-977-418-22	Sequence 22, Appl
34	61	2724	9	US-09-808-602-13	Sequence 13, Appl
35	61	2733	9	US-09-808-602-8	Sequence 8, Appli
36	61	2764	9	US-09-808-602-80	Sequence 80, Appl
37	61	2765	9	US-09-808-602-84	Sequence 84, Appl
38	61	2802	9	US-09-808-602-81	Sequence 81, Appl
39	61	4861	10	US-09-919-497-70	Sequence 70, Appl
40	58.8	35	10	US-09-864-761-44144	Sequence 44144, A
41	58.8	42	10	US-09-917-340-64	Sequence 64, Appl
42	58.8	50	10	US-09-764-869-985	Sequence 985, App
43	58.8	51	10	US-09-864-761-44562	Sequence 44562, A
44	58.8	53	10	US-09-864-761-48454	Sequence 48454, A
45	58.8	108	9	US-09-789-145-6	Sequence 6, Appli

#### ALIGNMENTS

RESULT 1  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (VSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798.869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-798-869-20

Query Match 100.0%; Score 51; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
DB 15 GPPVSCIKR 23

RESULT 2  
US-10-023-096-2  
; Sequence 2, Application US/10023096  
; Patent No. US20020160941A1  
; GENERAL INFORMATION:  
; APPLICANT: Kruzel, Marian L.  
; APPLICANT: Kurecki, Tomasz  
; APPLICANT: Gollnick, Paul D.

APPLICANT: Doyle, Darrell J.  
TITLE OF INVENTION: Cloning, Expression, and Uses of Human  
Lactoferrin  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/023,096  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,586  
FILING DATE: 30-SEPT-1996  
APPLICATION NUMBER: US 08/238,445  
FILING DATE: 05-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10505/P58185C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 694 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-023-096-2

Query Match 100.0%; Score 51; DB 9; Length 694;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 34 GPPVSCIQR 42

RESULT 3  
US-09-798-869-22  
Sequence 22, Application US/09798869  
Publication No. US20030022821A1  
GENERAL INFORMATION:  
APPLICANT: JOHN SIGURD SVENDSEN  
APPLICANT: (YSTEIN REKDAL  
APPLICANT: BALDUR SVEINBJ RNSSON  
APPLICANT: LARS VORLAND  
TITLE OF INVENTION: BIOACTIVE PEPTIDES  
CURRENT APPLICATION NUMBER: US/09/798,869  
CURRENT FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: PCT/GB99/02851  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: GB9818938.4  
PRIOR FILING DATE: 1998-08-28  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 25  
TYPE: PRT  
ORGANISM: MURINE  
US-09-798-869-22

Query Match 86.3%; Score 44; DB 9; Length 25;  
Best Local Similarity 66.7%; Pred. No. 0.12;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCIQR 9  
Db 15 GPPVSCIQR 23

RESULT 4  
US-09-389-442-145  
Sequence 145, Application US/09989442  
Publication No. US20030013649A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PZ08  
CURRENT APPLICATION NUMBER: US/09/989,442  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,447  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/218,290  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/216,647  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,267  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/216,880  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,270  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/251,869  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/235,834  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/234,274  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/234,223  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/228,924  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/224,518  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,369  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/224,519  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,964  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/241,809  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/249,299  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/236,327  
PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/241,785  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/251,856  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/251,868  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/229,344  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/234,997  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: 60/229,343  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,345  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135

PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,244  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,217  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,211  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,215  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,264  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,214  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,297  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/232,400  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/231,242  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,081  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,080  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,414  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,244  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,064  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/233,063  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,397  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,399  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,401  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/241,808  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,826  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,786  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,221  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,475  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/231,243  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,065  
PRIOR FILING DATE: 2000-09-14

Query Match 76.5%; Score 39; DB 9; Length 191;  
Best Local Similarity 85.7%; Pred. No. 7.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSCI 7

Db 180 GPPVSCL 186

RESULT 5  
US-09-866-557A-2  
; Sequence 2, Application US/09866557A  
; Patent No. US20020162126A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, S.  
; APPLICANT: Hannon, G.  
; APPLICANT: Beach, D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE  
; FILE REFERENCE: GNCRA-P02-007  
; CURRENT APPLICATION NUMBER: US/09/866,557A  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 60/189,739  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/243,097  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 1924  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-557A-2

Query Match 76.5%; Score 39; DB 9; Length 1924;  
Best Local Similarity 62.5%; Pred. No. 74;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 8  
DB 683 GPPMNSVCR 690

RESULT 6  
US-09-917-340-87  
; Sequence 87, Application US/09917340  
; Patent No. US20020090369A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Christopher J.  
; APPLICANT: McAnulty, Jonathan F.  
; APPLICANT: Reid, Ted W.  
; TITLE OF INVENTION: Transplant Media  
; FILE REFERENCE: TPLANT-06468  
; CURRENT APPLICATION NUMBER: US/09/917,340  
; CURRENT FILING DATE: 2001-07-29  
; PRIOR APPLICATION NUMBER: 60/221,632  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/249,602  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/290,932  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Capra hircus  
US-09-917-340-87

Query Match 70.6%; Score 36; DB 10; Length 64;  
Best Local Similarity 55.6%; Pred. No. 8;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
DB 55 GPPVKCCRK 63

RESULT 7  
US-09-917-340-88  
; Sequence 88, Application US/09917340

; Patent No. US20020090369A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Christopher J.  
; APPLICANT: McAnulty, Jonathan F.  
; APPLICANT: Reid, Ted W.  
; TITLE OF INVENTION: Transplant Media  
; FILE REFERENCE: TPLANT-06468  
; CURRENT APPLICATION NUMBER: US/09/917,340  
; CURRENT FILING DATE: 2001-07-29  
; PRIOR APPLICATION NUMBER: 60/221,632  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/249,602  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/290,932  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Capra hircus  
US-09-917-340-88

Query Match 70.6%; Score 36; DB 10; Length 64;  
Best Local Similarity 55.6%; Pred. No. 8;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
DB 55 GPPVKCCRK 63

RESULT 8  
US-09-854-133-203  
; Sequence 203, Application US/09854133  
; Publication No. US20020183499A1  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Raedon  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.475C10  
; CURRENT APPLICATION NUMBER: US/09/854,133  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 735  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 203  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-854-133-203

Query Match 70.6%; Score 36; DB 9; Length 164;  
Best Local Similarity 55.6%; Pred. No. 21;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
DB 53 GPSVACVKK 61

RESULT 9  
US-09-738-973-203  
; Sequence 203, Application US/09738973  
; Patent No. US20020110563A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Fling, Steven P.

; APPLICANT: Mohamath, Raodoh  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Secrist, Heather  
 ; APPLICANT: Indrias, Carol Yoseph  
 ; APPLICANT: Benson, Darin R.  
 ; APPLICANT: Elliot, Mark  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Kalos, Michael D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
 ; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.475C9  
 ; CURRENT APPLICATION NUMBER: US/09/738,973  
 ; CURRENT FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 587  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 203  
 ; LENGTH: 164  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-738-973-203

Query Match 70.6%; Score 36; DB 10; Length 164;  
 Best Local Similarity 55.6%; Pred. No. 21;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
 |||||  
 Db 53 GPSVACVKK 61

RESULT 10  
 US-09-977-034-24  
 ; Sequence 24, Application US/09977034  
 ; Patent No. US20020081664A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lo, Kin-Ming  
 ; APPLICANT: Sun, Yaping  
 ; APPLICANT: Gallies, Stephen D.  
 ; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
 ; TITLE OF INVENTION: FC Fusion Proteins  
 ; FILE REFERENCE: LEX-009  
 ; CURRENT APPLICATION NUMBER: US/09/977,034  
 ; CURRENT FILING DATE: 2001-10-11  
 ; PRIOR APPLICATION NUMBER: US/09/575,503  
 ; PRIOR FILING DATE: 2000-05-19  
 ; PRIOR APPLICATION NUMBER: US 60/134,895  
 ; PRIOR FILING DATE: 1999-05-19  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 24  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; OTHER INFORMATION: Mouse IFN alpha-4 protein  
 ; US-09-977-034-24

Query Match 68.6%; Score 35; DB 10; Length 162;  
 Best Local Similarity 71.4%; Pred. No. 31;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPSVCLK 8  
 |||||  
 Db 25 PPLSCLK 31

RESULT 11  
 US-09-925-297-810  
 ; Sequence 810, Application US/09925297  
 ; Patent No. US20020081659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA105  
 ; CURRENT APPLICATION NUMBER: US/09/925,297  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05989  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 928  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 810  
 ; LENGTH: 240  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (9)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (77)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (195)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-09-925-297-810

Query Match 68.6%; Score 35; DB 10; Length 240;  
 Best Local Similarity 66.7%; Pred. No. 45;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
 |||||  
 Db 83 GPPVLCPRR 91

RESULT 12  
 US-09-764-870-402  
 ; Sequence 402, Application US/09764870  
 ; Patent No. US20020042386A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: P1214  
 ; CURRENT APPLICATION NUMBER: US/09/764,870  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 646  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 402  
 ; LENGTH: 156  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-764-870-402

Query Match 66.7%; Score 34; DB 10; Length 156;  
 Best Local Similarity 83.3%; Pred. No. 44;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSC 6  
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 Db 10 GPPVAC 15

RESULT 13  
 US-09-864-761-45683  
 ; Sequence 45683, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Weisheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45683
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC015772.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
; OTHER INFORMATION: EST HUMAN HIT: AW003063.1, EVALUATE 3.00e-10
; OTHER INFORMATION: SWISSPROT HIT: P10286, EVALUATE 8.60e-02
US-09-864-761-45683

Query Match 64.7%; Score 33; DB 10; Length 33;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSC 6
| | | | |
DB 24 GPPVQC 29

RESULT 14
US-09-917-340-85
; Sequence 85, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.

; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45683
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC015772.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
; OTHER INFORMATION: EST HUMAN HIT: AW003063.1, EVALUATE 3.00e-10
; OTHER INFORMATION: SWISSPROT HIT: P10286, EVALUATE 8.60e-02
US-09-864-761-45683

Query Match 64.7%; Score 33; DB 10; Length 33;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSC 6
| | | | |
DB 24 GPPVQC 29

RESULT 14
US-09-917-340-85
; Sequence 85, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.

; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TELANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-85

Query Match 64.7%; Score 33; DB 10; Length 64;
Best Local Similarity 82.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIK 8
| | | | |
DB 26 GDPVTCIK 33

RESULT 15
US-09-764-878-165
; Sequence 165, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 165
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-878-165

Query Match 64.7%; Score 33; DB 10; Length 79;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIKR 9
| | | | |
DB 32 PPVSCCKK 39

Search completed: February 21, 2003, 08:11:59
Job time : 6.16279 secs
```



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01 ; Search time 7.95349 Seconds  
(without alignments)  
108.784 Million cell updates/sec

Title: US-09-743-107b-101

Perfect score: 51

Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73.\*

1: pirl.\*

2: pirl.\*

3: pirl.\*

4: pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	711	1 TFHUL	lactotransferrin p
2	44	86.3	707	1 A28438	lactoferrin precu
3	41	80.4	704	2 I47228	carbonic anhydrase
4	37	72.5	636	1 S01384	transferrin - pig
5	36	70.6	155	1 KRCHS	keratin, scale - c
6	36	70.6	170	2 AB2715	conserved hypotet
7	36	70.6	189	2 F97496	hypothetical prote
8	36	70.6	698	1 TFHUP	transferrin precu
9	35	70.6	723	2 T32136	hypothetical prote
10	35	68.6	186	1 IVMS24	interferon alpha-1
11	35	68.6	282	2 A71675	4-hydroxybenzoate
12	35	68.6	310	2 T31799	hypothetical prote
13	35	68.6	316	1 A38743	loricrin - human
14	35	68.6	450	2 D86356	hypothetical prote
15	35	68.6	479	2 F86356	T16E15.2 protein -
16	35	68.6	481	2 C86356	hypothetical prote
17	35	68.6	487	2 C86356	UDP-glucose glucos
18	35	68.6	489	2 H86356	probable UDP-gluc
19	35	68.6	1402	2 I46707	translation initia
20	34	66.7	121	2 AE3598	transposase BME110
21	34	66.7	470	2 A87508	hypothetical prote
22	34	66.7	1752	2 A45407	collagen alpha 3(I
23	34	66.7	3898	1 GNWVHB	genome polyprotein
24	33	64.7	64	2 A47438	airway epithelial
25	33	64.7	185	2 D82418	Mutfr/nudix family
26	33	64.7	185	2 T51003	hypothetical prote
27	33	64.7	187	2 A71328	probable survival
28	33	64.7	219	1 A37243	hemopoietic cell s
29	33	64.7	291	2 A81696	stationary-phase s

#### RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N.Alternate names: lactoferrin

C.Species: Homo sapiens (man)

C.Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C.Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R.Cho, Y.

submitted to the EMBL Data Library, March 1994

A.Reference number: G06820

A.Accession: G01394

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: mRNA

A.Residues: 1-711 <CHO>

A.Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R.Rev. M.W.; Moloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A>Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A.Reference number: S11228; MUID:90384839; PMID:2402455

A.Accession: S11228

A.Molecule type: mRNA

A.Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A.Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R.Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A>Title: Differential molecular mechanism of the estrogen action that regulates lactoferi

A.Reference number: A45401; MUID:93125571; PMID:1480183

A.Accession: A45401

A.Molecule type: DNA

A.Residues: 1-15 <TEN>

A.Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A.Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIP:122202)

R.Powell, M.J.; Ogdien, J.E.

Nucleic Acids Res. 18, 4013, 1990

A>Title: Nucleotide sequence of human lactoferrin cDNA.

A.Reference number: S10324; MUID:90326549; PMID:2374734

A.Accession: S10324

A.Molecule type: mRNA

A.Residues: 3-711 <POM>

A.Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R.Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A.Reference number: S15853; MUID:91264786; PMID:2049066

A.Accession: S15853

A.Status: nucleic acid sequence not shown; not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 20-31 <ST1>

A.Accession: S20841

A.Molecule type: protein

A.Residues: 20-26, 'X', 30-31 <ST2>

probable acid phos  
sugar-binding tran  
scription regu  
conserved hypotet  
heat shock transcr  
probable PurA - My  
polygalacturonase-  
DNA photolysase hom  
DNA helicase - Aqu  
protein P20B24.8 [  
hypothetical prote  
E-cadherin precurs  
diacylglycerol kin  
protein-tyrosine k  
DNA-directed RNA p  
titin, cardiac mus

#### ALIGNMENTS

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70, 989-993, 1987  
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A;Reference number: S07160; MUID:88001031; PMID:3477300  
 A;Accession: S07160  
 A;Molecule type: mRNA  
 A;Residues: 436-487, 'A', 489-711 <RAD>  
 A;Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA8665.1; PID:g386855  
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51, 3037-3043, 1991  
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A;Reference number: A61169; MUID:91235214; PMID:1674448  
 A;Accession: A61169  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 3-701, 'SWKPVN' <PAN>  
 A;Experimental source: normal breast tissue  
 R;Vet-Boutique, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984  
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other  
 A;Reference number: A31000; MUID:85076667; PMID:6510420  
 A;Accession: A31000  
 A;Molecule type: protein  
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-400  
 A;Note: this is the final paper in a series  
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norrskov, L.  
 Eur. J. Biochem. 241, 303-308, 1996  
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity chromatography  
 A;Reference number: S74119; MUID:97054624; PMID:8898921  
 A;Accession: S74119  
 A;Molecule type: protein  
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A;Experimental source: neutrophil granulocytes  
 C;Genetics:  
 A;Gene: GDB:LTF  
 A;Cross-references: GDB:119368; OMIM:150210  
 A;Map position: 3q21-3q23  
 C;Superfamily: transferrin; transferrin repeat homology  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-711/Product: lactotransferrin #status experimental <MAT>  
 F;21-356/Domain: transferrin repeat homology <TRH1>  
 F;360-699/Domain: transferrin repeat homology <TRH2>  
 F;29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status experimental  
 F;157, 498/Binding site: carbohydrate (asn) (covalent) #status experimental  
 F;368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #status experimental

Query Match 100.0%; Score 51; DB 1; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
 Db 51 GPPVSCIKR 59

RESULT 2  
 A28438  
 N;Alternate names: lactotransferrin  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A28438; A41205  
 R;Pentecost, B.T.; Teng, C.T.  
 J. Biol. Chem. 262, 10134-10139, 1987  
 A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretory gland  
 A;Reference number: A92596; MUID:87280033; PMID:3611056  
 A;Accession: A28438  
 A;Molecule type: mRNA  
 A;Residues: 3-707 <PEN>  
 A;Cross-references: EMBL:J03298  
 R;Lin, Y.; Teng, C.T.  
 J. Biol. Chem. 266, 21880-21885, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.  
 A;Reference number: A41205; MUID:92042099; PMID:1939212  
 A;Accession: A41205  
 A;Molecule type: DNA  
 A;Residues: 1-15 <LTU>  
 A;Cross-references: GB:M74778  
 C;Superfamily: transferrin; transferrin repeat homology  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-707/Product: lactotransferrin #status predicted <MAT>  
 F;358-695/Domain: transferrin repeat homology <TRH2>  
 F;494/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 86.3%; Score 44; DB 1; Length 707;  
 Best Local Similarity 66.7%; Pred. No. 3.1;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
 Db 49 GPPVSCIKR 57

RESULT 3  
 I47228  
 carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999  
 C;Accession: I47228  
 R;Roush, E.D.; Fierke, C.A.  
 Biochemistry 31, 12536-12542, 1992  
 A;Title: Purification and characterization of a carbonic anhydrase II inhibitor from porcine  
 A;Reference number: I47228; MUID:93099129; PMID:1463741  
 A;Accession: I47228  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-704 <ROU>  
 A;Cross-references: EMBL:U36916; NID:g1016329; PIDN:AAB58956.1; PID:g1016330  
 C;Genetics:  
 A;Gene: PICA  
 C;Superfamily: transferrin; transferrin repeat homology  
 F;20-350/Domain: transferrin repeat homology <TRH1>

Query Match 80.4%; Score 41; DB 2; Length 704;  
 Best Local Similarity 77.8%; Pred. No. 11;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
 Db 53 GPPVSCIKR 61

RESULT 4  
 S01384  
 transferrin - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 11-May-2000  
 C;Accession: S01384; A60520; A61573  
 R;Baldwin, G.S.; Weinstock, J.  
 Nucleic Acids Res. 16, 8720, 1988  
 A;Title: Nucleotide sequence of porcine liver transferrin.  
 A;Reference number: S01384; MUID:88335629; PMID:3419934  
 A;Accession: S01384  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-696 <BAL>  
 A;Cross-references: EMBL:X12386; NID:g2126; PIDN:CAA30943.1; PID:g833800  
 A;Note: 308-Arg was also found  
 R;Baldwin, G.S.; Bacic, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Tch, I  
 Comp. Biochem. Physiol. B 95, 261-268, 1990  
 A;Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine  
 A;Reference number: A60520; MUID:90227903; PMID:2328566  
 A;Accession: A60520

A/Molecule type: protein  
 A/Residues: 1-8,'X',10-11,'X',13-15 <BA2>  
 A/Experimental source: gastric mucosa  
 A/Note: the authors suggest transferrin from gastric mucosa may act in dietary iron uptake  
 R/Chung, W.C.M.; Chan, S.L.; Shimizu, S.  
 Int. J. Biochem. 23, 609-616, 1991  
 A/Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.  
 A/Reference number: A61573; MUID:91293379; PMID:2065820  
 A/Accession: A61573

A/Molecule type: protein  
 A/Residues: 1-8,'X',10-18,'XE' <CHU>  
 C/Superfamily: transferrin; transferrin repeat homology  
 C/Keywords: duplication; glycoprotein; iron transport; plasma  
 F/1-696/Product: transferrin status predicted <NAT>  
 F/1-335/Domain: transferrin repeat homology <TRH1>

Query Match 72.5%; Score 37; DB 1; Length 696;  
 Best Local Similarity 66.7%; Pred. No. 59;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
 |||||:  
 Db 33 GPLVSCVKQ 41

## RESULT 5

KRCHS  
 N/Alternate names: chicken keratin, scale - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 22-Jun-1999  
 C/Accession: A02851; B60136; I50168  
 R/Gregg, K.; Wilton, S.D.; Parry, D.A.D.; Rogers, G.E.  
 EMBO J. 3, 175-178, 1984  
 A/Title: A comparison of genomic coding sequences for feather and scale keratins: structure  
 A/Reference number: A90988; MUID:84158528; PMID:6200321

A/Molecule type: DNA  
 A/Residues: 1-155 <GRE>  
 A/Cross-references: GB:X00315; NID:963548; PIDN:CAA25084.1; PID:G63549  
 R/Wilton, S.D.; Crocker, L.A.; Rogers, G.E.  
 Biochim. Biophys. Acta 824, 201-208, 1985  
 A/Title: Isolation and characterization of keratin mRNA from the scale epidermis of the  
 A/Reference number: A60136; MUID:85122780; PMID:2578818  
 A/Accession: B60136  
 A/Molecule type: mRNA  
 A/Residues: 90-155 <WIL>  
 A/Cross-references: GB:M25642; NID:G212231; PIDN:AAA48931.1; PID:G212232  
 A/Note: this mRNA was designated clone CSK12. See entry A60136 for clone CSK9  
 R/Sawyer, R.H.; Shames, R.B.  
 Curr. Top. Dev. Biol. 22, 235-253, 1987

A/Title: Expression of beta-keratin genes during development of avian skin appendages.  
 A/Reference number: I50168; MUID:88003561; PMID:2443313  
 A/Accession: I50168  
 A/Status: preliminary; translated from GB/EMBL/DDBJ  
 A/Molecule type: DNA  
 A/Residues: 137-155 <SAW>  
 A/Cross-references: GB:M28422; NID:G211271; PIDN:AAA48631.1; PID:G211272  
 C/Superfamily: feather keratin  
 C/Keywords: duplication; epidermis; fibrous protein; horn; integument; tandem repeat  
 F/70-128/Region: 13-residue repeats (G-G-S-S-L-G-Y-G-G-L-Y-G-Y)

Query Match 70.6%; Score 36; DB 1; Length 155;  
 Best Local Similarity 75.0%; Pred. No. 23;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPVSCIKR 9  
 |||||:  
 Db 8 PPTSCISR 15

## RESULT 6

AB2715

conserved hypothetical protein Atul123 [imported] - Agrobacterium tumefaciens (strain C5)  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C/Accession: AB2715  
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
 erage, G.; Gillet, W.; Grant, C.; Guenther, T.; Kutayavin, T.; Levy, R.; Li, M.; McClell;  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.  
 ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; PMID:11743193

A/Accession: AB2715

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-170 <KUR>

A/Cross-references: GB:AE008688; PIDN:AA42136.1; PID:gl77739521; GSPDB:GN00186

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Gene: Atul123

A/Map position: circular chromosome

Query Match 70.6%; Score 36; DB 2; Length 170;  
 Best Local Similarity 62.5%; Pred. No. 25;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIKR 9  
 |||||:  
 Db 94 PPVECVKQ 101

## RESULT 7

F97496  
 Hypothetical protein AGR\_C 2080 [imported] - Agrobacterium tumefaciens (strain C58, Cere;  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
 C/Accession: F97496  
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A/Reference number: A97359; PMID:11743194

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-189 <KUR>

A/Cross-references: GB:AE007869; PIDN:AAK86927.1; PID:gl5156157; GSPDB:GN00169

C/Genetics:

A/Gene: AGR\_C 2080

A/Map position: circular chromosome

Query Match 70.6%; Score 36; DB 2; Length 189;  
 Best Local Similarity 62.5%; Pred. No. 28;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIKR 9  
 |||||:  
 Db 113 PPVECVKQ 120

## RESULT 8

TPHUP

transferrin precursor [validated] - human

N/Alternate names: siderophilin

C/Species: Homo sapiens (man)

C/Date: 15-Oct-1982 #sequence\_revision 30-Sep-1993 #text\_change 08-Dec-2000

C/Accession: A20981; A92417; A94044; A29090; A32739; I51559; I63133; I54011; I68160; A03;

R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin,

Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984

A/Title: Human transferrin: cDNA characterization and chromosomal localization.

A/Reference number: A20981; MUID:84194084; PMID:6585826

A/Contents: variant C

A/Accession: A20981

A;Molecule type: mRNA  
A;Residues: 1-698 <YAN>  
A;Cross-references: EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G339453  
A;Note: the authors translated the codon CAA for residue 203 as Glu  
R;Macgillivray, R.T.A.; Mendez, E.; Shewale, J.G.; Sinha, S.K.; Lineback-Zins, J.; Brew, J. Mol. Cell. Biol. 258, 3543-3553, 1983  
A;Title: The primary structure of human serum transferrin. The structures of seven cyano  
A;Reference number: A92417; MUID:83160878; PMID:6833213  
A;Accession: A92417  
A;Molecule type: protein  
A;Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-  
A;Note: the sequence shown is the predominant electrophoretic genetic variant (C or T/C)  
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985  
A;Title: Organization of the human transferrin gene: direct evidence that it originated  
A;Reference number: A94044; MUID:85216459; PMID:3859812  
A;Accession: A94044  
A;Molecule type: DNA  
A;Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>  
A;Cross-references: EMBL:M11361  
R;Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F. Gene 49, 167-175, 1986  
A;Title: The human transferrin gene: 5' region contains conserved sequences which match  
A;Reference number: A29090; MUID:87192006; PMID:3106157  
A;Accession: A29090  
A;Molecule type: DNA  
A;Residues: 1-72; 291-300 <ADR>  
A;Cross-references: EMBL:M15673  
R;Uzan, G.; Frain, M.; Park, I.; Beaumont, C.; Maessen, G.; Trepatt, J.S.; Zakari, M.M.; Ka  
Biochem. Biophys. Res. Commun. 119, 273-281, 1984  
A;Title: Molecular cloning and sequence analysis of cDNA for human transferrin.  
A;Reference number: A32739; MUID:84153910; PMID:6322780  
A;Accession: A32739  
A;Molecule type: mRNA  
A;Residues: 422-690, 'G', 692-698 <UZA>  
A;Cross-references: EMBL:M12525; NID:G339468; PIDN:AAA61142.1; PID:G339469  
R;Macgillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Lineback-Zins, J.; Brew, J. Mol. Cell. Biol. 258, 3543-3553, 1983  
A;Title: The complete amino acid sequence of human serum transferrin.  
A;Reference number: A93911; MUID:8222166; PMID:6953407  
A;Contents: annotation; disulfide bonds  
R;Hershberger, C.L.; Larson, J.L.; Arnold, B.; Rostock, P.R. Ann. N. Y. Acad. Sci. 646, 140-154, 1991  
A;Title: A cloned gene for human transferrin.  
A;Reference number: I51959; MUID:92231399; PMID:1809186  
A;Accession: I51959  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-698 <RES>  
A;Cross-references: GB:S95936; NID:G248647; PIDN:AA822049.1; PID:G248648  
R;Duguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W. Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989  
A;Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.  
A;Reference number: I48174; MUID:89386721; PMID:2780570  
A;Accession: I63133  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 636-696 <RE2>  
A;Cross-references: GB:M26641; NID:G339988; PIDN:AAA611233.1; PID:G339989  
R;Schaeffer, E.; Lucero, M.A.; Jeltsch, J.M.; Py, M.C.; Levin, M.J.; Chambon, P.; Cohen, Gene 56, 109-116, 1987  
A;Title: Complete structure of the human transferrin gene. Comparison with analogous chi  
A;Reference number: I54011; MUID:88056305; PMID:3678832  
A;Accession: I54011  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-72 <RE3>  
A;Cross-references: GB:M17611; NID:G339480; PIDN:AAA61147.1; PID:G339485  
A;Accession: I68160  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 564-698 <RE4>

A;Cross-references: GB:M17614; NID:G339483; PIDN:AAA61148.1; PID:G339486  
C;Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion  
C;Genetics: GDB:TF  
A;Gene: GDB:TF  
A;Cross-references: GDB:120432; OMIM:190000  
A;Map position: 3q21-3q21  
A;Introns: 15/1; 72/3; 119/1; 169/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 45  
C;Function:  
A;Description: binds iron for delivery into cells  
C;Superfamily: transferrin; transferrin repeat homology  
C;Keywords: duplication; glycoprotein; iron transport; metal binding; plasma  
F;19/Domain: signal sequence #status predicted <SIG>  
F;20-698/Product: transferrin #status experimental <MAT>  
F;20-350/Domain: transferrin repeat homology <TRH1>  
F;356-686/Domain: transferrin repeat homology <TRH2>  
F;38-67, 38-58, 137-213, 156-350, 177-193, 180-196, 190-198, 246-260, 358-615, 364-396, 374-387, 42  
F;432, 630/Binding site: carbohydrate (Asn) #status experimental  
Query Match 70.6%; Score 36; DB 1; Length 698;  
Best Local Similarity 55.6%; Pred. No. 91;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GPPVSCIKR 9  
DB 53 GPSVACVK 61  
RESULT 9  
T32136  
hypothetical protein R07C3.4 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 03-Nov-2000  
C;Accession: T32136  
R;Lamar, B.; Kramer, J. submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of C. elegans cosmid R07C3.  
A;Reference number: Z21125  
A;Accession: T32136  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-723 <LAM>  
A;Cross-references: EMBL:AF016696; PIDN:AA86234.1; GSPDB:GN00020; CSDP:R07C3.4  
A;Experimental source: strain Bristol N2; clone R07C3  
C;Genetics:  
A;Gene: CSDP:R07C3.4  
A;Map position: 2  
A;Introns: 25/3; 83/3; 149/3; 198/1; 326/2; 420/2; 622/3; 654/1  
C;Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homology  
F;133-691/Domain: acetate-CoA ligase homology <ACL>  
Query Match 70.6%; Score 36; DB 2; Length 723;  
Best Local Similarity 83.3%; Pred. No. 94;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPPVSC 6  
DB 497 GPPISC 502  
RESULT 10  
IVMSA4  
interferon alpha-I-4 precursor - mouse  
N;Alternate names: MuIFN-alpha-I-4; type I interferon  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 22-Jun-1999  
C;Accession: B23087  
R;Kelly, K.A.; Pitha, P.M. Nucleic Acids Res. 13, 805-823, 1985  
A;Title: Characterization of a mouse interferon gene locus. I. Isolation of a cluster of  
A;Reference number: A93600; MUID:85215516; PMID:2987811  
A;Accession: B23087  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-186 <REL>

A:Cross-references: GB:X01973; GB:M15456; GB:M23830; GB:X01967; NID:G51544; PIDN:CAA260d  
 C:Genetics:  
 A:Map position: 4  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral; glycoprotein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:1-186/Product: interferon alpha-I-4 #status predicted <MAT>  
 F:25-123,53-158/Bisulfide bonds: #status predicted  
 F:102/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 68.6%; Score 35; DB 1; Length 186;  
 Best Local Similarity 71.4%; Pred. No. 41;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCIK 8  
 |||||  
 Db 49 PPLSCLK 55

RESULT 11  
 A71675  
 4-hydroxybenzoate octaprenyltransferase (ubiA) RP686 - Rickettsia prowazekii  
 C:Species: Rickettsia prowazekii  
 C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 03-Nov-2000  
 C:Accession: A71675  
 R:Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.  
 Nature 396, 133-140, 1998  
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
 A:Reference number: A71675; MUID:99039499; PMID:9823893  
 A:Accession: A71675  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-282 <AND>  
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:G3861033; PIDN:CAA15123.1; PID:G386122  
 A:Experimental source: strain Madrid E  
 C:Genetics:  
 A:Gene: ubiA; RP686  
 C:Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 68.6%; Score 35; DB 2; Length 282;  
 Best Local Similarity 85.7%; Pred. No. 61;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVSCIKR 9  
 |||||  
 Db 260 PVNCIKR 266

RESULT 12  
 T31799  
 hypothetical protein F29G9.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T31799  
 R:Langston, Y.  
 submitted to the EMBL Data Library, July 1997  
 A:Description: The sequence of C. elegans cosmid F29G9.  
 A:Reference number: Z21088  
 A:Accession: T31799  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-310 <LAN>  
 A:Cross-references: EMBL:AF016440; PIDN:AB65905.1; GSPDB:GN00023; CESP:F29G9.4  
 A:Experimental source: strain Bristol N2; clone F29G9  
 C:Genetics:  
 A:Gene: CESP:F29G9.4  
 A:Map position: 5  
 A:Introns: 36/3; 203/3; 271/1

Query Match 68.6%; Score 35; DB 2; Length 310;  
 Best Local Similarity 71.4%; Pred. No. 66;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCIK 8  
 |||||  
 Db 145 PPISCIQ 151

RESULT 13  
 A38743  
 lorixin - human  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Sep-1991 #sequence\_revision 23-Aug-1996 #text\_change 20-Oct-2000  
 C:Accession: A38743; A43410  
 R:Hohl, D.; Mehret, T.; Lichti, U.; Turner, M.L.; Roop, D.R.; Steinert, P.M.  
 J. Biol. Chem. 266, 6626-6636, 1991  
 A:Title: Characterization of human lorixin. Structure and function of a new class of ep:  
 A:Reference number: A38743; MUID:91177926; PMID:2007607  
 A:Accession: A38743  
 A:Molecule type: mRNA  
 A:Residues: 1-316 <HOH>  
 A:Cross-references: GB:M61120; NID:G187184; PIDN:AAA36180.1; PID:G187185  
 A:Note: translation of Met-1 is not shown  
 R:Yoneda, K.; Hohl, D.; McBride, O.W.; Wang, M.; Cehrs, K.U.; Idler, W.W.; Steinert, P.M.  
 J. Biol. Chem. 267, 18060-18066, 1992  
 A:Title: The human lorixin gene.  
 A:Reference number: A43410; MUID:92388173; PMID:1355480  
 A:Accession: A43410  
 A:Molecule type: DNA  
 A:Residues: 2-151, C, 153-232, C, 234-316 <YON>  
 A:Cross-references: GB:M94077; NID:G187186; PIDN:AAA36181.1; PID:G187187  
 A:Note: sequence inconsistent with the nucleotide translation  
 A:Note: sequence extracted from NCBI backbone (NCBIN:112880, NCBIP:112882)  
 C:Comment: During the terminal differentiation of epidermal (stratum corneum) cell, this  
 n insoluble, cross-linked envelope (the cornified cell envelope) under the plasma membrar  
 C:Genetics:  
 A:Gene: GDB: LOR  
 A:Cross-references: GDB:132049; OMIM:152445  
 A:Map position: 1q21-1q21  
 A:Introns: #status absent  
 A:Note: polymorphisms include variants of different lengths  
 C:Superfamily: lorixin  
 C:Keywords: cornified cell envelope; disulfide bond; duplication; epidermis; tandem repe:  
 F:89/Cross-link: isopeptide (lys) (interchain to Gln-154) (partial) #status experimental  
 F:89/Cross-link: isopeptide (lys) (interchain to Gln-220) (partial) #status experimental  
 F:154/Cross-link: isopeptide (Gln) (interchain to Lys-89) #status experimental  
 F:216/Cross-link: isopeptide (Gln) (interchain to Lys-316) #status experimental  
 F:220/Cross-link: isopeptide (Gln) (interchain to Lys-89) #status experimental  
 F:316/Cross-link: isopeptide (lys) (interchain to Gln-216) (partial) #status experimental

Query Match 68.6%; Score 35; DB 1; Length 316;  
 Best Local Similarity 71.4%; Pred. No. 67;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIK 8  
 |||||  
 Db 12 PPVDCVK 18

RESULT 14  
 D86356  
 hypothetical protein T16E15.4 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
 C:Accession: D86356  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.  
 C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86356  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-450 <STO>  
 A;Cross-references: GB:AE005172; NID:g9392678; PIDN:AAF87258.1; GSPDB:GN00141  
 C;Genetics:  
 A;Map position: 1  
 C;Superfamily: flavonol O3-glucosyltransferase

Query Match 68.6%; Score 35; DB 2; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCI 7  
 Db 118 PPVSCI 123

RESULT 15  
 F86356  
 T16E15.2 protein - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Nov-2001  
 C;Accession: F86356  
 R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 arsen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: F86356  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-479 <STO>  
 A;Cross-references: GB:AE005172; NID:g9392678; PIDN:AAF87255.1; GSPDB:GN00141  
 C;Genetics:  
 A;Map position: 1  
 C;Superfamily: flavonol O3-glucosyltransferase

Query Match 68.6%; Score 35; DB 2; Length 479;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCI 7  
 Db 118 PPVSCI 123

Search completed: February 21, 2003, 08:02:53  
 Job time : 9.95349 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search time 3.90698 Seconds  
(without alignments)  
95.544 Million cell updates/sec

Title: US-09-743-107B-101  
Perfect score: 51  
Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	711	1 TRFL HUMAN	P02788 homo sapien
2	44	86.3	707	1 TRFL MOUSE	P08071 mus musculus
3	41	80.4	704	1 ICA FIG	Q29545 sus scrofa
4	38	74.5	1189	1 ITAH HUMAN	Q9UKX5 homo sapien
5	37	72.5	695	1 TRFL HORSE	O77811 equus caball
6	37	72.5	696	1 TRFE FIG	P09571 sus scrofa
7	36	70.6	64	1 BD01 CAPHI	O97946 capra hircu
8	36	70.6	64	1 BD01 SHEEP	O19038 ovis aries
9	36	70.6	154	1 KRSC CHICK	P04459 gallus gall
10	36	70.6	698	1 TRPE HUMAN	P02787 homo sapien
11	36	70.6	704	1 TRPE BOVIN	Q29443 bos taurus
12	36	70.6	708	1 TRPL CAMDR	Q9TUM0 camelus dro
13	35	68.6	186	1 INA4 MOUSE	P07351 mus musculus
14	35	68.6	316	1 LORI HUMAN	P23490 homo sapien
15	35	68.6	367	1 VE2 HEPV54	Q81021 human papil
16	35	68.6	1402	1 IF4G RABIT	P41110 cryptolagus
17	34	66.7	64	1 BD02 SHEEP	O19033 ovis aries
18	34	66.7	431	1 VE2 HEPV23	P50769 human papil
19	34	66.7	3898	1 POLG HCVB	P21530 hog cholera
20	33	64.7	64	1 BD02 HUMAN	O15263 homo sapien
21	33	64.7	64	1 TAP BOVIN	P25068 bos taurus
22	33	64.7	187	1 SURE TREPA	Q81434 treponema p
23	33	64.7	203	1 SHX HUMAN	Q9NGF3 homo sapien
24	33	64.7	219	1 CD53 HUMAN	P19397 homo sapien
25	33	64.7	283	1 SURE CHLMU	Q9PKH4 chlamydia m
26	33	64.7	283	1 SURE CHLTP	O84220 chlamydia t
27	33	64.7	314	1 SEHL HUMAN	Q9H418 homo sapien
28	33	64.7	401	1 VE2 HEPV1A	P03118 human papil
29	33	64.7	432	1 PURA MYCTU	O08381 mycobacteri
30	33	64.7	539	1 U175 MOUSE	Q925F4 mus musculus
31	33	64.7	875	1 XLNR ASPNG	O42804 aspergillus
32	33	64.7	887	1 CAD1 CHICK	P08641 gallus gall
33	33	64.7	1103	1 DPOD_MESAU	P97283 mesocricetu

#### RESULT 1

ID	TRFL HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9HLZ3; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
EX	MEDLINE=90384839; PubMed=2402455;			
RA	Ray M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.N.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RT	sequences.";			
RN	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RL	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

Q64398 mesocricetu  
P00522 drosophila  
P08968 trypanosoma  
Q09237 caenorhabdi  
P27716 drosophila  
P03121 cottontail  
Q9V9A7 drosophila  
Q00451 homo sapien  
P38915 saccharomyc  
Q92111 mus musculu  
P12346 rattus norv  
P97350 mus musculu

#### ALIGNMENTS

SEQUENCE OF 3-711 FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=90326549; PubMed=2374734;  
 RA Powell M.J., Ogden J.E.;  
 RT "Nucleotide sequence of human lactoferrin cDNA.";  
 RL Nucleic Acids Res. 18:4013-4013(1990).  
 RN [9]  
 RP SEQUENCE OF 20-711.  
 RX MEDLINE=85076667; PubMed=6510420;  
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
 RX LeGrand D., Spik G., Montreuil J., Jolles P.;  
 RT "Human lactotransferrin: amino acid sequence and structural  
 RX comparisons with other transferrins.";  
 RL Eur. J. Biochem. 145:659-666(1984).  
 RN [10]  
 RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
 RX MEDLINE=82046817; PubMed=6794640;  
 RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
 RX Jolles P.;  
 RT "The present state of the human lactotransferrin sequence. Study and  
 RX alignment of the cyanogen bromide fragments and characterization of  
 RX N- and C-terminal domains.";  
 RL Biochim. Biophys. Acta 670:243-254(1981).  
 RN [11]  
 RP SEQUENCE OF 609-711.  
 RX MEDLINE=82262043; PubMed=7049727;  
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
 RX Jolles P.;  
 RT "An 88 amino acid long C-terminal sequence of human  
 RX lactotransferrin.";  
 RL FEBS Lett. 142:107-110(1982).  
 RN [12]  
 RP SEQUENCE OF 436-711 FROM N.A.  
 RX MEDLINE=8801031; PubMed=3477300;  
 RA Rado T.A., Wei X., Benz E.J. Jr.;  
 RT "Isolation of lactoferrin cDNA from a human myeloid library and  
 RX expression of mRNA during normal and leukemic myelopoiesis.";  
 RL Blood 70:989-993(1987).  
 RN [13]  
 RP SEQUENCE OF 237-711 FROM N.A.  
 RA McCombie M.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
 RA Nnan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
 RA Gao J., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
 RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
 RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
 RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
 RA Sgripanti J.L.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
 RX MEDLINE=90064528; PubMed=2585506;  
 RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
 RT "Structure of human lactoferrin: crystallographic structure analysis  
 RX and refinement at 2.8-A resolution.";  
 RL J. Mol. Biol. 209:711-734(1989).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RA Haridas M., Anderson B.F., Baker E.N.;  
 RT "Structure of human diferric lactoferrin refined at 2.2-A  
 RX resolution.";  
 RL Acta Crystallogr. D 51:629-646(1995).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
 RX MEDLINE=97156796; PubMed=9003186;  
 RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
 RA Baker E.N.;  
 RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
 RX binding properties and crystal structure of the histidine-  
 RX 253--methionine mutant.";  
 RL Biochemistry 36:341-346(1997).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=99190892; PubMed=10089347;  
 RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
 RT "Structure of recombinant human lactoferrin expressed in *Aspergillus*  
 RX *awamori*.";  
 RL Acta Crystallogr. D 55:403-407(1999).  
 RN [18]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=99192677; PubMed=10089508;  
 RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
 RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
 RX and analysis of ligand-induced conformational change.";  
 RL Acta Crystallogr. D 54:1319-1335(1998).  
 RN [19]  
 RP CHARACTERIZATION OF LACTOFERROXINS.  
 RX MEDLINE=91166929; PubMed=1369293;  
 RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
 RT "Isolation and characterization of opioid antagonist peptides derived  
 RX from human lactoferrin.";  
 RL Agric. Biol. Chem. 54:1803-1810(1990).  
 RN [20]  
 RP VARIANTS THR-30 AND ARG-48.  
 RX PubMed=9873069;  
 RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
 RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
 RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,  
 RA El Matti L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
 RA Hejtmancik J.F., Teng C.T.;  
 RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
 RX corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
 RL Mol. Vision 4:31-32(1998).  
 CC -|- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE.  
 CC -|- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST  
 CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
 CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
 CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
 CC -|- SUBUNIT: MONOMER.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -|- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
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 CC -----  
 DR EMBL; X53961; CAA37914.1; -;  
 DR EMBL; U07643; AAB60324.1; -;  
 DR EMBL; M93150; AAA36159.1; -;  
 DR EMBL; M83202; AAA59511.1; -;  
 DR EMBL; M83205; AAA58656.1; -;  
 DR EMBL; M18642; AAA86665.1; -;  
 DR EMBL; AF332168; AAG48753.1; -;  
 DR EMBL; BC015822; AAH15822.1; -;  
 DR EMBL; BC015823; AAH15823.1; -;  
 DR EMBL; M73700; AAA59479.1; -;  
 DR EMBL; X52941; CAA37116.1; -;  
 DR EMBL; U95626; AAB57795.1; -;  
 DR PIR; S11228; TFHUL.  
 DR PDB; 1LCF; 31-AUG-94.  
 DR PDB; 1LCT; 31-OCT-93.  
 DR PDB; 1LFG; 31-JUL-94.  
 DR PDB; 1LFH; 31-OCT-93.  
 DR PDB; 1LEI; 31-OCT-93.  
 DR PDB; 1LGB; 31-AUG-94.  
 DR PDB; 1LGC; 31-AUG-94.  
 DR PDB; 1BKA; 08-NOV-96.  
 DR PDB; 1DSN; 08-MAR-96.  
 DR PDB; 1HSE; 12-MAR-97.  
 DR PDB; 1VPD; 21-APR-97.



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Query Match          100.0%; Score 51; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIQR 9
DB 51 GPPVSCIQR 59

RESULT 2
TRFL_MOUSE
ID TRFL_MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T.; Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
RT uterine secretions."
RL J. Biol. Chem. 262:10134-10139 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishita K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1939212;
RA Liu Y.; Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter."
RL J. Biol. Chem. 266:21880-21885 (1991).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC -----
DR EMBL; J03298; AAA40525.1; -
DR EMBL; D88510; BAA13633.1; -
DR EMBL; BC006904; AAA06904.1; -
DR EMBL; M74778; AAA39427.1; -
DR PIR; A28438; A28438.
DR HSP; P02788; ICB6.
DR MGD; MGI:96837; Lt1.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PRO0422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.

```

DR PROSITE; PS00205; TRANSFERRIN\_1; 1.  
DR PROSITE; PS00206; TRANSFERRIN\_2; 2.  
DR PROSITE; PS00207; TRANSFERRIN\_3; 2.  
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
KW Signal.  
FT CHAIN 1 19 BY SIMILARITY.  
FT REPEAT 20 707 LACTOTRANSFERRIN.  
FT REPEAT 358 707 1.  
FT REPEAT 358 707 2.  
FT DISULFID 27 63 BY SIMILARITY.  
FT DISULFID 37 54 BY SIMILARITY.  
FT DISULFID 133 216 BY SIMILARITY.  
FT DISULFID 175 191 BY SIMILARITY.  
FT DISULFID 188 199 BY SIMILARITY.  
FT DISULFID 249 263 BY SIMILARITY.  
FT DISULFID 366 398 BY SIMILARITY.  
FT DISULFID 376 389 BY SIMILARITY.  
FT DISULFID 423 702 BY SIMILARITY.  
FT DISULFID 443 665 BY SIMILARITY.  
FT DISULFID 475 550 BY SIMILARITY.  
FT DISULFID 499 693 BY SIMILARITY.  
FT DISULFID 509 523 BY SIMILARITY.  
FT DISULFID 520 533 BY SIMILARITY.  
FT DISULFID 591 605 BY SIMILARITY.  
FT DISULFID 643 648 BY SIMILARITY.  
FT METAL 78 78 IRON 1 (BY SIMILARITY).  
FT METAL 110 110 IRON 1 (BY SIMILARITY).  
FT METAL 210 210 IRON 1 (BY SIMILARITY).  
FT METAL 271 271 IRON 1 (BY SIMILARITY).  
FT METAL 413 413 IRON 2 (BY SIMILARITY).  
FT METAL 451 451 IRON 2 (BY SIMILARITY).  
FT METAL 544 544 IRON 2 (BY SIMILARITY).  
FT METAL 613 613 IRON 2 (BY SIMILARITY).  
FT BINDING 139 139 ANION (POTENTIAL).  
FT BINDING 481 481 ANION (POTENTIAL).  
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).  
FT CONFLICT 25 25 R -> Q (IN REF. 2).  
FT CONFLICT 82 82 M -> L (IN REF. 2).  
FT CONFLICT 359 359 S -> T (IN REF. 2).  
FT CONFLICT 382 382 A -> D (IN REF. 1).  
FT CONFLICT 449 449 E -> G (IN REF. 2).  
FT CONFLICT 629 629 L -> V (IN REF. 1).  
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;  
Query Match 86.3%; Score 44; DB 1; Length 707;  
Best Local Similarity 66.7%; Pred. No. 0.72;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPPVSCIQR 9  
DB 49 GPPVSCIQR 57  
RESULT 3  
ICA\_PIG  
ID ICA\_PIG STANDARD; PRT; 704 AA.  
AC Q29545;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Inhibitor of carbonic anhydrase precursor.  
GN ICA.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=97254619; PubMed=9100029;  
RA Wuebbens M.W.; Roush E.D.; Decastro C.M.; Fierke C.A.;  
RT "Cloning, sequencing, and recombinant expression of the porcine

RT inhibitor of carbonic anhydrase; a novel member of the transferrin  
 family".  
 RL Biochemistry 36:4327-4336(1997).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93099129; PubMed=1463741;  
 RA Roush E.D., Fierke C.A.;  
 RT "Purification and characterization of a carbonic anhydrase II  
 inhibitor from porcine plasma";  
 RL Biochemistry 31:12536-12542(1992).  
 CC -1- FUNCTION: SPECIFICALLY BINDS AND INHIBITS CARBONIC ANHYDRASE II  
 CC -1- WITH NANOMOLAR AFFINITY.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: N-GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
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 CC  
 CC EMBL; U36916; AAB58956.1; -.  
 CC HSPSP; P19134; ITFD.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SMC0094; TR\_FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN\_1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN\_2; 1.  
 CC PROSITE; PS00207; TRANSFERRIN\_3; 2.  
 CC KW Glycoprotein; Signal.  
 CC FT SIGNAL 1 19 POTENTIAL.  
 CC FT CHAIN 20 704 INHIBITOR OF CARBONIC ANHYDRASE.  
 CC FT CARBOHYD 491 491 N-LINKED (GLCNAC...) (POTENTIAL).  
 CC FT SEQUENCE 704 AA; 77634 MW; 16B80E65191E336 CRC64;  
 CC  
 CC Query Match 80.4%; Score 41; DB 1; Length 704;  
 CC Best Local Similarity 77.8%; Pred. No. 2.7;  
 CC Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC Qy 1 GPPVSCIKS 9  
 CC Db 53 GPHVSCVKR 61  
 CC  
 CC RESULT 4  
 CC ID ITAH HUMAN STANDARD; PRT; 1189 AA.  
 CC AC Q9UKX5; Q9UKQ1;  
 CC DT 16-OCT-2001 (Rel. 40, Created)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Integrin alpha-11 precursor.  
 CC GN ITGAL1  
 CC OS Homo sapiens (Human)  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC OX NCBI\_TaxID=9606;  
 CC [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Fetal heart, and Osteoblast;  
 CC RX MEDLINE=99417678; PubMed=10486209;  
 CC RA Lehnert K., Ni J., Leung E., Gough S.M., Weaver A., Yao W.P., Liu D.,  
 CC Wang S.-X., Morris C.M., Kriessansen G.W.;  
 CC RT "Cloning, sequence analysis, and chromosomal localization of the novel  
 CC human integrin alpha11 subunit (ITGAL11).";  
 CC RL Genomics 60:179-187(1999).  
 CC [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal muscle, and Uterus;  
 RX MEDLINE=93395147; PubMed=10464311;  
 RA Velling T., Kusche-Gullberg M., Seijersen T., Gullberg D.;  
 RT "cDNA Cloning and Chromosomal Localization of Human alpha(11)  
 RT Integrin. A collagen-binding, 1 domain-containing, beta(1)-associated  
 RT integrin alpha-chain present in muscle tissues.";  
 RL J. Biol. Chem. 274:25735-25742(1999).  
 RN [3]  
 RP SEQUENCE OF 954-1188 FROM N.A.  
 RC TISSUE=Fibroblast;  
 RA Andreu N., Estivill X., Escarceller M., Sunoy L.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INTEGRIN ALPHA-11/BETA-1 IS A RECEPTOR FOR COLLAGEN.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-11  
 CC ASSOCIATES WITH BETA-1.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: ACCORDING REF. 2 HIGHEST LEVELS IN UTERUS AND  
 CC HEART. INTERMEDIATE LEVELS IN SKELETAL MUSCLE AND INTERMEDIATE TO  
 CC LOW LEVELS IN PANCREAS, KIDNEY AND PLACENTA. ACCORDING REF.1 ALSO  
 CC FOUND IN BRAIN, COLON, LUNG, SMALL INTESTINE, STOMACH, TESTIS,  
 CC SALIVARY GLANDS, THYROID GLANDS AND PROSTATE. VERY LOW LEVELS IN  
 CC PERIPHERAL BLOOD LYMPHOCYTES, FETAL BRAIN AND FETAL LIVER.  
 CC -1- DEVELOPMENTAL STAGE: STRONGLY UP-REGULATED IN DIFFERENTIATING  
 CC FETAL MUSCLE CELLS (IN VITRO).  
 CC -1- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS  
 CC WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.  
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.  
 CC  
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 CC  
 CC EMBL; AF109681; AAF01258.1; -.  
 CC EMBL; AF137378; AAD51919.2; -.  
 CC EMBL; AL359064; CAB94392.1; -.  
 CC HSSP; P17301; IAOX.  
 CC MIM; 604789; -.  
 CC InterPro; IPR000413; Integrin\_alpha.  
 CC InterPro; IPR002035; VWF\_A.  
 CC Pfam; PF00092; vwa; 1.  
 CC Pfam; PF01839; FG-GAP; 5.  
 CC PRINTS; PR01185; INTEGRINA.  
 CC PRINTS; PR00453; VWFADOMAIN.  
 CC SMART; SMO0191; Int\_alpha; 5.  
 CC SMART; SMO0327; VWA\_1  
 CC PROSITE; PS00242; INTEGRIN\_ALPHA; FALSE\_NEG.  
 CC PROSITE; PS50234; VWFA; 1.  
 CC Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;  
 CC Signal; Repeat; Calcium; Magnesium; Polymorphism.  
 CC SIGNAL 1 22 POTENTIAL.  
 CC CHAIN 23 1189 INTEGRIN ALPHA-11.  
 CC DOMAIN 23 1142 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 1143 1165 POTENTIAL.  
 CC DOMAIN 1166 1189 CYTOPLASMIC (POTENTIAL).  
 CC REPEAT 38 94 FG-GAP 1.  
 CC REPEAT 102 163 FG-GAP 2.  
 CC REPEAT 167 345 VWFA.  
 CC DOMAIN 359 420 FG-GAP 3.  
 CC REPEAT 422 475 FG-GAP 4.  
 CC REPEAT 477 537 FG-GAP 5.  
 CC REPEAT 539 598 FG-GAP 6.  
 CC REPEAT 601 653 FG-GAP 7.  
 CC DOMAIN 1154 1162 POLY-LEU.  
 CC DOMAIN 1174 1177 POLY-ARG.  
 CC CA\_BIND 488 496 POTENTIAL.



## RESULT 6

TRFE\_PIG STANDARD; PRT; 696 AA.

AC P09571; (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 41, Last annotation update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Serotransferrin (Transferrin) (Siderophilin) (Beta-1-metal binding globulin).

GN TF.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=88335629; PubMed=3419934;

RA Baldwin G.S.; Weinstein J.;

RT "Nucleotide sequence of porcine liver transferrin."

CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE. IT IS RESPONSIBLE FOR THE TRANSPORT OF IRON FROM SITES OF ABSORPTION AND HEME DEGRADATION TO THOSE OF STORAGE AND UTILIZATION. SERUM TRANSFERRIN MAY ALSO HAVE A FURTHER ROLE IN STIMULATING CELL PROLIFERATION.

CC -1- SUBUNIT: MONOMER.

CC -1- TISSUE SPECIFICITY: Secreted.

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC EMBL; X12386; CAA30943.1; --

DR PIR; S01384; S01384.

DR HSP; P19134; ITFD.

DR InterPro; IPR001156; Transferrin.

DR Pfam; PF00405; transferrin; 2.

DR PRINTS; PR00422; TRANSFERRIN.

DR SMART; SM00094; TR\_FER; 2.

DR PROSITE; PS00205; TRANSFERRIN 1; 2.

DR PROSITE; PS00206; TRANSFERRIN 2; 2.

DR PROSITE; PS00207; TRANSFERRIN 3; 2.

KW Transport; iron transport; Glycoprotein; Metal-binding; Repeat.

FT REPEAT 1 340 1.

FT REPEAT 341 696 2.

FT DISULFID 9 47 BY SIMILARITY.

FT FT 19 38 BY SIMILARITY.

FT DISULFID 117 198 BY SIMILARITY.

FT DISULFID 157 173 BY SIMILARITY.

FT DISULFID 160 181 BY SIMILARITY.

FT DISULFID 170 183 BY SIMILARITY.

FT DISULFID 231 245 BY SIMILARITY.

FT DISULFID 343 605 BY SIMILARITY.

FT DISULFID 349 381 BY SIMILARITY.

FT DISULFID 359 372 BY SIMILARITY.

FT DISULFID 406 682 BY SIMILARITY.

FT DISULFID 423 646 BY SIMILARITY.

FT DISULFID 456 532 BY SIMILARITY.

FT DISULFID 480 673 BY SIMILARITY.

FT DISULFID 490 504 BY SIMILARITY.

FT DISULFID 501 515 BY SIMILARITY.

FT DISULFID 572 586 BY SIMILARITY.

FT DISULFID 624 629 BY SIMILARITY.

FT METAL 62 IRON 1 (BY SIMILARITY).

FT METAL 94 IRON 1 (BY SIMILARITY).

FT METAL 192 IRON 1 (BY SIMILARITY).

FT METAL 253 IRON 1 (BY SIMILARITY).

FT METAL 396 IRON 2 (BY SIMILARITY).

FT METAL 431 IRON 2 (BY SIMILARITY).

FT METAL 526 IRON 2 (BY SIMILARITY).

FT METAL 594 IRON 2 (BY SIMILARITY).

FT BINDING 123 ANION (POTENTIAL).

FT BINDING 462 ANION (POTENTIAL).

FT CARBOHYD 25 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 497 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 308 K -> R.

SQ SEQUENCE 696 AA; 76967 MW; 787C59F42D844B26 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 696;

Best Local Similarity 66.7%; Pred. No. 15; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 1;

QY 1 GPPVSCIKR 9

Db 33 GPLVSCVKK 41

## RESULT 7

ID -BD01\_CAPHI STANDARD; PRT; 64 AA.

AC O97946; (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Beta-defensin 1 precursor (BD-1).

GN DEFB1.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Capra.

OX NCBI\_TaxID=9925;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tongue;

RA Zhao C.; Nguyen T.; Lehrer R.I.;

RT "Molecular cloning and tissue expression of goat beta-defensin-1."

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.

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CC EMBL; Y17679; CAA76811.1; --

DR HSP; P46170; IBNB.

DR InterPro; IPR001855; Defensin beta.

DR InterPro; IPR001271; Defensin mammal.

DR Pfam; PF00711; Defensin beta; 1.

DR SMART; SM00048; DEFSN; 1.

KW Antibiotic; Signal.

FT SIGNAL 1 20 POTENTIAL.

FT PROPEP 21 26 POTENTIAL.

FT CHAIN 27 64 BETA-DEFENSIN 1.

FT DISULFID 31 60 BY SIMILARITY.

FT DISULFID 38 53 BY SIMILARITY.

FT DISULFID 43 61 BY SIMILARITY.

SQ SEQUENCE 64 AA; 7258 MW; 492B824C8F57B042 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 64;

Best Local Similarity 55.6%; Pred. No. 2.2;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
Db 55 GPPVKCKRK 63

## RESULT 8

BD01 SHEEP  
ID \_BD01\_SHEEP STANDARD; PRT; 64 AA.  
AC O19039;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Beta-defensin 1 precursor (BD-1) (sBD1).  
GN DFB1.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98138497; PubMed=9478010;  
RA Huttner K.M., Berezinski-Calguri D.J., Mahoney M.M., Diamond G.;  
RT "Antimicrobial peptide expression is developmentally regulated in the  
ovine gastrointestinal tract.";  
RL J. Nutr. 128:2978-2998(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Trachea;  
RX MEDLINE=98121317; PubMed=9461419;  
RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;  
RT "Localization and genomic organization of sheep antimicrobial peptides  
genes.";  
RL Gene 206:85-91(1998).

CC -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U75250; AAB61995.1; -  
CC HSP; P46170; IJNB.  
CC InterPro; IPR001855; Defensin\_beta.  
CC Pfam; PF00711; Defensin\_beta; 1.  
CC SMART; SM00048; DEFSN; 1.  
CC Antibiotic; Signal.  
FT SIGNAL 1 22 BY SIMILARITY  
FT CHAIN 23 64 BETA-DEFENSIN 1.  
FT DISULFID 31 60 BY SIMILARITY.  
FT DISULFID 38 53 BY SIMILARITY.  
FT DISULFID 43 61 BY SIMILARITY.  
SQ SEQUENCE 64 AA; 7244 MW; 3529A9B76ABD023A CRC64;  
Query Match 70.6%; Score 36; DB 1; Length 64;  
Best Local Similarity 55.6%; Pred. No. 2.2;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
Db 55 GPPVKCKRK 63

## RESULT 9

KRSC CHICK  
ID \_KRSC\_CHICK STANDARD; PRT; 154 AA.  
AC P04459;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Scale keratin (S-ker) (sKer).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84158528; PubMed=6200321;  
RA Gregg K., Wilton S.D., Parry D.A.D., Rogers G.E.;  
RT "A comparison of genomic coding sequences for feather and scale  
keratins: structural and evolutionary implications.";  
RL EMBO J. 3:1175-1178(1984).  
CC -!- SUBUNIT: THE AVIAN KERATINS (F-KER, S-KER, C-KER AND B-KER) ARE A  
COMPLEX MIXTURE OF VERY SIMILAR POLYPEPTIDES.  
CC -!- SIMILARITY: BELONGS TO THE AVIAN KERATIN FAMILY.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X00315; CAA25084.1; ALT\_SEQ.  
CC PIR; A02851; KRCHS.  
CC InterPro; IPR003461; Keratin.  
CC Pfam; PF02422; Keratin; 1.  
CC Keratin; Multigene family; Repeat.  
FT INIT MET 0 75 BY SIMILARITY.  
FT REPEAT 59 75  
FT REPEAT 76 88  
FT REPEAT 89 101  
FT REPEAT 102 114  
FT REPEAT 115 127  
SQ SEQUENCE 154 AA; 15710 MW; 65B337485EC00466 CRC64;  
Query Match 70.6%; Score 36; DB 1; Length 154;  
Best Local Similarity 75.0%; Pred. No. 5.3;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFVSCIKR 9  
Db 7 PPTSCISR 14

## RESULT 10

TRFE HUMAN  
ID \_TRFE\_HUMAN STANDARD; PRT; 698 AA.  
AC P02787; OSUHV0; O9NOB8; O43890;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal  
binding globulin) (PRO1400).  
GN TF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.; AND VARIANTS TF\*B2; TF\*CHI AND TF\*DI.  
RX MEDLINE=84194084; PubMed=6585826;  
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,  
RA van Bragt P.H., Baldwin W.D., Bowman B.H.;  
RT "Human transferrin: cDNA characterization and chromosomal

RT localization.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80056305; PubMed=3678832;  
 RA Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,  
 RA Chambon P., Cohen G.N., Zakim M.M.;  
 RT "Complete structure of the human transferrin gene. Comparison with  
 RT analogous chicken gene and human pseudogene.";  
 RL Gene 56:109-116(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=92231399; PubMed=1809186;  
 RA Hersheberger C.L., Larson J.L., Arnold B., Rostock P.R. Jr.,  
 RA Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W.,  
 RA Tice P.A.;  
 RT "A cloned gene for human transferrin.";  
 RL Ann. N.Y. Acad. Sci. 646:140-154(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A. AND VARIANT ATRANSFERRINEMIA PRO-477.  
 RX MEDLINE=20563920; PubMed=1110675;  
 RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,  
 RA Fairbanks V.F.;  
 RT "Molecular characterization of a case of atransferrinemia.";  
 RL Blood 96:4071-4074(2000).  
 RN [5]  
 RP SEQUENCE OF 99-698 FROM N.A.  
 RC TISSUE=Fetal liver;  
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,  
 RA He F.;  
 RT "Functional prediction of the coding sequences of 33 new genes deduced  
 RT by analysis of cDNA clones from human fetal liver.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 422-698 FROM N.A.  
 RX MEDLINE=84153910; PubMed=6327280;  
 RA Uzan G., Frain M., Kahn A.;  
 RA Zakim M.M., Park I., Desmond C., Maessen G., Trepat J.S.,  
 RT "Molecular cloning and sequence analysis of cDNA for human  
 RT transferrin.";  
 RL Biochem. Biophys. Res. Commun. 119:273-281(1984).  
 RN [7]  
 RP SEQUENCE OF 20-698  
 RX MEDLINE=83160878; PubMed=6833213;  
 RA McGilivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,  
 RA Lineback-Zins J., Brew K.;  
 RT "The primary structure of human serum transferrin. The structures of  
 RT seven cyanogen bromide fragments and the assembly of the complete  
 RT structure.";  
 RL J. Biol. Chem. 258:3543-3553(1983).  
 RN [8]  
 RP SEQUENCE OF 73-698 FROM N.A.  
 RX MEDLINE=85216459; PubMed=3858812;  
 RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,  
 RA Zakim M.M.;  
 RT "Organization of the human transferrin gene: direct evidence that it  
 RT originated by gene duplication.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).  
 RN [9]  
 RP SEQUENCE OF 1-14 FROM N.A.  
 RX MEDLINE=87066744; PubMed=3786138;  
 RA Lucero M.A., Schaeffer E., Cohen G.N., Zakim M.M.;  
 RT "The 5' region of the human transferrin gene: structure and potential  
 RT regulatory sites.";  
 RL Nucleic Acids Res. 14:8692-8692(1986).  
 RN [10]  
 RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.  
 RX MEDLINE=87192006; PubMed=3106157;  
 RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;  
 RT "The human transferrin gene: 5' region contains conserved sequences  
 RT which match the control elements regulated by heavy metals,  
 RT glucocorticoids and acute phase reaction.";  
 RL Gene 49:167-175(1986).  
 RN [11]  
 RP SEQUENCE OF 45-72 FROM N.A.  
 RX PubMed=10931525;  
 RA de Arriba Zarpa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,  
 RA Espinosa de los Monteros A., de Vellis J., Zakim M.M., Baron B.;  
 RT "Alternative splicing prevents transferrin secretion during  
 RT differentiation of a human oligodendrocyte cell line.";  
 RL J. Neurosci. Res. 61:388-395(2000).  
 RN [12]  
 RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF\*C2.  
 RC TISSUE=Brain;  
 RX MEDLINE=97418135; PubMed=9272172;  
 RA Namekata K., Oyama F., Imagawa M., Ihara Y.;  
 RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf  
 RT C1 or Tf C2 variant.";  
 RL Hum. Genet. 100:457-458(1997).  
 RN [13]  
 RP SEQUENCE OF 564-624 FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=96007936; PubMed=7498159;  
 RA Kovalyov L.S., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,  
 RA Erebova E.S., Egorov T.A., Musalyanov A.K.;  
 RT "The major protein expression profile and two-dimensional protein  
 RT database of human heart.";  
 RL Electrophoresis 16:1160-1169(1995).  
 RN [16]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=82222166; PubMed=6953407;  
 RA McGilivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,  
 RA Lineback-Zins J., Brew K.;  
 RT "The complete amino acid sequence of human serum transferrin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).  
 RN [17]  
 RP MUTAGENESIS.  
 RX MEDLINE=92031536; PubMed=1932003;  
 RA Woodworth R.C., Mason A.B., Funk W.D., McGilivray R.T.A.;  
 RT "Expression and initial characterization of five site-directed  
 RT mutants of the N-terminal half-molecule of human transferrin.";  
 RL Biochemistry 30:10824-10829(1991).  
 RN [18]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.  
 RX MEDLINE=98272865; PubMed=9609885;  
 RA McGilivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,  
 RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,  
 RA Woodworth R.C., Brayer G.D., Baker E.N.;  
 RT "Two high-resolution crystal structures of the recombinant N-lobe of  
 RT human transferrin reveal a structural change implicated in iron  
 RT release.";  
 RL Biochemistry 37:7919-7928(1998).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.  
 RX MEDLINE=98434369; PubMed=9760232;  
 RA Jeffrey P.D., Bewley M.C., McGilivray R.T.A., Mason A.B.,  
 RA Woodworth R.C., Baker E.N.;  
 RT "Ligand-induced conformational change in transferrins: crystal  
 RT structure of the open form of the N-terminal half-molecule of human  
 RT transferrin.";  
 RL Biochemistry 37:13978-13986(1998).  
 RN [20]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.  
 RX MEDLINE=99155227; PubMed=10029548;

RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,  
 RA Mason A.B., Woodworth R.C., Baker E.N., MacCallum R.A.,  
 RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe  
 RT of human transferrin expressed in *Pichia pastoris* is folded correctly  
 RL but is glycosylated on serine-32.";  
 RL Biochemistry 38:2535-2541(1999).  
 RN [21]  
 RN VARIANT SER-142.  
 RP MEDLINE=98019079; PubMed=9358047;  
 RA Evans P., Kemp J.;  
 RT "Exon/intron structure of the human transferrin receptor gene.";  
 RL Gene 199:133-131(1997).  
 RN [22]  
 RP VARIANT GLU-646.  
 RX PubMed=9803271;  
 RA Pang H., Koda Y., Soejima M., Kimura H.;  
 RT "Identification of a mutation (A1879G) of transferrin from cDNA  
 RT prepared from peripheral blood cells.";  
 RL Ann. Hum. Genet. 62:271-274(1998).  
 RN [23]  
 RP VARIANTS SER-277; SER-589 AND GLU-671, AND CHARACTERIZATION OF  
 RP VARIANT SER-277.  
 RX MEDLINE=21560268; PubMed=11703331;  
 RA Lee P.L., Halloran C., Trevino R., Pelitti V., Beutler E.;  
 RT "Human transferrin G277S mutation: a risk factor for iron deficiency  
 RT anaemia.";  
 RL Br. J. Haematol. 115:329-333(2001).  
 RN [24]  
 RP VARIANTS SER-277 AND SER-589.  
 RX MEDLINE=21558434; PubMed=11702220;  
 RA Douabin-Gicquel V., Soriano N., Ferran H., Wojcik F., Palierne E.,  
 RA Tamam S., Jovelin T., Mokie A.F., Le Gall J.-Y., David V., Mosser J.;  
 RT "Identification of 96 single nucleotide polymorphisms in eight genes  
 RT involved in iron metabolism: efficiency of bioinformatic extraction  
 RT compared with a systematic sequencing approach.";  
 RL Hum. Genet. 109:393-401(2001).

Query Match 70.6%; Score 36; DB 1; Length 698;  
 Best Local Similarity 55.6%; Pred. No. 24;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GPPVSCIKR 9  
 |||||  
 Db 53 GPSVACVK 61

RESULT 11  
 ID TRFE BOVIN STANDARD; PRT; 704 AA.  
 AC Q29443;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal  
 DE binding globulin).  
 GN TP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI TaxID=9913;  
 RN [1]\_TaxID=9913;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96132861; PubMed=8557646;  
 RA Retzer M.D., Kabani A., Button L.L., Yu R.H., Schryvers A.B.;  
 RT "Production and characterization of chimeric transferrins for the  
 RT determination of the binding domains for bacterial transferrin  
 RT receptors.";  
 RL J. Biol. Chem. 271:1166-1173(1996).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE. IT IS RESPONSIBLE FOR THE

CC TRANSPORT OF IRON FROM SITES OF ABSORPTION AND HEME DEGRADATION  
 CC TO THOSE OF STORAGE AND UTILIZATION. SERUM TRANSFERRIN MAY ALSO  
 CC HAVE A FURTHER ROLE IN STIMULATING CELL PROLIFERATION.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- TISSUE SPECIFICITY: Expressed in liver; secreted in plasma.  
 CC -!- DOMAIN: COMPOSED OF TWO HOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
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 CC -----  
 CC EMBL; U02564; AAA96735.1; -.  
 DR HSP; P19134; ITFD.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN\_1; 1.  
 DR PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN\_3; 1.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19 BY SIMILARITY.  
 FT CHAIN 20 704 SEROTRANSFERRIN.  
 FT REPEAT 20 359 1.  
 FT REPEAT 360 704 2.  
 FT DISULFID 28 66 BY SIMILARITY.  
 FT DISULFID 38 57 BY SIMILARITY.  
 FT DISULFID 136 192 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 179 200 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 362 622 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.  
 FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 699 BY SIMILARITY.  
 FT DISULFID 441 663 BY SIMILARITY.  
 FT DISULFID 473 549 BY SIMILARITY.  
 FT DISULFID 497 690 BY SIMILARITY.  
 FT DISULFID 507 521 BY SIMILARITY.  
 FT DISULFID 518 532 BY SIMILARITY.  
 FT DISULFID 589 603 BY SIMILARITY.  
 FT DISULFID 641 646 BY SIMILARITY.  
 FT METAL 81 81 IRON 1 (BY SIMILARITY).  
 FT METAL 113 113 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 449 449 IRON 2 (BY SIMILARITY).  
 FT METAL 543 543 IRON 2 (BY SIMILARITY).  
 FT METAL 611 611 IRON 2 (BY SIMILARITY).  
 FT BINDING 142 142 ANION (POTENTIAL).  
 FT BINDING 479 479 ANION (POTENTIAL).  
 FT CARBOHYD 514 514 N-LINKED (GLCNAC... (POTENTIAL).  
 SQ SEQUENCE 704 AA; 77753 MW; D87BB2AFE46C708D CRC64;

Query Match 70.6%; Score 36; DB 1; Length 704;  
 Best Local Similarity 66.7%; Pred. No. 24;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 GPPVSCIKR 9  
 |||||  
 Db 52 GPPVSCVK 60

RESULT 12

```

FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT METAL 140 140 ANION (BY SIMILARITY).
FT BINDING 482 482 ANION (BY SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)
FT CONFLICT 261 261 F -> S (IN REF. 2).
FT CONFLICT 304 304 G -> A (IN REF. 2).
FT CONFLICT 330 330 S -> P (IN REF. 2).
FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
FT CONFLICT 506 506 L -> F (IN REF. 2).
FT CONFLICT 609 609 A -> P (IN REF. 2).
FT CONFLICT 642 642 R -> Q (IN REF. 2).
SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 708;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9
|||:::
DB 50 GPSVTCVKK 58

RESULT 13
IN44 MOUSE STANDARD; PRT; 186 AA.
ID IN44 MOUSE
AC P07351;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interferon alpha-4 precursor.
GN IFNA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215516; PubMed=2987811;
RA Kelly K.A., Pitha P.M.;
RT "Characterization of a mouse interferon gene locus 1. Isolation of a
RT cluster of four alpha interferon genes.";
RL Nucleic Acids Res. 13:805-823(1985).
CC -1- FUNCTION. PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X01973; CAA26005.1; -.
CC PIR; B23087; IVM5A4.
CC DR HSSP; P01563; 2HIE.
CC DR MGD; MGI:107664; Ifna4.
CC DR InterPro; IPR000471; Interferon_abd.
CC DR Pfam; PF00143; Interferon_1.
CC DR PRINTS; PR00266; INTERFERONAB.
CC DR ProDom; PD000550; Interferon_abd; 1.

```



DR SMART: SM00076; IFabD; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Antiviral; Multigene family; Glycoprotein; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 186 INTERFERON ALPHA-4.  
 FT DISULFID 25 123 BY SIMILARITY.  
 FT DISULFID 53 158 BY SIMILARITY.  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (PROBABLE).  
 SQ SEQUENCE 186 AA; 21524 MW; FCS464D473741794 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 186;  
 Best Local Similarity 71.4%; Pred. No. 10;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCIK 8  
 DB 49 PPLSCLK 55

RESULT 14  
 LORI HUMAN  
 ID LORI HUMAN STANDARD; PRT; 316 AA.  
 AC P23450;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lorcin.  
 GN LOR OR LRN.

OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Forebrain;  
 RX MEDLINE=91177926; PubMed=2007607;  
 RA Hohl D., Mehrel T., Licht U., Turner M.L., Roop D.R., Steinert P.M.;  
 RT "Characterization of human lorcin. Structure and function of a new  
 class of epidermal cell envelope proteins.";  
 RL J. Biol. Chem. 266:6626-6636(1991).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92398173; PubMed=1355480;  
 RA Yoneda K., Hohl D., McBride O.W., Wang M., Cehrs K.U., Idler W.W.,  
 RT Steinert P.M.;  
 RA "The human lorcin gene.";  
 RL J. Biol. Chem. 267:18060-18066(1992).  
 CC -1- FUNCTION: MAJOR KERATINOCYTE CELL ENVELOPE PROTEIN.  
 CC -1- SUBUNIT: MONOMERS ARE CROSSLINKED BY DISULFIDE AND N-(GAMMA-  
 CC GLUTAMYL) LYSINE ISODIPEPTIDE BONDS.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; M61120; AAA36180.1; -.  
 CC EMBL; M94077; AAA36181.1; -.  
 DR PIR; A38743; A38743.  
 DR Genew; HGNC:6663; LOR.  
 DR MIM; 152445; -.  
 KW Keratinization.

SQ SEQUENCE 316 AA; 26033 MW; 100FEC52F9ACE8E CRC64;

Query Match 68.6%; Score 35; DB 1; Length 316;  
 Best Local Similarity 71.4%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIK 8  
 DB 49 PPLSCLK 55

Db 12 PPVDCVK 18  
 RESULT 15  
 ID\_V2 HPV54 STANDARD; PRT; 367 AA.  
 AC Q81021;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Regulatory protein E2.  
 GN E2.  
 OS Human papillomavirus type 54.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=37113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Delius H.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.  
 CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGGT-3') PRESENT  
 CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER  
 CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE/S POSITION  
 CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS  
 CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION  
 CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA  
 CC REPLICATION.  
 CC -1- SUBUNIT: BINDS DNA AS A DIMER.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.

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CC EMBL; U37488; AAA79190.1; -.  
 DR HSSP; P17383; LDHM.  
 DR InterPro; IPR000427; E2\_C.  
 DR InterPro; IPR001866; E2\_N.  
 DR Pfam; PF00508; E2\_N; 1.  
 DR Pfam; PF00511; E2\_C; 1.  
 DR ProDom; PD000672; E2\_C; 1.  
 DR ProDom; PD000678; E2\_N; 1.  
 KW Early protein; Transcription regulation; Activator; DNA-binding;  
 KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.  
 SQ SEQUENCE 367 AA; 41690 MW; 77FB3CF03EDD674 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 367;  
 Best Local Similarity 62.5%; Pred. No. 20;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPVSCIK 9  
 DB 105 PPTGCLKR 112

Search completed: February 21, 2003, 07:51:46  
 Job time : 5.90698 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 16.2558 Seconds  
(without alignments)  
114.078 Million cell updates/sec

Title: US-09-743-107b-101  
Perfect score: 51  
Sequence: 1 GPPVSCIKR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organalle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rendent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	711	4	Q8TCD2
2	46	90.2	1245	4	Q9ULD2
3	39	76.5	1521	4	Q9UQD2
4	39	76.5	1924	4	Q9UPY3
5	38	74.5	244	10	Q94JK1
6	38	74.5	823	4	Q8WY18
7	37	72.5	41	5	Q9NGM7
8	37	72.5	148	11	Q5CR70
9	37	72.5	148	11	Q8R2R7
10	37	72.5	184	4	Q9P0D5
11	37	72.5	223	5	Q9VJM2
12	37	72.5	499	5	Q960G4
13	37	72.5	576	15	Q55604
14	37	72.5	591	5	Q866U1
15	37	72.5	691	5	Q9SR88
16	37	72.5	704	5	Q9VVT8

17	37	72.5	718	4	Q05850
18	37	72.5	3895	12	Q9PZ97
19	36	70.6	64	6	Q97942
20	36	70.6	189	16	Q8UGB5
21	36	70.6	396	12	Q58869
22	36	70.6	551	4	Q9UK95
23	36	70.6	723	5	O16775
24	36	70.6	3989	12	Q9PYB2
25	35	68.6	203	4	Q9NUD3
26	35	68.6	204	4	Q9GZP1
27	35	68.6	282	16	Q9ZCN7
28	35	68.6	331	5	O16367
29	35	68.6	338	4	O60354
30	35	68.6	439	10	Q9SWS2
31	35	68.6	443	10	Q9SWS3
32	35	68.6	450	10	Q9LME9
33	35	68.6	466	5	Q8T282
34	35	68.6	479	10	Q9LMF0
35	35	68.6	481	10	Q8W4G1
36	35	68.6	481	10	Q9ZWJ3
37	35	68.6	487	10	Q9LME8
38	35	68.6	489	10	Q9M9E7
39	35	68.6	489	10	Q9SK82
40	35	68.6	830	10	Q9ZT05
41	34	66.7	121	16	Q8YC23
42	34	66.7	123	5	Q8WRN9
43	34	66.7	132	3	Q8XOD2
44	34	66.7	197	16	Q98AK3
45	34	66.7	243	5	Q8TIY6
					Q05850, homo sapien
					Q9PZ97, pestivirius
					Q97942, capra hircu
					Q8UGB5, agrobacteri
					Q58869, gallid herp
					Q9UK95, homo sapien
					O16775, caenorhabdi
					Q9PYB2, pestivirius
					Q9NUD3, homo sapien
					Q9GZP1, homo sapien
					Q9ZCN7, rickettsia
					O16367, caenorhabdi
					O60354, homo sapien
					Q9SWS2, glycine max
					Q9SWS3, glycine max
					Q9LME9, aradidopsis
					Q8T282, dictyostelli
					Q9LMF0, aradidopsis
					Q8W4G1, aradidopsis
					Q9ZWJ3, aradidopsis
					Q9LME8, aradidopsis
					Q9M9E7, aradidopsis
					Q9SK82, aradidopsis
					Q9ZT06, aradidopsis
					Q8YC23, bruceella me
					Q8WRN9, litopenaeus
					Q8XOD2, nitospora
					Q98AK3, rhizobium 1
					Q8TIY6, dictyostelli

## ALIGNMENTS

RESULT 1  
Q8TCD2 PRELIMINARY; PRT; 711 AA.  
ID Q8TCD2 PRELIMINARY; PRT; 711 AA.  
AC Q8TCD2; 2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC22347, AAH2347.1; -  
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7E5097C45FAF CRC64;

Query Match 100.0%; Score 51; DB 4; Length 711;  
Best Local Similarity 100.0%; Pred. No. 0.072; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;  
Qy 1 GPPVSCIKR 9  
Db 51 GPPVSCIKR 59  
RESULT 2  
Q9ULD2 PRELIMINARY; PRT; 1245 AA.  
ID Q9ULD2 PRELIMINARY; PRT; 1245 AA.  
AC Q9ULD2;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE KIAA1288 protein (Fragment).  
GN KIAA1288.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
RN NCBI\_TaxID=9606;  
[1]

RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=20039619; PubMed=10574462;

RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;  
RT Prediction of the coding sequences of unidentified human genes. XV.  
RT The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro.;  
RL DNA Res. 6:337-345(1999).  
DR EMBL; AB033114; BAA86602.1; .  
FT NON TER 1  
SQ SEQUENCE 1245 AA; 138533 MW; AB446CC36AC30ED4 CRC64;

Query Match 90.2%; Score 46; DB 4; Length 1245;

Best Local Similarity 77.8%; Pred. No. 1.1;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 9  
|||||:::

DB 705 GPPVSCILRR 713  
|||||:::

RESULT 3

ID Q9UQ02 PRELIMINARY; PRT; 1521 AA.  
AC Q9UQ02

DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE KIAA0928 protein (Fragment).

GN KIAA0928

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN NCBI\_TaxID=9606;  
[1]

RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=99246063; PubMed=10231032;

RA Nagase T., Ishikawa K., Suyama H., Kikuno R., Hirose M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RT Prediction of the coding sequences of unidentified human genes. XIII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro.;  
RL DNA Res. 6:63-70(1999).  
DR EMBL; AB023145; BAA76772.1; .  
DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001159; DS\_RBD.

DR InterPro; IPR005034; DUF283.

DR InterPro; IPR000532; Glucagon.

DR InterPro; IPR001650; Helicase\_C.

DR InterPro; IPR003100; PAZ.

DR InterPro; IPR000999; RNase\_3.

DR Pfam; PF00035; GERM; 1.

DR Pfam; PF03368; DUF283; 1.

DR Pfam; PF02170; PAZ; 1.

DR Pfam; PF00636; Ribonuclease\_3; 2.

DR PRINTS; PR00275; GLUCAGON.

DR SMART; SM00358; DSRM; 1.

DR SMART; SM00490; HELICC; 1.

DR SMART; SM00535; RIBOC; 2.

DR PROSITE; PS00137; DS\_RBD; 1.

DR PROSITE; PS00517; RNASE\_3; 1; 1.

DR PROSITE; PS0142; RNASE\_3; 2; 2.

KW ATP-binding; Helicase.

FT NON TER 1

SQ SEQUENCE 1521 AA; 172818 MW; D566C31E65081C19 CRC64;

Query Match

76.5%; Score 39; DB 4; Length 1521;

Best Local Similarity 62.5%; Pred. No. 33;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 8  
|||||:::

DB 280 GPPMSCVR 287  
|||||:::

RESULT 4

ID Q9UPY3 PRELIMINARY; PRT; 1924 AA.

AC Q9UPY3

DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Helicase-MOI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN NCBI\_TaxID=9606;  
[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20246304; PubMed=10786632;

RA Matsuda S., Ichigotani Y., Okuda T., Irimura T., Nakatsugawa S.,  
RA Hamaguchi M.;

RT "Molecular cloning and characterization of a novel human gene (HERNA)  
which encodes a putative RNA-helicase.";  
RL Biochim. Biophys. Acta 1490:163-169(2000).

DR EMBL; AB028449; BAA78691.1; .

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001159; DS\_RBD.

DR InterPro; IPR005034; DUF283.

DR InterPro; IPR001650; Helicase\_C.

DR InterPro; IPR003100; PAZ.

DR InterPro; IPR000999; RNase\_3.

DR Pfam; PF00270; DEAD; 1.

DR Pfam; PF00035; GERM; 1.

DR Pfam; PF03368; DUF283; 1.

DR Pfam; PF00271; Helicase\_C; 1.

DR Pfam; PF02170; PAZ; 1.

DR Pfam; PF00636; Ribonuclease\_3; 2.

DR SMART; SM00487; DEXDC; 1.

DR SMART; SM00358; DSRM; 1.

DR SMART; SM00490; HELICC; 1.

DR SMART; SM00535; RIBOC; 2.

DR PROSITE; PS00137; DS\_RBD; 1.

DR PROSITE; PS00517; RNASE\_3; 1; 1.

DR PROSITE; PS0142; RNASE\_3; 2; 2.

KW ATP-binding; Helicase.

SQ SEQUENCE 1924 AA; 218811 MW; BA5D3020995B5F89 CRC64;

Query Match 76.5%; Score 39; DB 4; Length 1924;

Best Local Similarity 62.5%; Pred. No. 41;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSCIKR 8  
|||||:::

DB 683 GPPMSCVR 690  
|||||:::

RESULT 5

ID Q94JK1 PRELIMINARY; PRT; 244 AA.

AC Q94JK1

DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE P0434B04.22 protein.

GN P0434B04.22

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzae; Oryza.

OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
 RT clone: P0434B04.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF002540; BAB44001.1; -;  
 DR InterPro: IPR003902; GCM motif.  
 SQ SEQUENCE 244 AA; 27252 MW; 445B5CEBA06064FA CRC64;

Query Match 74.5%; Score 38; DB 10; Length 244;  
 Best Local Similarity 55.6%; Pred. No. 11;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPPVSCIKR 9  
 ||| |||  
 Db 81 GPPAACLR 89

RESULT 6  
 ID Q8W18 PRELIMINARY; PRT; 823 AA.  
 AC Q8W18;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE MSTP018.  
 GN MST018.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=AORTA;  
 RA Xu Y.Y., Sun L.Z., Wu Q.Y., Liu Y.Q., Liu B., Zhao B., Wang X.Y.,  
 RA Song L., Ye J.J., Sheng H., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,  
 RA Sun Y.H., Jiang X.X., Zhao X.W., Liu S., Liu L.S., Ding J.P.,  
 RA Gao R.L., Qiang B.Q., Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF111799; AAL39001.1; -;  
 DR InterPro: IPR000413; Integrin\_alpha.  
 DR Pfam: PF01839; FG-GAP; 4.  
 DR PRINTS; PRO1185; INTEGRINA.  
 DR SMART; SM00191; Int\_alpha; 4.  
 SQ SEQUENCE 823 AA; 92672 MW; DE4E78079DCD4925 CRC64;

Query Match 74.5%; Score 38; DB 4; Length 823;  
 Best Local Similarity 77.8%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPPVSCIKR 9  
 ||| |||  
 Db 618 GPPFSCIFR 626

RESULT 7  
 ID Q9NGM7 PRELIMINARY; PRT; 41 AA.  
 AC Q9NGM7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Myosin-like protein MipB (Fragment).  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=20440049; PubMed=10984411;  
 RA Sirotkin V., Seipel S., Krendel M., Bonder E.M.;  
 RT "Characterization of sea urchin unconventional myosins and analysis of  
 RT their patterns of expression during early embryogenesis.";  
 RL MCL. Reprod. Dev. 57:111-126(2000).  
 DR EMBL; AF247514; AAF1726.1; -;  
 FT NON TER 1  
 FT NON TER 41  
 SQ SEQUENCE 41 AA; 4693 MW; 54CD7BF60626D599 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 41;  
 Best Local Similarity 75.0%; Pred. No. 3.6;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PPVSCIKR 9  
 ||| |||  
 Db 25 PPVECIER 32

RESULT 8  
 ID Q9CR70 PRELIMINARY; PRT; 148 AA.  
 AC Q9CR70;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE 1110049G11Rik protein.  
 GN 1110049G11Rik.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=EMBRYO, AND KIDNEY;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Hono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK004210; BAB23222.1; -;  
 DR EMBL; AK002539; BAB22174.1; -;  
 DR MGD; MGI:1913442; 1110049G11Rik.  
 SQ SEQUENCE 148 AA; 15824 MW; 17C28868F7E064CC CRC64;

Query Match 72.5%; Score 37; DB 11; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSC 6  
 ||| |||  
 Db 143 GPPVSC 148

RESULT 9  
 ID Q8R2R7 PRELIMINARY; PRT; 148 AA.

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AC Q8R2R7;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1110049G11 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=1090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027305; AAB27305.1; -.
SQ SEQUENCE 148 AA; 15957 MW; 19DDIC9A5FE31D83 CRC64;

Query Match 72.5%; Score 37; DB 11; Length 148;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPPVSC 6
Db 143 GPPVSC 148

RESULT 10
Q9P0D5 PRELIMINARY; PRT; 184 AA.
ID Q9P0D5
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE HSPC101 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.X., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from c334+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161364; AAF28924.1; -.
FT NON_TER 1
SQ SEQUENCE 184 AA; 20857 MW; 05D569073D334F5D CRC64;

Query Match 72.5%; Score 37; DB 4; Length 184;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPVSCIKR 9
Db 149 PPLNCLKR 156

RESULT 11
Q9VJM2 PRELIMINARY; PRT; 223 AA.
ID Q9VJM2
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE BG:DS04095.2 protein.
GN BG:DS04095.2 OR CG4892.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod W.F., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AB003650; AAF53502.1; -.
DR FlyBase; FBgn0028884; BG:DS04095.2.
SQ SEQUENCE 223 AA; 25233 MW; C72A405F7BEF981E CRC64;

Query Match 72.5%; Score 37; DB 5; Length 223;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPVSCIKR 9
Db 25 PPMSCIKR 32

RESULT 12
Q960G4 PRELIMINARY; PRT; 499 AA.
ID Q960G4
OC Q960G4
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE SD02971P.
GN CG3961.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

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RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY052074; RAK93498.1; -  
 DR Flybase: FBgn0036821; CG3961.  
 DR InterPro: IPR000873; AMP-Bind.  
 DR Pfam: PF00501; AMP-binding; 1.  
 DR PROSITE: PS00455; AMP BINDING; UNKNOWN 1.  
 SQ SEQUENCE 499 AA; 55517 MW; CAD577FC98873421 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 499;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSC 6  
 |||||  
 Db 283 GPPVSC 288

## RESULT 13

Q65604 PRELIMINARY; PRT; 576 AA.

ID Q65604  
 AC Q65604  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE Surface envelope protein (Fragment).  
 OS Bovine immunodeficiency-like virus.  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11647;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FL491;  
 RX MEDLINE=96010247; PubMed=7571444;  
 RA Suarez D.L., Whetstone C.A.;  
 RT "Identification of hypervariable and conserved regions in the surface  
 envelope gene in the bovine lentivirus.";  
 RL Virology 212:728-733 (1995).  
 DR EMBL: L43127; AAC42157.1; -  
 KW Envelope protein.  
 FT NON TER 576  
 SQ SEQUENCE 576 AA; 64168 MW; 5690B759A5FC51C7 CRC64;

Query Match 72.5%; Score 37; DB 15; Length 576;  
 Best Local Similarity 55.6%; Pred. No. 36;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPPVSCIKR 9  
 |||||  
 Db 475 GRPISCVK 483

## RESULT 14

Q966U1 PRELIMINARY; PRT; 591 AA.

ID Q966U1  
 AC Q966U1  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Transcription factor ems/emx.  
 GN HREMx.  
 OS Halocynthia roretzi (sea squirt).  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Pyruidae; Halocynthia.  
 OX NCBI\_TaxID=7729;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21359114; PubMed=11465524;  
 RA Oda I., Saiga H.;  
 RT "Hremx, the ascidian homologue of ems/emx, is expressed in the  
 anterior and posterior-lateral epidermis but not in the central  
 nervous system during embryogenesis.";  
 RL Dev. Genes Evol. 211:291-298 (2001).  
 DR EMBL: AB055144; BAB61733.1; -

DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00045; homeobox; 1.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; UNKNOWN 1.  
 DR PROSITE: PSS0071; HOMEBOX\_2; 1.  
 SQ SEQUENCE 591 AA; 65943 MW; 11E74AA8237CC53B CRC64;

Query Match 72.5%; Score 37; DB 5; Length 591;  
 Best Local Similarity 85.7%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPPVSCI 7  
 |||||  
 Db 326 GPPTSCI 332

## RESULT 15

Q95R88 PRELIMINARY; PRT; 691 AA.

ID Q95R88  
 AC Q95R88  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE S001152p.  
 GN CG3961.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY061568; AAL29116.1; -  
 DR Flybase: FBgn0036821; CG3961.  
 DR InterPro: IPR000873; AMP-bind.  
 DR Pfam: PF00501; AMP-binding; 1.  
 DR PROSITE: PS00455; AMP BINDING; UNKNOWN 1.  
 SQ SEQUENCE 691 AA; 77346 MW; FBB4EAB69BC7C6B9 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 691;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPPVSC 6  
 |||||  
 Db 475 GPPVSC 480

Search completed: February 21, 2003, 08:00:52  
 Job time : 18.2558 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56,502 Million cell updates/sec

Title: US-09-743-107B-47  
Perfect score: 71  
Sequence: 1 CFQWQNRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum Match 100%  
Listing first 45 summaries

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23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	12	21	AAV78038 Human lactoferrin
2	71	100.0	12	21	AAV78046 Human lactoferrin
3	71	100.0	12	21	AAV78047 Human lactoferrin
4	71	100.0	13	21	AAV78037 Human lactoferrin
5	71	100.0	13	21	AAV78048 Human lactoferrin
6	71	100.0	13	21	AAV78049 Human lactoferrin
7	71	100.0	14	21	AAV78036 Human lactoferrin
8	71	100.0	14	21	AAV78050 Human lactoferrin
9	71	100.0	14	21	AAV78051 Human lactoferrin
10	71	100.0	15	17	AAV98554 Peptide for anti-u

11	71	100.0	15	21	AAV78035 Human lactoferrin
12	71	100.0	15	21	AAV78062 Human lactoferrin
13	71	100.0	15	21	AAV78063 Human lactoferrin
14	71	100.0	16	21	AAV78031 Human lactoferrin
15	71	100.0	16	21	AAV78064 Human lactoferrin
16	71	100.0	16	21	AAV78065 Human lactoferrin
17	71	100.0	17	21	AAV78034 Human lactoferrin
18	71	100.0	17	21	AAV78066 Human lactoferrin
19	71	100.0	17	21	AAV78067 Human lactoferrin
20	71	100.0	18	15	AAV69352 Human lactoferrin
21	71	100.0	18	17	AAV13397 Advanced glycosylase
22	71	100.0	18	21	AAV78033 Human lactoferrin
23	71	100.0	19	21	AAV68867 Amino acid sequenc
24	71	100.0	19	21	AAV78032 Human lactoferrin
25	71	100.0	20	13	AAV21810 Anti microbial pep
26	71	100.0	20	14	AAV44841 Lactoferrin-relate
27	71	100.0	20	15	AAV48530 Lactoferrin derive
28	71	100.0	20	15	AAV48531 Lactoferrin derive
29	71	100.0	20	15	AAV57461 Lactoferrin derive
30	71	100.0	20	15	AAV57462 Lactoferrin derive
31	71	100.0	20	16	AAV84698 Bovine lactoferrin
32	71	100.0	20	16	AAV84699 Bovine lactoferrin
33	71	100.0	20	16	AAV80263 Anti-parasitic lac
34	71	100.0	20	16	AAV80264 Anti-parasitic lac
35	71	100.0	20	17	AAV98553 Peptide for anti-u
36	71	100.0	20	17	AAV98552 Lactoferrin-derive
37	71	100.0	20	17	AAV91852 Lactoferrin-derive
38	71	100.0	20	17	AAV90607 Lactoferrin-derive
39	71	100.0	20	17	AAV87621 Lactoferrin-derive
40	71	100.0	20	17	AAV87622 Lactoferrin-derive
41	71	100.0	20	18	AAV26150 Lactoferrin derive
42	71	100.0	20	18	AAV14036 Anti-parasitic pep
43	71	100.0	20	19	AAV70310 Thrombus formation
44	71	100.0	20	19	AAV53224 Lactoferrin hydrol
45	71	100.0	20	19	AAV53225 Lactoferrin hydrol

#### ALIGNMENTS

RESULT 1  
AAV78038  
ID AAV78038 standard; Peptide; 12 AA.  
XX AAV78038;  
AC AAV78038;  
XX  
XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:38.  
DE Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; candida infection; fungicidal;  
KW bactericidal; preservative.  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200001730-A1.  
XX  
XX 13-JAN-2000.  
XX  
XX 06-JUL-1999; 99WO-SE01230.  
XX  
XX 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX  
XX (ASCI-) A+ SCI INVEST AB.  
XX  
XX Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;  
PI WPI; 2000-147388/13.  
DR

XX New peptides used for treatment and prevention of infections, -  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX  
XX  
XX Sequence 12 AA;  
SQ

Query Match 100.0%; Score 71; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12  
DB |||||  
1 CFQWQRNMRKVR 12

RESULT 2  
AAY78046  
ID AAY78046 standard; Peptide; 12 AA.  
XX  
AC AAY78046;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:46.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
DR WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections, -  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 15; Page 35; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX  
XX  
XX Sequence 12 AA;  
SQ

Query Match 100.0%; Score 71; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12  
DB |||||  
1 CFQWQRNMRKVR 12

RESULT 3  
AAY78047  
ID AAY78047 standard; Peptide; 12 AA.  
XX  
AC AAY78047;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:47.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
DR WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections, -  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 18; Page 73; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human



CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 12 AA;  
 SQ Query Match 100.0%; Score 71; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12  
 DB 1 CFQWQNRMRKVR 12

RESULT 4  
 AAY78037  
 ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;  
 SQ Query Match 100.0%; Score 71; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12  
 DB 2 CFQWQNRMRKVR 13

RESULT 5  
 AAY78048  
 ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;

XX Query Match 100.0%; Score 71; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12  
 DB 2 CFQWQNNRKVR 13

## RESULT 6

AAAY78049  
 ID AAY78049 standard; Peptide; 13 AA.

XX AC AAY78049;  
 XX DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.  
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PS Claim 18; Page 74; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 71; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12  
 DB 2 CFQWQNNRKVR 13

## RESULT 7

AAAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:36.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.  
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PS Claim 12; Page 69; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 71; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12  
 DB 3 CFQWQNNRKVR 14

## RESULT 8

AAAY78050  
 ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:50.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 PD  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PS Claim 15; Page 75; 102pp; English.  
 XX  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 XX SQ Sequence 14 AA;  
 Query Match 100.0%; Score 71; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMRKVR 12  
 Db 3 CFQWQRNMRKVR 14  
 RESULT 9  
 AAY78051  
 ID AAY78051 standard; Peptide; 14 AA.  
 XX  
 AC AAY78051;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT  
 XX Human lactoferrin derived peptide SEQ ID NO:51.  
 DE  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 XX Homo sapiens.

OS Synthetic.  
 XX WO200001730-A1.  
 PN  
 XX 13-JAN-2000.  
 PD  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PS Claim 18; Page 75; 102pp; English.  
 XX  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 XX SQ Sequence 14 AA;  
 Query Match 100.0%; Score 71; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMRKVR 12  
 Db 3 CFQWQRNMRKVR 14  
 RESULT 10  
 AAR98554  
 ID AAR98554 standard; Peptide; 15 AA.  
 XX  
 AC AAR98554;  
 XX  
 XX 12-NOV-1996 (first entry)  
 DT  
 XX Peptide for anti-ulcer agent.  
 DE  
 XX anti-ulcer agent; low toxicity; stable; heat-resistant.  
 KW  
 XX Synthetic.  
 OS  
 XX JF08143468-A.  
 PN  
 XX 04-JUN-1996.  
 PD  
 XX 17-NOV-1994; 94JP-0283869.  
 PP  
 XX 17-NOV-1994; 94JP-0283869.  
 PR  
 XX (MORG ) MORINAGA MILK IND CO LTD.  
 PA



Query Match 100.0%; Score 71; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12  
 DB 4 CFQWQNNRKR 15

RESULT 13  
 AAY78063  
 ID AAY78063 standard; Peptide; 15 AA.  
 AC AAY78063;  
 DT 25-APR-2000 (first entry)  
 DE Human lactoferrin derived peptide SEQ ID NO:63.

Human; lactoferrin; modification; infection; inflammation; tumour;  
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 urinary tract infection; colitis; Candida infection; fungicidal;  
 bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.  
 PN WO200001730-A1.  
 PD 13-JAN-2000.  
 PF 06-JUL-1999; 99WO-SE01230.  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 DR WPI; 2000-147388/13.  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 Claim 18; Page 81; 102pp; English.

AAV78001 to AAV78100 represent peptides having sequences based on human  
 lactoferrin. The peptides are taken up in the intestine through  
 binding to specific lactoferrin receptors and are then transported  
 through the circulation. A medicinal product of the peptide or fragment  
 can be used for treating and/or prevention of infections (such as  
 urinary tract infections, colitis, and Candida infection on a mucosal  
 membrane), inflammations and/or tumours. The peptides can also be used  
 in food stuffs such as infant formula food. The peptides are also  
 fungicidal and bactericidal and may also be used as preservatives.  
 Even though native human lactoferrin have been shown to have desired  
 anti-inflammatory anti-infectious and anti-tumoural properties they  
 cannot be used clinically on a broad basis because of high production  
 costs. Therefore, provision of peptides based on lactoferrin would  
 enable them to be used for the same purposes as lactoferrin at lower  
 cost.

QY 1 CFQWQNNRKR 12  
 DB 4 CFQWQNNRKR 15

Query Match 100.0%; Score 71; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 AAY78031  
 ID AAY78031 standard; Peptide; 16 AA.  
 AC AAY78031;  
 DT 25-APR-2000 (first entry)  
 DE Human lactoferrin derived peptide SEQ ID NO:31.

Human; lactoferrin; modification; infection; inflammation; tumour;  
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 urinary tract infection; colitis; Candida infection; fungicidal;  
 bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.  
 PN WO200001730-A1.  
 PD 13-JAN-2000.  
 PF 06-JUL-1999; 99WO-SE01230.  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 DR WPI; 2000-147388/13.  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 Claim 11; Page 68; 102pp; English.

AAV78001 to AAV78100 represent peptides having sequences based on human  
 lactoferrin. The peptides are taken up in the intestine through  
 binding to specific lactoferrin receptors and are then transported  
 through the circulation. A medicinal product of the peptide or fragment  
 can be used for treating and/or prevention of infections (such as  
 urinary tract infections, colitis, and Candida infection on a mucosal  
 membrane), inflammations and/or tumours. The peptides can also be used  
 in food stuffs such as infant formula food. The peptides are also  
 fungicidal and bactericidal and may also be used as preservatives.  
 Even though native human lactoferrin have been shown to have desired  
 anti-inflammatory anti-infectious and anti-tumoural properties they  
 cannot be used clinically on a broad basis because of high production  
 costs. Therefore, provision of peptides based on lactoferrin would  
 enable them to be used for the same purposes as lactoferrin at lower  
 cost.

QY 1 CFQWQNNRKR 12  
 DB 5 CFQWQNNRKR 16

Query Match 100.0%; Score 71; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
 AAY78064  
 ID AAY78064 standard; Peptide; 16 AA.  
 AC AAY78064;

Tue Dec 9 06:51:21 2003

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XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:64.
DE
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX
XX 13-JAN-2000.
PD
XX 06-JUL-1999; 99WO-SE01230.
PF
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
FA
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food -
XX
XX Claim 15; Page 82; 102pp; English.
XX
XX AAV78001 to AAV78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
XX through the circulation. A medicinal product of the peptide or fragment
XX can be used for treating and/or prevention of infections (such as
XX urinary tract infections, colitis, and Candida infection on a mucosal
XX membrane), inflammations and/or tumours. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also
XX fungicidal and bactericidal and may also be used as preservatives.
XX Even though native human lactoferrin have been shown to have desired
XX anti-inflammatory anti-infectious and anti-tumoural properties they
XX cannot be used clinically on a broad basis because of high production
XX costs. Therefore, provision of peptides based on lactoferrin would
XX enable them to be used for the same purposes as lactoferrin at lower
XX cost.
XX
XX SQ Sequence 16 AA;
XX
XX Query Match 100.0%; Score 71; DB 21; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CFQWQENMKYR 12
XX |||||
XX Db 5 CFQWQENMKYR 16
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Search completed: February 21, 2003, 07:37:10  
Job time : 29.35 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-47

Perfect score: 71

Sequence: 1 CFQQRNKKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	71	100.0	18	1	US-08-204-487-3
2	71	100.0	18	2	US-08-485-948-8
3	71	100.0	18	2	US-08-628-380-8
4	71	100.0	18	2	US-08-475-055-8
5	71	100.0	20	1	US-07-755-161A-3
6	71	100.0	20	1	US-07-891-174-3
7	71	100.0	20	1	US-08-204-487-1
8	71	100.0	20	1	US-08-256-771-24
9	71	100.0	20	1	US-08-256-771-25
10	71	100.0	20	1	US-08-381-984-24
11	71	100.0	20	1	US-08-381-984-25
12	71	100.0	22	4	US-09-508-734-4
13	71	100.0	24	4	US-09-508-734-6
14	71	100.0	25	1	US-07-755-161A-10
15	71	100.0	25	1	US-07-891-174-10
16	71	100.0	25	1	US-08-204-487-7
17	71	100.0	29	4	US-09-508-734-8
18	71	100.0	36	1	US-07-755-161A-8
19	71	100.0	36	1	US-07-891-174-8
20	71	100.0	36	1	US-08-256-771-30
21	71	100.0	36	1	US-08-381-984-29
22	71	100.0	47	2	US-08-464-182A-6
23	71	100.0	47	2	US-08-406-271-6
24	71	100.0	50	2	US-08-693-274A-7
25	71	100.0	52	4	US-09-017-043A-3
26	71	100.0	53	2	US-08-464-182A-5
27	71	100.0	53	2	US-08-406-271-5

28 71 100.0 54 2 US-08-464-182A-2  
29 71 100.0 54 2 US-08-406-271-2  
30 71 100.0 694 3 US-08-724-586-2  
31 71 100.0 694 4 US-09-421-632-2  
32 71 100.0 694 4 US-09-932-190-2  
33 71 100.0 705 2 US-08-655-640-2  
34 71 100.0 708 2 US-08-655-640-4  
35 71 100.0 711 1 US-08-154-019-4  
36 71 100.0 711 1 US-08-461-333-4  
37 71 100.0 711 3 US-08-464-167-4  
38 71 100.0 711 3 US-09-158-313-4  
39 71 100.0 711 4 US-08-476-798-4  
40 68 95.8 711 1 US-08-145-681-2  
41 68 95.8 711 1 US-08-250-308-2  
42 68 95.8 711 1 US-08-453-703-2  
43 68 95.8 711 2 US-08-456-106-2  
44 68 95.8 711 3 US-08-456-108-2  
45 68 95.8 711 4 US-09-265-577-2

## ALIGNMENTS

RESULT 1  
US-08-204-487-3  
Sequence 3, Application US/08204487  
Patent No. 5565425  
GENERAL INFORMATION:  
APPLICANT: YAMAMOTO, NAOKI  
APPLICANT: NAKASHIMA, HIDEKI  
APPLICANT: MOSUCHI, WATARU  
APPLICANT: TANAKA, SHIGEKI  
APPLICANT: DOSAKO, SHUN'ICHI  
APPLICANT: KAWASAKI, YOSHIHIRO  
APPLICANT: UCHIDA, TOSHIKI  
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
TITLE OF INVENTION: INHIBITORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
ADDRESSEE: THIBEAULT  
STREET: 53 STATE STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,487  
FILING DATE: 02-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPELL, PAULA A.  
REGISTRATION NUMBER: 32,503  
REFERENCE/DOCKET NUMBER: RJN-019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..18  
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37) "  
US-08-204-487-3

Query Match 100.0%; Score 71; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.1e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12  
| | | | | | | | | | | | | | | | | |  
DB 1 CFQWQNRKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882

GENERAL INFORMATION:

APPLICANT: YONG MING LI

APPLICANT: HELEN VLASSARA

APPLICANT: ANTHONY CERAMI

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,948

FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/488,217

FILING DATE: JUNE 7, 1995

APPLICATION NUMBER: 08/418,642

FILING DATE: APRIL 7, 1995

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 947-1-008A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

DESCRIPTION: LF-Cl, 8-25

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 100.0%; Score 71; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.1e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12  
| | | | | | | | | | | | | | | | | |  
DB 1 CFQWQNRKVR 12

## RESULT 3

US-08-628-380-8

; Sequence 8, Application US/08628380

; Patent No. 5891341

GENERAL INFORMATION:

APPLICANT: LI, YONG MING

APPLICANT: VLASSARA, HELEN

APPLICANT: CERAMI, ANTHONY

TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,380

FILING DATE: April 4, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/418,642

FILING DATE: APRIL 7, 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 947-1-008 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

DESCRIPTION: LF-Cl, 8-25

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 100.0%; Score 71; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.1e-06;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12

| | | | | | | | | | | | | | | | | |

DB 1 CFQWQNRKVR 12

## RESULT 4

US-08-475-055-8

; Sequence 8, Application US/08475055

; Patent No. 5962245

GENERAL INFORMATION:

APPLICANT: YONG MING LI

APPLICANT: HELEN VLASSARA

APPLICANT: ANTHONY CERAMI

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

NUMBER OF SEQUENCES: 9



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/489,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 100.0%; Score 71; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWRNNRKVR 12
Db 1 CFQWRNNRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 100.0%; Score 71; DB 1; Length 20;
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Best Local Similarity 100.0%, Pred. No. 7.9e-06; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 CFQWQRNMRKV 12
    |||||
Db 2 CFQWQRNMRKV 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Porack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

; LOCATION: 2
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 19"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 19
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 2"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-3

Query Match 100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKV 12
    |||||
Db 2 CFQWQRNMRKV 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGRAKI
; APPLICANT: DOSAKO, SHUN-ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: EFN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
```

```
TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: 1..20
;   OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
;   OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match      100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
   |||||
Db 2 CFQWRNMRKVR 13

RESULT 8
US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; PRODUCT: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are linked by
; OTHER INFORMATION: disulfide bond"
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US-08-256-771-24

Query Match      100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
   |||||
Db 2 CFQWRNMRKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; PRODUCT: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25

Query Match      100.0%; Score 71; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
   |||||
Db 2 CFQWRNMRKVR 13

RESULT 10
US-08-381-984-24
```

; Sequence 24, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,984  
; FILING DATE: April 11, 1995  
; CLASSIFICATION: 252  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "cysteine residues as well as  
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
; US-08-381-984-24  
  
Query Match 100.0%; Score 71; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CFQWQRNRKVR 12  
Db 2 CFQWQRNRKVR 13  
  
RESULT 11  
US-08-381-984-25  
; Sequence 25, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,984  
; FILING DATE: April 11, 1995  
; CLASSIFICATION: 252  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
; US-08-381-984-25  
  
Query Match 100.0%; Score 71; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CFQWQRNRKVR 12  
Db 2 CFQWQRNRKVR 13  
  
RESULT 12  
US-09-508-734-4  
; Sequence 4, Application US/09508734  
; Patent No. 6423509  
; GENERAL INFORMATION:  
; APPLICANT: Samyang Genex Corporation  
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
; TITLE OF INVENTION: useful microorganism thereof  
; FILE REFERENCE: PA/SYG/00139  
; CURRENT APPLICATION NUMBER: US/09/508,734  
; CURRENT FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: PCT/KR99/00373  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: KR1998-29351  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 4



RESULT 15  
US-07-891-174-10  
; Sequence 10, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 4  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 21"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 21

; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 4"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
; US-07-891-174-10  
; Query Match 100.0%; Score 71; DB 1; Length 25;  
; Best Local Similarity 100.0%; Pred. No. 9.8e-06;  
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; QY 1 CFQWQNRMKVR 12  
; Db 4 CFQWQNRMKVR 15  
; Search completed: February 21, 2003, 07:50:32  
; Job time : 9.7 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107B-47  
Perfect score: 71  
Sequence: 1 CFQWQNNRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	15	9	US-09-798-869-2
2	71	100.0	25	9	US-09-798-869-20
3	71	100.0	694	9	US-10-023-096-2
4	63	88.7	15	9	US-09-798-869-6
5	54	76.1	15	9	US-09-798-869-3
6	54	76.1	25	9	US-09-798-869-23
7	46	64.8	15	9	US-09-798-869-7
8	45	63.4	15	9	US-09-798-869-4
9	45	63.4	25	9	US-09-798-869-22
10	42	59.2	15	9	US-09-798-869-8
11	42	59.2	15	9	US-09-798-869-29
12	42	59.2	15	9	US-09-798-869-30
13	38	53.5	489	9	US-09-888-320-2
14	37	52.1	21	10	US-09-864-761-47985
15	37	52.1	747	9	US-10-066-500-58
16	37	52.1	747	9	US-10-002-796-58
17	37	52.1	747	9	US-10-066-273-58
18	37	52.1	747	9	US-10-066-494-58
19	36	50.7	86	9	US-09-738-626-5715

20	36	50.7	209	10	US-09-904-536-8	Sequence 8, Appli
21	36	50.7	209	10	US-09-904-536-9	Sequence 9, Appli
22	36	50.7	209	10	US-09-904-536-11	Sequence 11, Appli
23	36	50.7	209	10	US-09-904-536-12	Sequence 12, Appli
24	36	50.7	209	10	US-09-904-536-13	Sequence 13, Appli
25	36	50.7	209	10	US-09-904-536-14	Sequence 14, Appli
26	36	50.7	209	10	US-09-904-536-15	Sequence 15, Appli
27	36	50.7	209	10	US-09-904-536-16	Sequence 16, Appli
28	36	50.7	209	10	US-09-904-536-17	Sequence 17, Appli
29	36	50.7	209	10	US-09-904-536-18	Sequence 18, Appli
30	36	50.7	212	10	US-09-904-536-10	Sequence 10, Appli
31	36	50.7	235	9	US-10-035-449-6	Sequence 6, Appli
32	36	50.7	235	10	US-09-448-378-1	Sequence 1, Appli
33	36	50.7	235	10	US-09-983-806-6	Sequence 1, Appli
34	36	50.7	235	10	US-09-904-536-1	Sequence 1, Appli
35	36	50.7	338	9	US-09-978-295A-119	Sequence 119, App
36	36	50.7	338	9	US-09-978-697-119	Sequence 119, App
37	36	50.7	338	9	US-09-978-192A-119	Sequence 119, App
38	36	50.7	338	9	US-09-999-832A-119	Sequence 119, App
39	36	50.7	338	9	US-09-978-189-119	Sequence 119, App
40	36	50.7	553	9	US-09-796-753-14	Sequence 14, App
41	36	50.7	553	10	US-09-981-649A-6	Sequence 6, Appli
42	36	50.7	553	10	US-09-981-649A-24	Sequence 24, Appli
43	36	50.7	554	10	US-09-981-649A-30	Sequence 30, Appli
44	36	50.7	554	10	US-09-981-649A-32	Sequence 32, Appli
45	36	50.7	559	10	US-09-981-649A-28	Sequence 28, Appli

## ALIGNMENTS

RESULT 1  
US-09-798-869-2  
; Sequence 2, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/SE99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 100.0%; Score 71; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12  
|||  
Db 3 CFQWQNNRKVR 14

RESULT 2  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match      100.0%; Score 71; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFQWQRNMRKVR 12
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DB      3 CFQWQRNMRKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2
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Query Match      100.0%; Score 71; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFQWQRNMRKVR 12
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DB      22 CFQWQRNMRKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6
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Query Match      88.7%; Score 63; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CFQWQRNMRKVR 12
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DB      3 CFQWQRNMRKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3
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Query Match      76.1%; Score 54; DB 9; Length 15;
Best Local Similarity 72.7%; Pred. No. 0.0041;
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Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKRV 11  
|:|||||  
Db 3 CYQWQRMKRL 13

RESULT 6  
US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 76.1%; Score 54; DB 9; Length 25;  
Best Local Similarity 72.7%; Pred. No. 0.0066;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKRV 11  
|:|||||  
Db 3 CYQWQRMKRL 13

RESULT 7  
US-09-798-869-7  
; Sequence 7, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-7

Query Match 64.8%; Score 46; DB 9; Length 15;  
Best Local Similarity 63.8%; Pred. No. 0.0086;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRMKRV 11  
|:|||||  
Db 3 CYQWQRMKRL 13

RESULT 8  
US-09-798-869-4  
; Sequence 4, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-4

Query Match 63.4%; Score 45; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.13;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMKRV 11  
|:|||||  
Db 3 CLRQWQRMKRV 13

RESULT 9  
US-09-798-869-22  
; Sequence 22, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-22

Query Match 63.4%; Score 45; DB 9; Length 25;  
Best Local Similarity 63.6%; Pred. No. 0.2;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMKRV 11  
|:|||||  
Db 3 CLRQWQRMKRV 13

RESULT 10  
US-09-798-869-8  
; Sequence 8, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine  
; OTHER INFORMATION: sequence)  
US-09-798-869-8

Query Match 59.2%; Score 42; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.39; Indels 3; Gaps 0;  
Matches 7; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

QY 1 CFQWQRMNRKV 11  
| : | | | |  
DB 3 CLRWQWEMRKV 13

RESULT 11  
US-09-798-869-29  
; Sequence 29, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-29

Query Match 59.2%; Score 42; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.39; Indels 2; Gaps 0;  
Matches 6; Conservative 3; Mismatches 3; Indels 2; Gaps 0;

QY 1 CFQWQRMNRKV 11  
| : | | | |  
DB 3 CFQWQWEMRKV 13

RESULT 12  
US-09-798-869-30

; Sequence 30, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-30

Query Match 59.2%; Score 42; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.39; Indels 2; Gaps 0;  
Matches 6; Conservative 3; Mismatches 3; Indels 2; Gaps 0;

QY 1 CFQWQRMNRKV 11  
| : | | | |  
DB 3 CFQWQWEMRKV 13

RESULT 13  
US-09-888-320-2  
; Sequence 2, Application US/09888320  
; Publication No. US20030013090A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry III, Clifton E.  
; APPLICANT: DeBarber, Andrea E.  
; APPLICANT: Mdululi, Khisimuzi  
; APPLICANT: Bekker, Linda-Gail  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis  
; FILE REFERENCE: 015280-413100US  
; CURRENT APPLICATION NUMBER: US/09/888,320  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/214,187  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)  
US-09-888-320-2

Query Match 53.5%; Score 38; DB 9; Length 489;  
Best Local Similarity 54.5%; Pred. No. 47; Indels 3; Gaps 0;  
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

QY 1 CFQWQRMNRKV 11  
| : | | | |  
DB 253 CQWFRMRMRKM 263

RESULT 14  
US-09-864-761-47985  
; Sequence 47985, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:

```

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47985
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL096701.14
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06
; US-09-864-761-47985
;
; Query Match 52.1%; Score 37; DB 10; Length 21;
; Best Local Similarity 83.3%; Pred. No. 3.6;
; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 CFQWR 6
; Db 16 CFQWR 21
;
; RESULT 15
; US-10-066-500-58
; Sequence 58, Application US/10066500
; Patent No. US2002017165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066840
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/095998
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/097000
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/099601
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
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;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099812  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/100858  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: 60/101922  
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;; PRIOR APPLICATION NUMBER: 60/106032  
;; PRIOR FILING DATE: 1998-10-28  
;; PRIOR APPLICATION NUMBER: 60/109304  
;; PRIOR FILING DATE: 1998-11-20  
;; PRIOR APPLICATION NUMBER: 60/125778  
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;; PRIOR APPLICATION NUMBER: 60/145070  
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;; PRIOR FILING DATE: 1999-12-07  
;; PRIOR APPLICATION NUMBER: 08/918874  
;; PRIOR FILING DATE: 1997-08-26  
;; PRIOR APPLICATION NUMBER: 08/933821  
;; PRIOR FILING DATE: 1997-09-19  
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;; PRIOR FILING DATE: 1997-10-29  
;; PRIOR APPLICATION NUMBER: 09/114844  
;; PRIOR FILING DATE: 1998-07-14  
;; PRIOR APPLICATION NUMBER: 09/136801  
;; PRIOR FILING DATE: 1998-08-19  
;; PRIOR APPLICATION NUMBER: 09/136804  
;; PRIOR FILING DATE: 1998-08-19  
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;; PRIOR APPLICATION NUMBER: 09/158342  
;; PRIOR FILING DATE: 1998-09-21  
;; PRIOR APPLICATION NUMBER: 09/180997  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 09/202088  
;; PRIOR FILING DATE: 1998-12-08  
;; PRIOR APPLICATION NUMBER: 09/254311  
;; PRIOR FILING DATE: 1999-03-03  
;; PRIOR APPLICATION NUMBER: 09/254460  
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;; PRIOR FILING DATE: 1999-10-18  
;; PRIOR APPLICATION NUMBER: 09/403297  
;; PRIOR FILING DATE: 1999-10-18  
;; PRIOR APPLICATION NUMBER: 09/423741  
;; PRIOR FILING DATE: 1999-11-10  
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;; PRIOR FILING DATE: 1999-11-12

;; PRIOR APPLICATION NUMBER: 09/522342  
;; PRIOR FILING DATE: 2000-03-09  
;; PRIOR APPLICATION NUMBER: 09/548815  
;; PRIOR FILING DATE: 2000-04-13  
;; PRIOR APPLICATION NUMBER: 09/664610  
;; PRIOR FILING DATE: 2000-09-18  
;; PRIOR APPLICATION NUMBER: 09/665350  
;; PRIOR FILING DATE: 2000-09-18  
;; PRIOR APPLICATION NUMBER: 09/709238  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 09/767609  
;; PRIOR FILING DATE: 2001-01-22  
;; PRIOR APPLICATION NUMBER: 09/802706  
;; PRIOR FILING DATE: 2001-03-09  
;; PRIOR APPLICATION NUMBER: 09/808689  
;; PRIOR FILING DATE: 2001-03-14  
;; PRIOR APPLICATION NUMBER: 09/866028  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 09/870574  
;; PRIOR FILING DATE: 2001-05-30  
;; PRIOR APPLICATION NUMBER: 09/872035  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: 09/886342  
;; PRIOR FILING DATE: 2001-06-19  
;; PRIOR APPLICATION NUMBER: PCT/US98/14552  
;; PRIOR FILING DATE: 1998-07-14  
;; PRIOR APPLICATION NUMBER: PCT/US98/18824  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: PCT/US98/19093  
;; PRIOR FILING DATE: 1998-09-14  
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;; PRIOR APPLICATION NUMBER: PCT/US98/19437  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: PCT/US98/24855  
;; PRIOR FILING DATE: 1998-11-20  
;; PRIOR APPLICATION NUMBER: PCT/US98/25108  
;; PRIOR FILING DATE: 1998-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US98/25190  
;; PRIOR FILING DATE: 1998-11-25  
;; PRIOR APPLICATION NUMBER: PCT/US99/05028  
;; PRIOR FILING DATE: 1999-03-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: 1999-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/20111  
;; PRIOR FILING DATE: 1999-09-01  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 52.1%; Score 37; DB 9; Length 747;  
Best Local Similarity 45.5%; Pred. No. 1e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFOWQRMKRV 11  
Db 311 CVRWQINSRI 321

Search completed: February 21, 2003, 08:08:02  
Job time : 10.55 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-47

Perfect score: 71

Sequence: 1 CFQQRNMRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	711	1	TFHUL
2	54	76.1	708	2	lactotransferrin p
3	51	71.8	33	2	lactoferrin - goat
4	45	63.4	707	1	lactoferrin - sheep
5	44	62.0	4568	2	lactoferrin precursor
6	42	59.2	298	2	dynamin beta heavy
7	42	59.2	511	2	hypothetical prote
8	41	57.7	275	2	hypothetical prote
9	41	57.7	932	2	hypothetical prote
10	40	56.3	681	2	hypothetical prote
11	39	54.9	594	2	hypothetical prote
12	38	53.5	121	2	hypothetical prote
13	38	53.5	205	2	26S proteasome SU
14	38	53.5	274	2	apolipoprotein B-1
15	38	53.5	282	2	hypothetical prote
16	38	53.5	489	2	probable monooxyge
17	38	53.5	515	2	probable cytochrom
18	38	53.5	543	2	cytochrome P450 ho
19	38	53.5	1432	2	trichonayalin like
20	37	52.1	206	2	pyridoxamine 5'-ph
21	37	52.1	206	2	pyridoxamine 5'-ph
22	37	52.1	208	2	probable pyridoxam
23	37	52.1	222	2	hypothetical prote
24	37	52.1	275	1	interleukin-2 rece
25	37	52.1	275	1	interleukin-2 rece
26	37	52.1	289	2	33.3K hypothetical
27	37	52.1	361	2	hypothetical prote
28	37	52.1	365	2	MHC class I histoc
29	37	52.1	500	2	protein kinase (BC

## RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence, revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S741

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: Placenta

A:Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70: 989-993, 1987  
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A;Reference number: S07160; MUID:88001031; PMID:3477300  
 A;Accession: S07160  
 A;Molecule type: mRNA  
 A;Residues: 436-487, 'A', 489-711 <RAD>  
 A;Cross-references: EMBL:M18642; NID:G186815; PID:G386855  
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51: 3037-3043, 1991  
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A;Reference number: A61169; MUID:91235214; PMID:1674448  
 A;Accession: A61169  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 3-701, 'SWKPVN' <PAN>  
 A;Experimental source: normal breast tissue  
 R;Merz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;  
 Eur. J. Biochem. 145: 659-666, 1984  
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other  
 A;Reference number: A31000; MUID:85076667; PMID:6510420  
 A;Accession: A31000  
 A;Molecule type: protein  
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4  
 A;Note: this is the final paper in a series  
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.  
 Eur. J. Biochem. 241: 303-308, 1996  
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affinity  
 A;Reference number: S74119; MUID:97054624; PMID:8899921  
 A;Accession: S74119  
 A;Molecule type: protein  
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A;Experimental source: neutrophil granulocytes  
 C;Genetics:  
 A;Gene: GDB:150210  
 A;Cross-references: GDB:119368; OMIM:150210  
 A;Map position: 3q21-3q23  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein; iron binding; milk  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-711/Product: lactotransferrin #status experimental <MAT>  
 F;21-356/Domain: transferrin repeat homology <TRH1>  
 F;360-699/Domain: transferrin repeat homology <TRH2>  
 F;29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e  
 F;157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;368-400, 378-391, 425-706, 747-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat  
 Query Match 100.0%; Score 71; DB 1; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFQWQRMNRKV 12  
 DB 39 CFQWQRMNRKV 50  
 RESULT 2  
 JC2323  
 lactoferrin - goat  
 C;Species: Capra aegagrus hircus (domestic goat)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C;Accession: JC2323  
 R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.  
 Biochem. Biophys. Res. Commun. 203: 1324-1332, 1994  
 A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus  
 A;Reference number: JC2323; MUID:94380047; PMID:8093048  
 A;Accession: JC2323  
 A;Molecule type: mRNA  
 A;Residues: 1-708 <LEP>  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein  
 F;359-696/Domain: transferrin repeat homology <TRH2>  
 F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.1%; Score 54; DB 2; Length 708;  
 Best Local Similarity 72.7%; Pred. No. 0.14;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKV 11  
 DB 38 CYQWQRMNRKV 48

## RESULT 3

S52107

lactoferrin - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 14-Jul-1995 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997

A;Accession: S52107

R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

Biochim. Biophys. Acta 1243: 25-32, 1995

A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a

A;Reference number: S52107; MUID:95127729; PMID:7827104

A;Accession: S52107

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-33 &lt;QIA&gt;

C;Superfamily: transferrin; transferrin repeat homology

C;Keywords: duplication

Query Match 71.8%; Score 51; DB 2; Length 33;

Best Local Similarity 63.6%; Pred. No. 0.023;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKV 11

DB 19 CYQWQRMNRKV 29

## RESULT 4

A28438

lactoferrin precursor - mouse

N;Alternate names: lactotransferrin

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

A;Accession: A28438; A41205

R;Pentecost, B.T.; Teng, C.T.

J. Biol. Chem. 262: 10314-10319, 1987

A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre

A;Reference number: A92596; MUID:87280033; PMID:3611056

A;Accession: A28438

A;Molecule type: mRNA

A;Residues: 3-707 &lt;PEN&gt;

A;Cross-references: EMBL:J03298

R;Liu, Y.; Teng, C.T.

J. Biol. Chem. 266: 21880-21895, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A;Reference number: A41205; MUID:92042099; PMID:1939212

A;Accession: A41205

A;Molecule type: DNA

A;Residues: 1-15 &lt;LIU&gt;

A;Cross-references: GB:M74778

C;Superfamily: transferrin; transferrin repeat homology

C;Keywords: duplication; glycoprotein

F;1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F;20-707/Product: lactotransferrin #status predicted &lt;MAT&gt;

F;358-695/Domain: transferrin repeat homology &lt;TRH2&gt;

F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.4%; Score 45; DB 1; Length 707;

Best Local Similarity 63.6%; Pred. No. 5.3;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKV 11

DB 37 CLRQWQRMNRKV 47

```

RESULT 5
T08030
dynein beta heavy chain - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C:Accession: T08030
R:Mitchell, D.R.; Brown, K.S.
J:Cell Sci. 107, 635-644, 1994
A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A:Reference number: Z16302; MUID:94274778; PMID:8006077
A:Accession: T08030
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4568 <MIT>
A:Cross-references: EMBL:U02963; NID:g409965; PIDN:AA19556.1; PID:g514215
A:Experimental source: strain 21gr
C:Genetics:
A:Gene: ODA4
A:Map position: IX
A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 359/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3892/3; 4240/3
C:Superfamily: dynein heavy chain, ciliary
C:Keywords: nucleotide binding; P-loop
F:1919-1926/Region: nucleotide-binding motif A (P-loop)
F:2202-2209/Region: nucleotide-binding motif A (P-loop)
F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 62.0%; Score 44; DB 2; Length 4568;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNRKVR 12
||||| : : :
Db 1852 CFQWQSLRVIQ 1863

RESULT 6
AD2346
hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AD2346
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2346
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA876022.1; PID:g17133459; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4323

Query Match 59.2%; Score 42; DB 2; Length 298;
Best Local Similarity 77.8%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRNRK 10
||||| : : :
Db 163 FHWQRNRK 171

RESULT 7
AB0858
hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi

```

```

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0858
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerthon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AB0858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
C:Genetics:
A:Gene: STY3070

Query Match 59.2%; Score 42; DB 2; Length 511;
Best Local Similarity 58.3%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQRNRKVR 12
||||| : : :
Db 350 CFQWQRNRKVR 361

RESULT 8
T22597
hypothetical protein F53H4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T22597
R:Dobson, R.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19587
A:Accession: T22597
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <WIL>
A:Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A:Experimental source: clone F53H4
C:Genetics:
A:Gene: CESP:F53H4.4
A:Map position: X
A:Introns: 67/1; 153/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 57.7%; Score 41; DB 2; Length 275;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRNRKVR 12
||||| : : :
Db 262 FQWQRNRKVR 272

RESULT 9
T28820
hypothetical protein F07C3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28820
R:Favella, A.; Gartung, S.
Submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid F07C3.
A:Reference number: Z20528
A:Accession: T28820
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-932 <FAV>
A:Cross-references: EMBL:U50308; PIDN:AA48001.1; GSPDB:GN00023; CESP:F07C3.1
A:Experimental source: strain Bristol N2; clone F07C3
C:Genetics:

```

AH3147  
 Hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C/Accession: AH3147  
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
 erage, G.; Gillet, W.; Grant, C.; Guentchner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 284, 2317-2323, 2001  
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A/Reference number: AB2577; PMID:11743193  
 A/Accession: AH3147  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-121 <KUR>  
 A/Cross-references: GB:AE008689; PID: AAL45598.1; PID: g17743317; GSPDB: GNC00187  
 A/Experimental source: strain C58 (Dupont)  
 C/Genetics:  
 A/Gene: Atu4804  
 A/Map position: linear chromosome

Query Match	53.5%;	Score 38;	DB 2;	Length 121;
Best Local Similarity	54.5%;	Pred. No. 16;		
Matches	6;	Conservative 1;	Mismatches 4;	Indels 0;
Gaps	0;			

QY 1 CFQWQNRKVV 11  
 DB 14 CLAWQRNRRV 24  
 |||||  
 |||||

RESULT 13  
 E90094  
 26S proteasome SU B5 [imported] - Guillardia theta nucleomorph  
 C/Species: nucleomorph Guillardia theta  
 C/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
 C/Accession: E90094  
 R/Doughlas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei  
 Nature 410, 1091-1096, 2001  
 A/Title: The highly reduced genome of an enslaved algal nucleus.  
 A/Reference number: A99082; MUID: 11323671; PMID: 11323671  
 A/Accession: E90094  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-205 <DOU>  
 A/Cross-references: GB:AF165818; NID: g13794510; PID: AAK39885.1; GSPDB: GNC00150  
 C/Genetics:  
 A/Gene: prsB5  
 A/Map position: 1  
 A/Gene: nucleomorph  
 C/Keywords: nucleomorph

Query Match	53.5%;	Score 38;	DB 2;	Length 205;
Best Local Similarity	62.5%;	Pred. No. 26;		
Matches	5;	Conservative 2;	Mismatches 1;	Indels 0;
Gaps	0;			

QY 1 CFQWQNRNM 8  
 DB 63 CFFWERNL 70  
 |||||  
 |||||

RESULT 14  
 B60950  
 apolipoprotein B-100 - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 31-Dec-1993 #sequence\_revision 09-Sep-1994 #text\_change 07-Oct-1994  
 C/Accession: B60950  
 F/Law, A.; Scott, J.  
 J. Lipid Res. 31, 1109-1120, 1990  
 A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
 A/Reference number: A60950; MUID: 90324804; PMID: 2373961



A;Accession: B60950  
 A;Molecule type: mRNA  
 A;Residues: 1-274 <LAW>  
 A;Note: authors translated the codon ATA for residue 8 as Val  
 C;Superfamily: apolipoprotein B  
 C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 53.5%; Score 38; DB 2; Length 274;  
 Best Local Similarity 66.7%; Pred. No. 35;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WQNRMRKV 12  
 | | | | |  
 DB 39 WDRNRKR 47

## RESULT 15

F90580  
 hypothetical protein MYPU\_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
 C;Species: Mycoplasma pulmonis  
 C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
 C;Accession: F90580  
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samsen, D.; Galisson, F.; Moszer, I.;  
 Nucleic Acids Res. 29, 2145-2153, 2001  
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
 A;Reference number: A99512; MUID:21267165; PMID:11353084  
 A;Accession: F90580  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-282 <KUR>  
 A;Cross-references: GB:AL445566; PID:G14089965; PIDN:CAC13723.1; GSPDB:GN00153  
 A;Experimental source: strain UAB CTIP  
 C;Genetics:  
 A;Gene: MYPU\_5500  
 A;Genetic code: SGC3

Query Match 53.5%; Score 38; DB 2; Length 282;  
 Best Local Similarity 50.0%; Pred. No. 36;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWRMRKV 11  
 | | | | |  
 DB 20 FAWQNNIKI 29

Search completed: February 21, 2003, 07:47:34  
 Job time : 12.65 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107B-47

Perfect score: 71

Sequence: 1 CFQWQNMRRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	71	100.0	711	1	TRFL_HUMAN
2	54	76.1	708	1	TRFL_CAMDR
3	54	76.1	708	1	TRFL_CAPHI
4	46	64.8	695	1	TRFL_HORSE
5	45	63.4	707	1	TRFL_MOUSE
6	44	62.0	4568	1	DYHB_CHLRE
7	39	54.9	292	1	NLA_DROME
8	38	53.5	146	1	RPOB_LIBAF
9	37	52.1	62	1	RL28_THETN
10	37	52.1	275	1	IL2A_BOVIN
11	37	52.1	275	1	IL2A_SHEEP
12	37	52.1	385	1	IA34_HUMAN
13	37	52.1	455	1	YKYL_CABEL
14	37	52.1	749	1	VP4_ROTGA
15	37	52.1	783	1	YNR2_CABEL
16	36	50.7	214	1	VIF_SIVS4
17	36	50.7	235	1	FL3L_HUMAN
18	36	50.7	306	1	BUB2_YEAST
19	36	50.7	1135	1	PHYC_SORBI
20	36	50.7	2671	1	IP3T_HUMAN
21	35	49.3	85	1	PMRD_SALTY
22	35	49.3	211	1	LOLB_VIBCH
23	35	49.3	238	1	YBM9_SCHPO
24	35	49.3	428	1	SVH_CHLMU
25	35	49.3	435	1	DCOR_PANRE
26	35	49.3	502	1	C911_ARATH
27	35	49.3	663	1	PD11_HUMAN
28	35	49.3	665	1	YL14_CABEL
29	35	49.3	708	1	TRFL_BUBBU
30	35	49.3	728	1	KDGL_ARATH
31	35	49.3	765	1	Y008_HUMAN
32	35	49.3	962	1	YBX7_SCHPO
33	34	47.9	60	1	RL28_BACST

34 34 47.9 62 1 RL28\_LISMO  
35 34 47.9 62 1 RL28\_STAAM  
36 34 47.9 152 1 YE83\_METJA  
37 34 47.9 215 1 VIF\_HV2SB  
38 34 47.9 215 1 VIF\_HV2ST  
39 34 47.9 246 1 Y495\_SYNY3  
40 34 47.9 267 1 Y125\_MYCCA  
41 34 47.9 272 1 IL2A\_HUMAN  
42 34 47.9 316 1 NORC\_CHLTR  
43 34 47.9 334 1 CATL\_MOUSE  
44 34 47.9 334 1 CATL\_RAT  
45 34 47.9 369 1 SP11\_MYXVL

Q92a12 listeria mo  
Q99up4 staphylococ  
Q58878 methanococc  
P24452 human immun  
P20878 human immun  
Q55185 synechocyst  
P53661 mycoplasma  
P01589 homo sapien  
O84281 chlamydia t  
P06797 mus musculu  
P07154 rattus norv  
P12393 myxoma viru

#### ALIGNMENTS

RESULT 1  
TRFL\_HUMAN  
ID TRFL\_HUMAN STANDARD; PRT; 711 AA.  
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;  
AC Q96KZ5;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;  
DE Lactoferrin B; Lactoferrin C]  
GN LTF OR LF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90384839; PubMed=2402455;  
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;  
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";  
RL Nucleic Acids Res. 18:5288-5288(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cho Y.Y.;  
RL Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Connely O.M.;  
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Liang Q., Jimenez-Flores R., Richardson T.;  
RL "Molecular cloning and sequence analysis of human lactoferrin.";  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Wei X., Han J., Rado T.A.;  
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA  
sequences.";  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cheng H., Chen X., Huan L.;  
RL "cDNA cloning and sequence analysis of human lactoferrin.";  
RN [7]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE=Mammary Gland.  
RX MEDLINE=9036549; PubMed=2374734;  
RA Powell M.J., Ogden J.E.;  
RT "Nucleotide sequence of human lactoferrin cDNA.";  
RL Nucleic Acids Res. 18:4013-4013(1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
Legrand D., Spik G., Montreuil J., Jolles P.;  
RT "Human lactotransferrin: amino acid sequence and structural  
comparisons with other transferrins.";  
RL Eur. J. Biochem. 145:659-666(1984).  
RN [10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
alignment of the cyanogen bromide fragments and characterization of  
N- and C-terminal domains.";  
RL Biochim. Biophys. Acta 670:243-254(1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
lactotransferrin.";  
RL FEBS Lett. 142:107-110(1982).  
RN [12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
expression of mRNA during normal and leukemic myelopoiesis.";  
RL Blood 70:989-993(1987).  
RN [13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
Gao L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
Sagripanti J.L.;  
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2555506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
and refinement at 2.8-A resolution.";  
RL J. Mol. Biol. 209:711-734(1989).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
resolution.";  
RL Acta Crystallogr. D 51:629-646(1995).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
binding properties and crystal structure of the histidine-  
253-->methionine mutant.";  
RL Biochemistry 36:341-346(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in Aspergillus  
awamori.";  
RL Acta Crystallogr. D 55:403-407(1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
and analysis of ligand-induced conformational change.";  
RL Acta Crystallogr. D 54:1319-1335(1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioid antagonist peptides derived  
from human lactoferrin.";  
RL Agric. Biol. Chem. 54:1803-1810(1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,  
El Matri L., Iwata F., Kasser-Kupfer M., Nagata M., Nakayasu K.,  
Hejtmancik J.F., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RL Mol. Vision 4:31-32(1998).  
RN [21]  
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
OF AN ANION, USUALLY BICARBONATE.  
CC  
RP FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST  
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC  
RP SUBUNIT: MONOMER.  
CC  
RP SUBCELLULAR LOCATION: Secreted.  
CC  
RP DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC  
RP SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC  
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CC  
EMBL; X53961; CAA37914.1; -  
EMBL; U07643; AAB60324.1; -  
EMBL; M93150; AAA36159.1; -  
EMBL; M83202; AAA59511.1; -  
EMBL; M83205; AAA58656.1; -  
EMBL; M18642; AAA86665.1; -  
EMBL; AF332168; AAC48753.1; -  
EMBL; BC015822; AAH15822.1; -  
EMBL; BC015823; AAH15823.1; -  
EMBL; M73700; AAA59479.1; -  
EMBL; X52941; CAA37116.1; -  
EMBL; U95626; AAB57795.1; -  
PIR; S11228; TFFUL.  
DR PDB; 1LCP; 31-AUG-94.  
DR PDB; 1LCT; 31-OCT-93.  
DR PDB; 1LFG; 31-JUL-94.  
DR PDB; 1LFH; 31-OCT-93.  
DR PDB; 1LFI; 31-OCT-93.  
DR PDB; 1LGB; 31-AUG-94.  
DR PDB; 1LGC; 31-AUG-94.  
DR PDB; 1BXA; 08-NOV-96.  
DR PDB; 1DSN; 08-VAR-96.  
DR PDB; 1HSE; 12-VAR-97.  
DR PDB; 1VFD; 21-APR-97.

Query Match 100.0%; Score 71; DS 1; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 4,9e-05; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0;

QY 1 CFQWQRNKKVR 12  
 |||||  
 Db 39 CFQWQRNKKVR 50

## RESULT 2

TRFL\_CAMDR STANDARD; PRT; 708 AA.  
 AC Q9TUMG; Q9MZS5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhah Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).

-!- SUBUNIT: MONOMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Secreted.

-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; AJ131674; CAB53387.1; -  
 EMBL; AF165879; AAF82241.1; -  
 DR HSP; 077811; IBI.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 Signal.  
 FT CHAIN 1 19 BY SIMILARITY.  
 FT REPEAT 20 708 LACTOTRANSFERRIN.  
 FT REPEAT 363 363 1.  
 FT REPEAT 364 708 2.  
 FT DISULFID 28 64 BY SIMILARITY.  
 FT DISULFID 38 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 76.1%; Score 54; DB 1; Length 708;

Best Local Similarity 75.0%; Pred. No. 0.048;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNKKVR 12  
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 Db 38 CAQWQRNKKVR 49

## RESULT 3

TRFL\_CAPHI STANDARD; PRT; 708 AA.  
 ID TRFL\_CAPHI  
 AC Q29477; Q29479;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (lactoferrin).  
 GN LTF.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=94380047; PubMed=9093048;  
 RA Le Provost F.; Nocart M.; Guerin G.; Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntenic group."  
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.



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FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 66 66
FT METAL 98 98
FT METAL 198 198
FT METAL 259 259
FT METAL 401 401
FT METAL 439 439
FT METAL 532 532
FT METAL 601 601
FT BINDING 127 127
FT BINDING 469 469
FT CARBOHYD 143 143
FT CARBOHYD 287 287
FT CARBOHYD 482 482
SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 64.8%; Score 46; DB 1; Length 695;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
Db 25 CAKQNRKVR 36

RESULT 5
TRFL MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactoferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Pentecost B.T., Teng C.T.;
RX MEDLINE=87280033; PubMed=3611056;
RT "Lactoferrin is the major estrogen inducible protein of mouse
   uterine secretions.";
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishita K.;
RX Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strauberg R.;
RX Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX Liu Y., Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
RL J. Biol. Chem. 266:21880-21885(1991).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION. USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; J03298; AAA40525.1; -  
EMBL; D8510; BAA13633.1; -  
EMBL; BC006904; AAA06904.1; -  
EMBL; M74778; AAA39427.1; -  
PIR; A28438; A28438.  
HSP; P02788; 1CB6.  
MGD; MGI:96837; Ltf.  
InterPro; IPR001156; Transferrin.  
Pfam; PF00405; transferrin; 2.  
PRINTS; PR00422; TRANSFERRIN.  
SMART; SM00094; TR\_FER; 2.  
PROSITE; PS00205; TRANSFERRIN\_1; 1.  
PROSITE; PS00206; TRANSFERRIN\_2; 2.  
PROSITE; PS00207; TRANSFERRIN\_3; 2.  
Signal.  
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
Signal.  
FT CHAIN 1 19 BY SIMILARITY.  
FT SIGNAL 20 707 LACTOTRANSFERRIN.  
FT REPEAT 20 357 1.  
FT REPEAT 358 707 2.  
FT DISULFID 27 63 BY SIMILARITY.  
FT DISULFID 37 54 BY SIMILARITY.  
FT DISULFID 133 216 BY SIMILARITY.  
FT DISULFID 175 191 BY SIMILARITY.  
FT DISULFID 188 199 BY SIMILARITY.  
FT DISULFID 249 263 BY SIMILARITY.  
FT DISULFID 366 398 BY SIMILARITY.  
FT DISULFID 376 389 BY SIMILARITY.  
FT DISULFID 423 702 BY SIMILARITY.  
FT DISULFID 443 665 BY SIMILARITY.  
FT DISULFID 475 550 BY SIMILARITY.  
FT DISULFID 499 693 BY SIMILARITY.  
FT DISULFID 509 523 BY SIMILARITY.  
FT DISULFID 520 533 BY SIMILARITY.  
FT DISULFID 591 605 BY SIMILARITY.  
FT DISULFID 643 648 BY SIMILARITY.  
FT METAL 78 78 IRON 1 (BY SIMILARITY).  
FT METAL 110 110 IRON 1 (BY SIMILARITY).  
FT METAL 210 210 IRON 1 (BY SIMILARITY).  
FT METAL 271 271 IRON 1 (BY SIMILARITY).  
FT METAL 413 413 IRON 2 (BY SIMILARITY).  
FT METAL 451 451 IRON 2 (BY SIMILARITY).  
FT METAL 544 544 IRON 2 (BY SIMILARITY).  
FT METAL 613 613 IRON 2 (BY SIMILARITY).  
FT BINDING 139 139 ANION (POTENTIAL).  
FT BINDING 481 481 ANION (POTENTIAL).  
FT CARBOHYD 118 118 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 494 494 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).  
FT CONFLICT 25 25 R -> Q (IN REF. 2).  
FT CONFLICT 82 82 M -> L (IN REF. 2).  
FT CONFLICT 359 359 S -> T (IN REF. 2).  
FT CONFLICT 382 382 A -> D (IN REF. 1).  
FT CONFLICT 449 449 E -> G (IN REF. 2).  
FT CONFLICT 529 529 L -> V (IN REF. 1).  
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;

Query Match 63.4%; Score 45; DB 1; Length 707;  
Best Local Similarity 63.6%; Pred. No. 1.8;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 11  
Db 37 CLRQWQNRKVR 47

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RESULT 6
DYHB CHLRE
ID QY9565; STANDARD; PRT; 4568 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=219F;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes";
RL J. Cell Sci. 107:635-644(1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC -----
DR EMBL; U02963; AAA19556.1; -
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3239 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 62.0%; Score 44; DB 1; Length 4568;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
Db 1852 CFQWQSLRYIQ 1863

RESULT 7
NLA DROME
ID NLA DROME
AC Q9XZL8; Q9V391; PRT; 292 AA.
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
GN NLA OR CG6072.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA McCormick A.V., Goldberg M.L.;
RT "Gene required for elongation of meiosis I spindle in Drosophila
females";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Dustin K., Evans G., Gabor C., Garg N.S., Gelbart W.M., Glasser K.,
Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hoskins D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mout R.D., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Smith H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
CC -----
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CC -----
DR EMBL; AF147700; AAD33987.1; -
DR EMBL; AE003712; AAF55285.1; -
DR FlyBae; FBgn0026629; nla.
SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

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Query Match      54.9%; Score 39; DB 1; Length 292;
Best Local Similarity 54.5%; Pred. No. 8.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12
DB 150 FQWLSFRRLR 160

RESULT 8
RPOB LIBAF
ID RPOB LIBAF STANDARD; PRT; 146 AA.
AC P41187; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (transcriptase
  beta chain) (RNA polymerase beta subunit) (fragment).
GN RPOB
OS Liberibacter africanus (Liberibacter africanus).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Candidatus Liberibacter.
OX NCBI_TaxID=34020;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nelepruit;
RA Planet P., Jagoueix S., Bove J.M., Garnier M.;
RT "Detection and characterization of the African Citrus Greening
  RT Liberibacter by amplification, cloning and sequencing of the rplKJL-
  RT rpoBC operon.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION. DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
  OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
  SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
  {RNA}(N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
  ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
  BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC
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CC
CC EMBL; U09675; AAA19557.1;
CC InterPro; IPR001572; RNA_pol_B.
CC Pfam; PF00562; RNA_pol_B_1.
CC PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
KW Transferase; Transcription; DNA-directed RNA polymerase.
FT NON_TER 146
SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD6GFD8943 CRC64;

Query Match      53.5%; Score 38; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 6.2;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 10
DB 10 CFQWQNRGARK 19

RESULT 9
RL28_THETN
ID RL28_THETN STANDARD; PRT; 62 AA.
AC Q8R9U1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE 50S ribosomal protein L28.
GN RPB4 OR TTE1495.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
  RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
  RA Tan H., Chen R., Wang J., Yu J., Yang H.;
  RA "A complete sequence of T. tengcongensis genome.";
  RL Genome Res. 12:689-700(2002).
CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL; AE013107; ANM24713.1;
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;

Query Match      52.1%; Score 37; DB 1; Length 62;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRKVR 12
DB 27 RWKPNRKVR 36

RESULT 10
IL2A_BOVIN
ID IL2A_BOVIN STANDARD; PRT; 275 AA.
AC P12342;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
  subunit) (P85) (TAC antigen) (CD25).
GN IL2RA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88212503; PubMed=2835311;
RA Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
  RA Reeves R., Magnuson J.A.;
  RA "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
  RL Immunology 63:603-610(1988).
CC [2]
CC SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=96116968; PubMed=8563178;
RA Yoo J., de Leon F.A., Stone R.T., Beattie C.W.;
  RA "Cloning and chromosomal assignment of the bovine interleukin-2
  receptor alpha (IL-2R alpha) gene.";
  RL Mamm. Genome 6:751-753(1995).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
  EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
  AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
  CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
  WITH A GAMMA CHAIN.
CC

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CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; M20818; AAA51414.1; -
CC  EMBL; U24226; AAC48487.1; -
CC  PIR; S07442; S07442.
CC  HSP; P01589; IILM.
CC  InterPro; IPR000436; Sush1_SCR_CCP.
CC  Pfam; PF00084; sush1; 2.
CC  SMART; SM00032; CCP; 2.
CC  Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sush1.
CC  SIGNAL 1 21
CC  CHAIN 22 243
CC  DOMAIN 22 243
CC  TRANSMEM 244 262
CC  DOMAIN 263 275
CC  DOMAIN 23 78
CC  DOMAIN 122 185
CC  DOMAIN 24 64
CC  DISULFID 24 64
CC  DISULFID 751 77
CC  DISULFID 123 168
CC  DISULFID 152 184
CC  DISULFID 80 80
CC  CARBOHYD 109 109
CC  CARBOHYD 109 109
CC  N-LINKED (GLCNAC...) (POTENTIAL).
CC  N-LINKED (GLCNAC...) (POTENTIAL).
CC  SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;
CC
CC  Query Match 52.1%; Score 37; DB 1; Length 275;
CC  Best Local Similarity 50.0%; Pred. No. 18;
CC  Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
CC
CC  QY 1 CFQWQRNMRKVR 12
CC  Db 261 CLTWQRNMRKVR 272
CC
CC  RESULT 11
CC  IL2A_SHEEP
CC  ID IL2A_SHEEP STANDARD; PRT; 275 AA.
CC  AC P26998;
CC  DT 01-AUG-1992 (Rel. 23, Created)
CC  DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC  DT 01-FEB-1996 (Rel. 33, Last annotation update)
CC  DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
CC  DE subunit) (P55) (TAC antigen) (CD25).
CC  GN IL2RA.
CC  OS Ovis aries (Sheep).
CC  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC  OC Bovidae; Caprinae; Ovis.
CC  OX NCBI_TaxID=9940;
CC  RN [1]
CC  RP SEQUENCE FROM N.A.
CC  RC TISSUE=T-cell;
CC  RA Verhagen A.A.;
CC  RL Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
CC  [2]
CC  SEQUENCE FROM N.A.
CC  RX MEDLINE=92241682; PubMed=1572550;
CC  RA Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;
CC  RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
CC  RT protein, CD25."
CC  RL Gene 113:283-284 (1992).
CC  CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC  CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC  CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE

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CC  AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC  CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC  WITH A GAMMA CHAIN.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC  -----
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CC  -----
CC  EMBL; Z11560; CAA77652.1; -
CC  EMBL; X60149; CAA42723.1; -
CC  EMBL; A9167; CAA01447.1; -
CC  PIR; S18910; S18910.
CC  PIR; S18899; S18899.
CC  PIR; JC1113; JC1113.
CC  HSP; P01589; IILM.
CC  InterPro; IPR000436; Sush1_SCR_CCP.
CC  Pfam; PF00084; sush1; 2.
CC  SMART; SM00032; CCP; 2.
CC  Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sush1.
CC  SIGNAL 1 21
CC  CHAIN 22 275
CC  DOMAIN 22 243
CC  TRANSMEM 244 262
CC  DOMAIN 263 275
CC  DOMAIN 122 185
CC  DOMAIN 24 64
CC  DISULFID 24 64
CC  DISULFID 751 77
CC  DISULFID 123 168
CC  DISULFID 152 184
CC  DISULFID 80 80
CC  CARBOHYD 166 166
CC  CONFLICT 166 166
CC  S -> T (IN REF. 2).
CC  SEQUENCE 275 AA; 30904 MW; 1101A2DE5A5A088 CRC64;
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CC  Best Local Similarity 50.0%; Pred. No. 18;
CC  Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
CC
CC  QY 1 CFQWQRNMRKVR 12
CC  Db 261 CLTWQRNMRKVR 272
CC
CC  RESULT 12
CC  IL2A_HUMAN
CC  ID IL2A_HUMAN STANDARD; PRT; 365 AA.
CC  AC P30453; P30454;
CC  DT 01-APR-1993 (Rel. 25, Created)
CC  DT 01-APR-1993 (Rel. 25, Last sequence update)
CC  DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC  DE HLA class I histocompatibility antigen, A*34(A-10) alpha chain
CC  DE precursor.
CC  GN HLA-A OR HLA-A.
CC  OS Homo sapiens (Human).
CC  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC  OX NCBI_TaxID=9606;
CC  RN [1]
CC  RP SEQUENCE FROM N.A. (A*3401/A*3402).
CC  RX MEDLINE=93056508; PubMed=1431115;
CC  RA Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
CC  RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
CC  RA Martell R.W., du Toit E.D., Parham P.;
CC  RT "Distinctive HLA-A,B antigens of black populations formed by
CC  RT interallelic conversion."
CC  RL J. Immunol. 149:3411-3415 (1992).
CC  [2]

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RP SEQUENCE FROM N.A. (A\*3401/A\*3402).  
 RX MEDLINE-93235211; PubMed-8475492;  
 RA Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,  
 RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzi-Erler M.L.,  
 RA du Toit E.D., Farham P.;  
 RT "Structural diversity in the HLA-A10 family of alleles: correlations  
 RT with serology.";  
 RL Tissue Antigens 41:72-80(1993).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC -!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A\*3401  
 CC (AW-34.1) AND A\*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF  
 CC A\*3401.  
 CC -----  
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 CC -----  
 DR EMBL; X61704; CAA43873.1; -;  
 DR EMBL; X61705; CAA43874.1; -;  
 DR PIR; S16767; S16767.  
 DR PIR; S16771; S16771.  
 DR HSP; Q19673; 1HSP.  
 DR MIM; 142800; -;  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGH1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.  
 FT SIGNAL 1 24  
 FT CHAIN 25 365  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 308  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 365  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 FT VARIANT 3 3  
 FT VARIANT 90 90  
 FT VARIANT 121 121  
 FT VARIANT 129 129  
 FT VARIANT 138 138  
 FT VARIANT 180 180  
 FT VARIANT 312 312  
 FT SEQUENCE 365 AA; 41055 MW; 063BF63E6E01F6 CRC64;  
 SQ  
 Query Match 52.1%; Score 37; DB 1; Length 365;  
 Best Local Similarity 66.7%; Pred. No. 24;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 WQNRKRVK 12  
 | | | | |  
 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 AW-34 (A-10) ALPHA CHAIN.  
 EXTRACELLULAR ALPHA-1.  
 EXTRACELLULAR ALPHA-2.  
 EXTRACELLULAR ALPHA-3.  
 CONNECTING PEPTIDE.  
 CYTOPLASMIC TAIL.  
 N-LINKED (GLCNAC. .) (BY SIMILARITY).  
 BY SIMILARITY.  
 BY SIMILARITY.  
 I -> V (IN A\*3402).  
 /FTID=VAR 004379.  
 K -> N (IN A\*3402).  
 /FTID=VAR 004380.  
 R -> I (IN A\*3402).  
 /FTID=VAR 004381.  
 P -> S (IN A\*3402).  
 /FTID=VAR 004382.  
 Q -> R (IN A\*3402).  
 /FTID=VAR 004383.  
 W -> L (IN A\*3402).  
 /FTID=VAR 004384.  
 L -> I (IN A\*3402).  
 /FTID=VAR 004385.

Db 84 WDRNTRKVK 92  
 RESULT 13  
 YKYL\_CABEL STANDARD; PRT; 455 AA.  
 ID YKYL\_CABEL  
 AC Q19910;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein F30B5.4 in chromosome IV.  
 DE F30B5.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Miller N., Bradshaw H.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP REVISIONS.  
 RP Waterston R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U42437; AAA83493.2; -;  
 DR WormPeP; F30B5.4; CE28552.  
 DR Hypothetical protein.  
 KW SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;  
 SQ  
 Query Match 52.1%; Score 37; DB 1; Length 455;  
 Best Local Similarity 50.0%; Pred. No. 30;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWRNWK 10  
 | | | | |  
 Db 102 CIQWELNRR 111  
 RESULT 14  
 VP4\_ROTGA STANDARD; PRT; 749 AA.  
 ID VP4\_ROTGA  
 AC Q04916;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).  
 DE S4.  
 OS Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 OX NCBI\_TaxID=12705;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE-93233240; PubMed-8386274;  
 RA Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;  
 RT "Identification and baculovirus expression of the VP4 protein of the  
 RT human group B rotavirus ADRV.";  
 RL J. Virol. 67:2730-2738(1993).  
 CC -!- SUBCELLULAR LOCATION: Outer capsid.  
 CC -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.  
 CC -----  
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CC -----  
DR EMBL; M91434; AAA47338.1; -  
DR InterPro; IPR000416; Cap\_VP4.  
DR Pfam; PF00426; VP4; 1.  
KW Coat protein; Glycoprotein.  
FT CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 527 527 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 568 568 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 620 620 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 681 681 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 698 698 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 749 AA; 84362 MW; D1223527DEAE0F21 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 749;  
Best Local Similarity 50.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKKVR 12  
Db 195 CFTWDMNCANVR 206

## RESULT 15

YNR2 CAEEL STANDARD; PRT; 783 AA.  
AC Q21988;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical protein R13G10.2 in chromosome III.  
GN R13G10.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Gardner A.E.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP REVISIONS.  
RA Durbin R.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- COFACTOR: FAD (POTENTIAL).  
CC -!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; Z35602; CAA84671.2; -  
DR WormPep; R13G10.2; CE25088.  
DR InterPro; IPR002937; Amino\_Oxidase.  
DR Pfam; PF01593; Amino\_Oxidase; 1.  
KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.  
FT NP\_BIND 311 366 FAD (ADP PART) (POTENTIAL).  
SQ SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 783;

Best Local Similarity 50.0%; Pred. No. 52;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKKVR 12  
Db 540 CIDWGRDRKVK 551

Search completed: February 21, 2003, 07:27:38  
Job time : 7.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107b-47  
Perfect score: 71  
Sequence: 1 CFQWQRNRKV 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL.21.\*  
1: sp.archaea.\*  
2: sp.bacteria.\*  
3: sp.fungi.\*  
4: sp.human.\*  
5: sp.invertebrate.\*  
6: sp.mammal.\*  
7: sp.mhc.\*  
8: sp.organella.\*  
9: sp.phage.\*  
10: sp.plant.\*  
11: sp.rodent.\*  
12: sp.virus.\*  
13: sp.vertebrate.\*  
14: sp.unclassified.\*  
15: sp.virus.\*  
16: sp.bacteriaph.\*  
17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	93.0	711	4 Q8TCD2	Q8Tcd2 homo sapien
2	62	87.3	38	4 Q9UCY5	Q9ucy5 homo sapien
3	51	71.8	33	6 Q9TR80	Q9tr80 ovis aries
4	42	59.2	298	16 Q8IP77	Q8yp77 anabaena sp
5	42	59.2	511	16 Q8Z462	Q8z462 salmorella
6	41	57.7	148	10 Q9XHP1	Q9xhpi sesamum ind
7	41	57.7	275	5 Q93780	Q93780 caenorhabdi
8	41	57.7	932	5 Q19153	Q19153 caenorhabdi
9	40	56.3	279	16 Q8XSE2	Q8xse2 ralstonia s
10	40	56.3	469	9 Q38115	Q38115 bacterioph
11	40	56.3	681	5 Q9XVD1	Q9xvdi caenorhabdi
12	39	54.9	105	10 Q9XFD5	Q9xfid5 oryza sativ
13	39	54.9	273	2 Q31090	Q31090 rhizobium l
14	39	54.9	274	4 Q96M21	Q96m21 homo sapien
15	39	54.9	306	4 Q8TAX2	Q8tax2 homo sapien
16	39	54.9	372	10 Q81653	Q81653 hemerocalli

Q9nu22 homo sapien  
Q8s334 diospyros k  
Q9hpa3 halobacteri  
Q77855 human immun  
Q77856 human immun  
Q8u8k3 agrobacteri  
Q98r22 guillardia  
Q98q19 mycoplasma  
Q8r2a4 mus musculu  
Q9n2w0 homo sapien  
Q9n2w3 homo sapien  
P96223 mycobacteri  
Q22185 arabidopsis  
Q22188 arabidopsis  
Q94937 homo sapien  
Q8s487 zea mays (m  
Q62582 encephalito  
Q8srq3 encephalito  
Q8sq16 encephalito  
Q9fhi9 arabidopsis  
Q23230 arabidopsis  
Q9n906 trypanosoma  
Q8r9u1 thermonaer  
Q9ygc1 human immun  
Q9ygc0 human immun  
Q9yqb9 human immun  
Q9yqb8 human immun  
Q9yji7 human immun  
Q9yji2 human immun

39 54.9 466 4 Q9NUS2  
39 54.9 488 10 Q8S934  
39 54.9 584 17 Q9HPA3  
38 53.5 91 15 Q77855  
38 53.5 91 15 Q77856  
38 53.5 121 16 Q8U8K3  
38 53.5 205 8 Q98RR2  
38 53.5 282 16 Q98Q19  
38 53.5 341 11 Q8R2A4  
38 53.5 459 4 Q9NZW0  
38 53.5 460 4 Q9NZW3  
38 53.5 489 16 P96223  
38 53.5 513 10 Q22185  
38 53.5 543 10 Q22188  
38 53.5 570 10 Q8S487  
38 53.5 632 4 Q94937  
38 53.5 864 5 Q62582  
38 53.5 864 5 Q8SRG3  
38 53.5 864 5 Q8SQ16  
38 53.5 866 10 Q9FHI9  
38 53.5 1432 10 Q23230  
38 53.5 2186 5 Q9N906  
37 52.1 62 16 Q8R9U1  
37 52.1 109 15 Q9YQC1  
37 52.1 109 15 Q9YQC0  
37 52.1 109 15 Q9YQB9  
37 52.1 109 15 Q9YQB8  
37 52.1 109 15 Q9YJI7  
37 52.1 109 15 Q9YJI2

#### ALIGNMENTS

RESULT 1  
Q8TCD2  
ID Q8TCD2 PRELIMINARY; PRT; 711 AA.  
AC Q8TCD2;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCB1\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022347; AAH22347.1; -.  
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 93.0%; Score 66; DB 4; Length 711;  
Best Local Similarity 100.0%; Pred. No. 0.00077;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWQRNRKV 11  
Dd 39 CFQWQRNRKV 49

RESULT 2  
Q9UCY5  
ID Q9UCY5 PRELIMINARY; PRT; 38 AA.  
AC Q9UCY5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Lactoferrin homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP MEDLINE=96081613; PubMed=8551695;  
 RA Sato I.;  
 RT "Characterization of the 84-kDa protein with ABH activity in human  
 seminal plasma";  
 RL Jpn. J. Legal Med. 49:281-293(1995).  
 DR HSP, P02788; 18XA.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 1.  
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDBB CRC64;

Query Match 87.3%; Score 62; DB 4; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12  
 Db 21 FQWQNRKVR 31  
 |||||  
 |||||

RESULT 3  
 Q9TR80 PRELIMINARY; PRT; 33 AA.  
 ID Q9TR80;  
 AC Q9TR80;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Lactoferrin (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]\_SEQUENCE.  
 RP MEDLINE=95127729; PubMed=7827104;  
 RX Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;  
 RA Biochim. Biophys. Acta 1243:25-32(1995).  
 RL HSP; O77698; 1CE2.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 1.  
 SQ SEQUENCE 33 AA; 3514 MW; D1904CAE15A73961 CRC64;

Query Match 71.8%; Score 51; DB 6; Length 33;  
 Best Local Similarity 63.6%; Pred. No. 0.017;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 11  
 Db 19 CYQWQNRKVR 29  
 |||||  
 |||||

RESULT 4  
 Q9YP77 PRELIMINARY; PRT; 298 AA.  
 ID Q9YP77;  
 AC Q9YP77;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein Alr4323.  
 GN Alr4323.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP MEDLINE=21595285; PubMed=11759840;  
 RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A.,

RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL; AF003596; BAB76022.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 298 AA; 34513 MW; 64036B6B5229A9F CRC64;

Query Match 59.2%; Score 42; DB 16; Length 298;  
 Best Local Similarity 77.8%; Pred. No. 8.2;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 10  
 Db 163 FQWQNRKVR 171  
 |||||  
 |||||

RESULT 5  
 Q8Z462 PRELIMINARY; PRT; 511 AA.  
 ID Q8Z462;  
 AC Q8Z462;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein STY3070.  
 GN STY3070.  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Cherkar C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.F., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 DR EMBL; AL627276; CAD06049.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;

Query Match 59.2%; Score 42; DB 16; Length 511;  
 Best Local Similarity 58.3%; Pred. No. 15;  
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12  
 Db 350 CFQWQNRKVR 361  
 |||||  
 |||||

RESULT 6  
 Q9XHP1 PRELIMINARY; PRT; 148 AA.  
 ID Q9XHP1;  
 AC Q9XHP1;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE 2S albumin.  
 OS Sesamum indicum (Oriental sesame) (Gingelly).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.  
 OX NCBI\_TaxID=4182;  
 RN [1]\_SEQUENCE FROM N.A.

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RP SEQUENCE FROM N.A.
RC STRAIN=TAINAN 1;
RX MEDLINE=20074970; PubMed=10606554;
RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RL storage proteins in sesame.";
RL J. Agric. Food Chem. 47:4932-4938(1999).
DR EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000617; Napin.
DR InterPro; IPR001765; try/amy1 inhbr.
DR Pfam; PF00234; try2_alpha_ami1; 1.
DR PRINTS; PR00496; NAPIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 57.7%; Score 41; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOWQRNMR 9
| | | | |
Db 54 CMQWRSMR 62

RESULT 7
Q93780
ID Q93780 PRELIMINARY; PRT; 275 AA.
AC Q93780;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F53H4.4 protein.
GN F53H4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81089; CAB03137.1; -.
SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 57.7%; Score 41; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRMKRV 12
| | | | |
Db 262 FQWISMRTK 272

RESULT 8
Q19153
ID Q19153 PRELIMINARY; PRT; 932 AA.
AC Q19153;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 105.1 kDa protein.
GN F07C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

```

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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Favell A., Gattung S.;
RT "The sequence of C. elegans cosmid F07C3.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50308; AAG24025.1; -.
DR InterPro; IPR000731; HMGCR/patch_5TM.
DR PROSITE; PS50156; SSD; 1.
DR Hypothetical protein.
SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFDS CRC64;

Query Match 57.7%; Score 41; DB 5; Length 932;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRMKRV 12
| | | | |
Db 579 FQWQSRARLVK 589

RESULT 9
Q8XSE2
ID Q8XSE2 PRELIMINARY; PRT; 279 AA.
AC Q8XSE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ICC protein homolog.
GN ICC OR RSP0534 OR RS00414.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguiet P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646079; CAD17685.1; -.
DR InterPro; IPR004843; Mppsstrase.
DR InterPro; IPR004844; S/T_phosphatase.
DR Pfam; PF00149; Metallophos; 1.
DR Plasmid; Complete proteome.
KW SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 56.3%; Score 40; DB 16; Length 279;
Best Local Similarity 41.7%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```



RL Mcl. Biol. (Mosc) 32:797-804(1998).  
 DR EMBL; AF028810; AAB8891.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;

Query Match 54.9%; Score 39; DB 2; Length 273;  
 Best Local Similarity 60.0%; Pred. No. 27;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRKVR 12  
 DB 245 RWLRNLRKLR 254

## RESULT 14

Q96M21 PRELIMINARY; PRT; 274 AA.  
 AC Q96M21;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE CDNA FLJ32891 fis, clone TESTI2004929.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,  
 RA Arita M., Musashino K., Yuki H., Hara H., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
 RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,  
 RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;  
 RT "NEDO human cDNA sequencing project";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK057453; BAB71493.1; -  
 SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

Query Match 54.9%; Score 39; DB 4; Length 274;  
 Best Local Similarity 50.0%; Pred. No. 27;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12  
 DB 66 CFQWRWGVYLR 77

## RESULT 15

Q8TAX2 PRELIMINARY; PRT; 306 AA.  
 AC Q8TAX2;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Similar to hypothetical protein FLJ11175.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PANCREAS;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025708; AAB25708.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;

Query Match 54.9%; Score 39; DB 4; Length 306;  
 Best Local Similarity 55.6%; Pred. No. 30;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKVR 9  
 DB 269 CFQWESTLR 277

Search completed: February 21, 2003, 07:44:14  
 Job time : 23.8 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107B-68  
Perfect score: 66  
Sequence: 1 AFGWQRNRKVR 12  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: A\_Geneseq\_101002.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	12	21	AAV78068 Human lactoferrin
2	62	93.9	11	21	AAV57318 Human lactoferrin
3	62	93.9	11	21	AAV78039 Human lactoferrin
4	62	93.9	11	21	AAV78044 Human lactoferrin
5	62	93.9	11	21	AAV78045 Human lactoferrin
6	62	93.9	11	22	AAV78046 Human lactoferrin
7	62	93.9	12	21	AAV78038 Human lactoferrin
8	62	93.9	12	21	AAV78046 Human lactoferrin
9	62	93.9	12	21	AAV78047 Human lactoferrin
10	62	93.9	13	21	AAV78037 Human lactoferrin

11	62	93.9	13	21	AAV78048 Human lactoferrin
12	62	93.9	13	21	AAV78049 Human lactoferrin
13	62	93.9	14	21	AAV78036 Human lactoferrin
14	62	93.9	14	21	AAV78050 Human lactoferrin
15	62	93.9	14	21	AAV78051 Human lactoferrin
16	62	93.9	14	21	AAV78056 Human lactoferrin
17	62	93.9	14	21	AAV78057 Human lactoferrin
18	62	93.9	14	21	AAV78098 Human lactoferrin
19	62	93.9	15	17	AAV78055 Peptide for anti-u
20	62	93.9	15	20	AAV04008 Antibacterial lact
21	62	93.9	15	21	AAV57317 Human lactoferrin
22	62	93.9	15	21	AAV78035 Human lactoferrin
23	62	93.9	15	21	AAV78062 Human lactoferrin
24	62	93.9	15	21	AAV78063 Human lactoferrin
25	62	93.9	16	21	AAV78031 Human lactoferrin
26	62	93.9	16	21	AAV78064 Human lactoferrin
27	62	93.9	16	21	AAV78065 Human lactoferrin
28	62	93.9	17	21	AAV78034 Human lactoferrin
29	62	93.9	17	21	AAV78066 Human lactoferrin
30	62	93.9	17	21	AAV78067 Human lactoferrin
31	62	93.9	18	15	AAV69352 Human lactoferrin
32	62	93.9	18	17	AAV13397 Advanced glycosyla
33	62	93.9	18	21	AAV78033 Human lactoferrin
34	62	93.9	19	21	AAV68867 Amino acid sequenc
35	62	93.9	19	21	AAV78032 Human lactoferrin
36	62	93.9	20	13	AAV21810 Anti microbial pep
37	62	93.9	20	13	AAV21811 Anti microbial pep
38	62	93.9	20	14	AAV44841 Lactoferrin-relate
39	62	93.9	20	15	AAV48530 Lactoferrin derive
40	62	93.9	20	15	AAV48531 Lactoferrin derive
41	62	93.9	20	15	AAV57461 Lactoferrin derive
42	62	93.9	20	15	AAV57462 Lactoferrin derive
43	62	93.9	20	16	AAV84698 Bovine lactoferrin
44	62	93.9	20	16	AAV84699 Bovine lactoferrin
45	62	93.9	20	16	AAV80263 Anti-parasitic lac

#### ALIGNMENTS

#### RESULT 1

AAV78068  
ID AAV78068 standard; Peptide; 12 AA.  
AC AAV78068;  
XX  
XX 25-APR-2000 (first entry)  
DE Human lactoferrin derived peptide SEQ ID NO:68.  
XX  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200001730-A1.  
XX  
XX 13-JAN-2000.  
XX  
XX 06-JUL-1999; 99WO-SE01230.  
XX  
XX 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX  
XX (ASCI-) A+ SCI INVEST AB.  
XX  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
XX WPI; 2000-147388/13.  
DR

XX New peptides used for treatment and prevention of infections, -  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX PS Claim 22; Page 35; 102pp; English.  
XX  
CC AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.  
XX  
XX SQ Sequence 12 AA;  
XX  
XX Query Match 100.0%; Score 66; DB 21; Length 12;  
XX Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 AFQWRNMRKVR 12  
XX | | | | | | | | | | | | | |  
XX Db 1 AFQWRNMRKVR 12  
XX  
XX RESULT 2  
XX AAY57318  
XX ID AAY57318 standard; peptide; 11 AA.  
XX  
XX AC AAY57318;  
XX  
XX DT 13-JUN-2000 (first entry)  
XX  
XX DE Human lactoferrin partial peptide sequence.  
XX  
XX KW Lactoferrin; anti-microbial; adhesive; coating material; clothing;  
XX waste water treatment; leather; fiber; human.  
XX  
XX OS Homo sapiens.  
XX  
XX PN JP2000045182-A.  
XX  
XX PD 15-FEB-2000.  
XX  
XX PF 23-JUL-1998; 98JP-0207751.  
XX  
XX PR 23-JUL-1998; 98JP-0207751.  
XX  
XX PA (PEPU-) PEPUCHIDO SCI YG.  
XX (FUJI-) FUJII KAIHATSU KENKYUSHO YG.  
XX (NARU-) MARUJU KK.  
XX  
XX DR WPI; 2000-306598/27.  
XX  
XX AT antimicrobial fiber for bandage, gauze, sheet and fiber goods comprises  
PT anti-microbial component fixed to fiber by water soluble resin -  
XX  
XX PS Claim 3; Page 2; 10pp; Japanese.  
XX  
XX The invention provides water soluble resin-based fixing agent which  
CC dissociates the anionic polymer component in water, fixes cationic anti-  
CC microbial component into a fiber to form anti-microbial fiber. Cow or  
CC human lactoferrin peptides may be used as the anti-microbial component  
CC in the anti-microbial fiber of the invention. The agent is useful as  
CC adhesive, coating material, waste water treatment and in fixing

CC antimicrobial component to a fiber to form antimicrobial fiber useful as  
CC a bandage, gauze, sheet, clothing others or leathers, and fiber goods.  
CC The antimicrobial activity is measured against S. coli, S. aureus,  
CC methicillin-resistant S. aureus and P. aeruginosa. The antimicrobial  
CC fiber formed has excellent antimicrobial activity and wash durability.  
CC The leather used has excellent antimicrobial processing agent. Fixing of  
CC lactoferrin to the fiber is reliable. The present sequence represents a  
CC human lactoferrin partial peptide fragment.  
XX  
XX SQ Sequence 11 AA;  
XX  
XX Query Match 93.9%; Score 62; DB 21; Length 11;  
XX Best Local Similarity 100.0%; Pred. No. 0.00026;  
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 2 FQWRNMRKVR 12  
XX | | | | | | | | | | | | | |  
XX Db 1 FQWRNMRKVR 11  
XX  
XX RESULT 3  
XX AAY78039  
XX ID AAY78039 standard; Peptide; 11 AA.  
XX  
XX AC AAY78039;  
XX  
XX DT 25-APR-2000 (first entry)  
XX  
XX DE Human lactoferrin derived peptide SEQ ID NO:39.  
XX  
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.  
XX  
XX OS Homo sapiens.  
XX  
XX OS Synthetic.  
XX  
XX PN WO200001730-A1.  
XX  
XX PD 13-JAN-2000.  
XX  
XX PF 06-JUL-1999; 99WO-SE01230.  
XX  
XX PR 06-JUL-1998; 98SE-0002441.  
XX 17-JUL-1998; 98SE-0002562.  
XX 29-DEC-1998; 98SE-0004614.  
XX  
XX PA (ASCI-) A+ SCI INVEST AB.  
XX  
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
XX DR WPI; 2000-147388/13.  
XX  
XX PT New peptides used for treatment and prevention of infections,  
XX inflammations and tumors and for use in infant formula food -  
XX  
XX PS Claim 12; Page 70; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower

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CC cost.
XX Sequence 11 AA;
SQ

Query Match 93.9%; Score 62; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12
Db 1 FQWRNMRKVR 11

RESULT 4
AAV78044
ID AAV78044 standard; Peptide; 11 AA.
XX
AC AAV78044;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:44.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 15; Page 72; 102pp; English.
XX
CC AAV78001 to AAV78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 11 AA;

Query Match 93.9%; Score 62; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 FQWRNMRKVR 12
Db 1 FQWRNMRKVR 11

RESULT 5
AAV78045
ID AAV78045 standard; Peptide; 11 AA.
XX
AC AAV78045;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:45.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 18; Page 72; 102pp; English.
XX
CC AAV78001 to AAV78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 11 AA;

Query Match 93.9%; Score 62; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 FQWRNMRKVR 12
Db 1 FQWRNMRKVR 11

```

RESULT 6

AAB97384  
 ID AAB97384 standard; peptide; 11 AA.  
 AC AAB97384;  
 XX  
 DT 17-AUG-2001 (first entry)  
 XX  
 DE Human lactoferrin fragment hLF (21-3).  
 XX  
 KW Human; lactoferrin; hLF; N-terminal; antimicrobial; heparin;  
 KW inflammatory response; cytokine production reduction;  
 KW neutrophil degranulation; myelopoiesis inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200134641-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 10-NOV-2000; 2000WO-NL00821.  
 XX  
 PR 11-NOV-1999; 99BP-0203775.  
 PR 11-NOV-1999; 99US-0164975.  
 XX  
 PA (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.  
 XX  
 PI Van Berkel PHC, Nibbering PH, Nuijens JH;  
 XX  
 DR WPI; 2001-335909/35.  
 XX  
 XX New polypeptides comprising the N-terminal region of human lactoferrin  
 PT protein exhibit higher antimicrobial activity than the full length  
 PT protein and are useful to treat bacterial infections  
 XX  
 PS Example 1; Page 22; 59pp; English.  
 XX  
 CC This invention relates to fragments (between 6 and 26 amino acids) of the  
 CC human lactoferrin hLF protein, such as that represented in the present  
 CC sequence. N-terminal hLF peptides have antimicrobial activity. The  
 CC peptides of the invention are used to treat microbial infections,  
 CC especially infections by gram positive or negative bacteria, particularly  
 CC *Listeria*, *Staphylococcus*, *Klebsiella* or *Bacterichia* species, especially  
 CC *L. monocytogenes*, *S. aureus* and *E. coli*. Other uses include reducing  
 CC inflammatory response by neutralising heparin or lipopolysaccharide or by  
 CC reducing cytokine production and neutrophil degranulation, inhibiting  
 CC entry of viruses such as cytomegalovirus, herpes simplex virus 1 or HIV  
 CC into cells, inhibiting myelopoiesis and reducing production of GM-CSF  
 CC (granulocyte/macrophage colony stimulating factor).  
 XX  
 SQ Sequence 11 AA;  
 Query Match 93.9%; Score 62; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00026;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FQWRNMRKVR 12  
 DB 1 FQWRNMRKVR 11  
 RESULT 7  
 AAY78038  
 ID AAY78038 standard; Peptide; 12 AA.  
 AC AAY78038;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:38.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 XX

KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SB01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147389/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food  
 XX  
 PS Claim 12; Page 70; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 93.9%; Score 62; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00028;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FQWRNMRKVR 12  
 DB 2 FQWRNMRKVR 12  
 RESULT 8  
 AAY78046  
 ID AAY78046 standard; Peptide; 12 AA.  
 XX  
 AC AAY78046;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:46.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX

PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCII-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 15; Page 35; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 93.9%; Score 62; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00028;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FQWQNRMKVR 12  
 Db 2 FQWQNRMKVR 12  
 RESULT 9  
 AAY78047  
 ID AAY78047 standard; Peptide; 12 AA.  
 XX  
 AC AAY78047;  
 XX  
 DT 25-APR-2000 (first entry)  
 DE Human lactoferrin derived peptide SEQ ID NO:47.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 OS  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 PF  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCII-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX

XX  
 PA (ASCII-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 18; Page 73; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 93.9%; Score 62; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00028;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FQWQNRMKVR 12  
 Db 2 FQWQNRMKVR 12  
 RESULT 10  
 AAY78037  
 ID AAY78037 standard; Peptide; 13 AA.  
 XX  
 AC AAY78037;  
 XX  
 DT 25-APR-2000 (first entry)  
 DE Human lactoferrin derived peptide SEQ ID NO:37.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 OS  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 PF  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCII-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX

PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PS Claim 12; Page 70; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides are also  
 CC in food stuffs such as infant formula food. The peptides can also be used  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX SQ Sequence 13 AA;  
 Query Match 93.9%; Score 62; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00031;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FQWQNNRKVR 12  
 DB 3 FQWQNNRKVR 13  
 RESULT 11  
 AAY78048  
 ID AAY78048 standard; Peptide; 13 AA.  
 AC AAY78048;  
 XX  
 DT 25-APR-2000 (first entry)  
 DE Human lactoferrin derived peptide SEQ ID NO:48.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 15; Page 74; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX SQ Sequence 13 AA;  
 Query Match 93.9%; Score 62; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00031;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FQWQNNRKVR 12  
 DB 3 FQWQNNRKVR 13  
 RESULT 12  
 AAY78049  
 ID AAY78049 standard; Peptide; 13 AA.  
 AC AAY78049;  
 XX  
 DT 25-APR-2000 (first entry)  
 DE Human lactoferrin derived peptide SEQ ID NO:49.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 18; Page 74; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 13 AA;

Query Match 93.9%; Score 62; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00031;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12  
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 Db 3 FQWRNMRKVR 13

RESULT 13

AAAY78036  
 ID AAY78036 standard; Peptide; 14 AA.

XX AAY78036;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:36.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

SQ Sequence 14 AA;

Query Match 93.9%; Score 62; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12  
 |||||  
 Db 4 FQWRNMRKVR 14

RESULT 14

AAAY78050  
 ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:50.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

SQ Sequence 14 AA;

Query Match 93.9%; Score 62; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNMRKVR 12

Db 4 FQWRNRKVR 14

## RESULT 15

AAV78051  
 ID AAV78051 standard; Peptide; 14 AA.  
 XX AC AAV78051;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:51.  
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PN WO200001730-A1.  
 XX PD 13-JAN-2000.  
 XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX PA (ASCI-) A+ SCI INVEST AB.  
 XX PI Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 75; 102pp; English.  
 XX PS AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
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 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 14 AA;

Query Match 93.9%; Score 62; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWRNRKVR 12

Db 4 FQWRNRKVR 14

Search completed: February 21, 2003, 07:37:10  
 Job time : 28.35 secs



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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)

56.502 Million cell updates/sec

Title: US-09-743-107B-70

Perfect score: 70

Sequence: 1 CFAWRNMRKV 12

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
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9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
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11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78070 Human lactoferrin
2	66	94.3	12	21	AAV78094 Human lactoferrin
3	65	92.9	12	21	AAV78038 Human lactoferrin
4	65	92.9	12	21	AAV78046 Human lactoferrin
5	65	92.9	12	21	AAV78047 Human lactoferrin
6	65	92.9	13	21	AAV78037 Human lactoferrin
7	65	92.9	13	21	AAV78048 Human lactoferrin
8	65	92.9	13	21	AAV78049 Human lactoferrin
9	65	92.9	14	21	AAV78036 Human lactoferrin
10	65	92.9	14	21	AAV78050 Human lactoferrin

11	65	92.9	14	21	AAV78051 Human lactoferrin
12	65	92.9	15	17	AAV78054 Peptide for anti-u
13	65	92.9	15	21	AAV78035 Human lactoferrin
14	65	92.9	15	21	AAV78062 Human lactoferrin
15	65	92.9	15	21	AAV78063 Human lactoferrin
16	65	92.9	16	21	AAV78031 Human lactoferrin
17	65	92.9	16	21	AAV78064 Human lactoferrin
18	65	92.9	16	21	AAV78065 Human lactoferrin
19	65	92.9	17	21	AAV78034 Human lactoferrin
20	65	92.9	17	21	AAV78066 Human lactoferrin
21	65	92.9	17	21	AAV78067 Human lactoferrin
22	65	92.9	18	15	AAV78067 Human lactoferrin
23	65	92.9	18	17	AAV78032 Human lactoferrin
24	65	92.9	18	21	AAV78033 Human lactoferrin
25	65	92.9	19	21	AAV78067 Amino acid sequenc
26	65	92.9	19	21	AAV78032 Human lactoferrin
27	65	92.9	20	13	AAV78051 Anti microbial pep
28	65	92.9	20	14	AAV78051 Lactoferrin-relate
29	65	92.9	20	15	AAV78051 Lactoferrin derive
30	65	92.9	20	15	AAV78051 Lactoferrin derive
31	65	92.9	20	15	AAV78051 Lactoferrin derive
32	65	92.9	20	15	AAV78051 Lactoferrin derive
33	65	92.9	20	16	AAV78051 Bovine lactoferrin
34	65	92.9	20	16	AAV78051 Bovine lactoferrin
35	65	92.9	20	16	AAV78051 Anti-parasitic lac
36	65	92.9	20	16	AAV78051 Anti-parasitic lac
37	65	92.9	20	16	AAV78051 Peptide for anti-u
38	65	92.9	20	17	AAV78051 Lactoferrin-derive
39	65	92.9	20	17	AAV78051 Lactoferrin-derive
40	65	92.9	20	17	AAV78051 Lactoferrin-derive
41	65	92.9	20	17	AAV78051 Lactoferrin-derive
42	65	92.9	20	17	AAV78051 Lactoferrin-derive
43	65	92.9	20	18	AAV78051 Lactoferrin deriva
44	65	92.9	20	18	AAV78051 Anti-parasitic pep
45	65	92.9	20	19	AAV78051 Thrombus formation

#### ALIGNMENTS

#### RESULT 1

AAV78070

ID AAV78070 standard; Peptide; 12 AA.

XX AAV78070;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:70.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PD 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;

DR WPI; 2000-147388/13.

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XX New peptides used for treatment and prevention of infections,
PT Inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 35; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 70; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFAWQRNMRKVR 12
Db 1 CFAWQRNMRKVR 12
RESULT 2
AAY78094
ID AAY78094 standard; Peptide; 12 AA.
XX
AC AAY78094;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:94.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PE 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 38; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human

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CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 94.3%; Score 66; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 8.6e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFAWQRNMRKVR 12
Db 1 CFAWQRNMRKVR 12
RESULT 3
AAY78038
ID AAY78038 standard; Peptide; 12 AA.
XX
AC AAY78038;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:38.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PE 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
XX
PR 17-JUL-1998; 98SE-0002562.
XX
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 12; Page 70; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

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CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00013;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 12  
 |||||  
 Db 1 CFQWQNRKVR 12

RESULT 4  
 AAY78046  
 ID AAY78046 standard; Peptide; 12 AA.  
 XX AC AAY78046;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:46.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.  
 XX PN W0200001730-A1.  
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 XX FT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00013;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 12  
 |||||  
 Db 1 CFQWQNRKVR 12

RESULT 5  
 AAY78047  
 ID AAY78047 standard; Peptide; 12 AA.  
 XX AC AAY78047;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.  
 XX PN W0200001730-A1.  
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 XX FT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00013;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 12  
 |||||  
 Db 1 CFQWQNRKVR 12

RESULT 5  
 AAY78047  
 ID AAY78047 standard; Peptide; 12 AA.  
 XX AC AAY78047;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:47.  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX PN W0200001730-A1.  
 XX PD 13-JAN-2000.  
 XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.  
 XX PA (ASCI-) A+ SCI INVEST AB.  
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX DR WPI; 2000-147388/13.  
 XX PT New peptides used for treatment and prevention of infections,  
 XX FT inflammations and tumors and for use in infant formula food -  
 XX PS Claim 18; Page 73; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

QY 1 CFAWQNMREKVR 12  
 |||||  
 Db 1 CFQWQNMREKVR 12

## RESULT 6

AAV78037  
 ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;  
 DT 25-APR-2000 (first entry)  
 XX Human lactoferrin derived peptide SEQ ID NO:37.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX

OS Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

PF 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -

PS Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 0.00014;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNMREKVR 12  
 |||||  
 Db 2 CFQWQNMREKVR 13

## RESULT 7

AAV78048

ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;  
 XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:48.

DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX

OS Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

PF 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -

PS Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 0.00014;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNMREKVR 12  
 |||||  
 Db 2 CFQWQNMREKVR 13

## RESULT 8

AAV78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;  
 XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:49.

XX

XX Human, lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.00014;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNNRKVR 12

Db 2 CFAWQNNRKVR 13

RESULT 9

AAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:36.

XX Human, lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 14 AA;

Query Match 92.9%; Score 65; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00015;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNNRKVR 12

Db 3 CFAWQNNRKVR 14

RESULT 10

AAY78050

ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:50.

XX Human, lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

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XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 15; Page 75; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 14 AA;
XX
XX Query Match 92.9%; Score 65; DB 21; Length 14;
XX Best Local Similarity 91.7%; Pred. No. 0.00015;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CFAWQRNMRKVR 12
XX |||||
XX Db 3 CFAWQRNMRKVR 14
XX
XX RESULT 11
XX AAY78051
XX ID AAY78051 standard; Peptide; 14 AA.
XX
XX AC AAY78051;
XX
XX DT 25-APR-2000 (first entry)
XX
XX DE Human lactoferrin derived peptide SEQ ID NO:51.
XX
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX PN WO200001730-A1.
XX
XX PD 13-JAN-2000.
XX
XX PF 06-JUL-1999; 99WO-SE01230.
XX
XX PR 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX

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```

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 18; Page 75; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 14 AA;
XX
XX Query Match 92.9%; Score 65; DB 21; Length 14;
XX Best Local Similarity 91.7%; Pred. No. 0.00015;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CFAWQRNMRKVR 12
XX |||||
XX Db 3 CFAWQRNMRKVR 14
XX
XX RESULT 12
XX AAR98554
XX ID AAR98554 standard; Peptide; 15 AA.
XX
XX AC AAR98554;
XX
XX DT 12-NOV-1996 (first entry)
XX
XX DE Peptide for anti-ulcer agent.
XX
XX KW anti-ulcer agent; low toxicity; stable; heat-resistant.
XX
XX OS Synthetic.
XX
XX PN JP08143468-A.
XX
XX PD 04-JUN-1996.
XX
XX PF 17-NOV-1994; 94JP-0283869.
XX
XX PR 17-NOV-1994; 94JP-0283869.
XX
XX PA (MORG ) MORINAGA MILK IND CO LTD.
XX
XX DR WPI; 1996-318857/32.
XX
XX PT Anti-ulcer agent contg. peptide - has low toxicity, is
XX heat-resistant and water-soluble
XX
XX PS Claim 1; Page 11; 11pp; Japanese.
XX
XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
CC administered orally and be produced in large amounts.
XX
XX SQ Sequence 15 AA;

```

Query Match 92.9%; Score 65; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00016;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12  
 DB 2 CFQWQNNRKVR 13

RESULT 13  
 AAY78035  
 ID AAY78035 standard; Peptide; 15 AA.  
 XX  
 AC AAY78035;  
 DT 25-APR-2000 (first entry)  
 XX Human lactoferrin derived peptide SEQ ID NO:35.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 PD 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 69; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 15 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00016;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12  
 DB 4 CFQWQNNRKVR 15

RESULT 15  
 AAY78063  
 ID AAY78063 standard; Peptide; 15 AA.  
 XX  
 AC AAY78063;

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XX 25-APR-2000 (first entry)
DT XX
DE XX
DE XX
DE XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX
XX 17-JUL-1998; 98SE-0002562.
XX
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI
XX
DR WPI; 2000-147398/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food, -
PT
XX
XX Claim 18; Page 81; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX
SQ Sequence 15 AA;
Query Match 92.9%; Score 65; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFAWQENMRKVR 12
Db 4 CFWQENMRKVR 15

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Search completed: February 21, 2003, 07:37:11  
 Job time : 28.35 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-70

Perfect score: 70

Sequence: 1 CFAWQNMKRV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/55 COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-09-508-734-4
13	65	92.9	24	4	US-09-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	36	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-693-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28	65	92.9	54	2	US-08-454-182A-2
29	65	92.9	54	2	US-08-406-271-2
30	65	92.9	694	3	US-08-724-586-2
31	65	92.9	694	4	US-09-421-632-2
32	65	92.9	694	4	US-09-932-190-2
33	65	92.9	705	2	US-08-655-640-2
34	65	92.9	708	2	US-08-655-640-4
35	65	92.9	711	1	US-08-154-019-4
36	65	92.9	711	1	US-08-481-333-4
37	65	92.9	711	3	US-08-484-167-4
38	65	92.9	711	3	US-09-158-313-4
39	65	92.9	711	4	US-08-476-798-4
40	62	88.6	711	1	US-08-145-681-2
41	62	88.6	711	1	US-08-250-308-2
42	62	88.6	711	1	US-08-453-703-2
43	62	88.6	711	2	US-08-456-106-2
44	62	88.6	711	3	US-08-456-108-2
45	62	88.6	711	4	US-09-265-577-2

#### ALIGNMENTS

RESULT 1  
US-08-204-487-3  
; Sequence 3, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 51A  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..18  
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 6.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQRMNRKVR 12  
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Db 1 CFQWQRMNRKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,948  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

## US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 6.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQRMNRKVR 12  
||| |||||  
Db 1 CFQWQRMNRKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI, YONG MING  
; APPLICANT: VLASSARA, HELEN  
; APPLICANT: CERAMI, ANTHONY  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

US-08-628-380-8  
Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 6.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQRMNRKVR 12  
||| |||||  
Db 1 CFQWQRMNRKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE  
; NUMBER OF SEQUENCES: 9

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CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LP-CL, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match          92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12
Db 1 CFQWQNRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match          92.9%; Score 65; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAQWRNRKVR 12  
Db 2 CFQWRNRKVR 13

RESULT 6  
US-07-891-174-3  
; Sequence 3, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHEICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site

LOCATION: 2  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 19"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 19  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 2"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAQWRNRKVR 12  
Db 2 CFQWRNRKVR 13

RESULT 7  
US-08-204-487-1  
; Sequence 1, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: RJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE  
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"  
US-08-204-487-1

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFAWQNNMKVR 12  
Db 2 CFAWQNNMKVR 13

RESULT 8  
US-08-256-771-24  
Sequence 24, Application US/08256771  
Patent No. 5656591  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
TITLE OF INVENTION: PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are linked by  
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNNMKVR 12  
Db 2 CFAWQNNMKVR 13

RESULT 9  
US-08-256-771-25  
Sequence 25, Application US/08256771  
Patent No. 5656591  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
TITLE OF INVENTION: PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are protected to  
OTHER INFORMATION: prevent disulfide bond"  
US-08-256-771-25

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQNNMKVR 12  
Db 2 CFAWQNNMKVR 13

RESULT 10  
US-08-381-984-24

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; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

```

INFORMATION FOR SEQ ID NO: 24:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"

```

```

US-08-381-984-24
Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 CFAWQRNMRKVR 12
DB 2 CFQWQRNMRKVR 13

```

US-08-381-984-24

```

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CFAWQRNMRKVR 12
DB 2 CFQWQRNMRKVR 13

```

RESULT 11

```

US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

```

```

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

```

INFORMATION FOR SEQ ID NO: 25:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"

```

```

US-08-381-984-25
Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 CFAWQRNMRKVR 12
DB 2 CFQWQRNMRKVR 13

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RESULT 12

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US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4

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LENGTH: 22  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;  
Best Local Similarity 91.7%; Pred. No. 7.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQNNRKVR 12  
Db 2 CFQWQNNRKVR 13

## RESULT 13

US-09-508-734-6  
Sequence 6, Application US/09508734  
Patent No. 6423509  
GENERAL INFORMATION:  
APPLICANT: Samyang Genex Corporation  
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
FILE REFERENCE: PA/SYG/00139  
CURRENT APPLICATION NUMBER: US/09/508,734  
CURRENT FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: PCT/KR99/00373  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: KR1998-29351  
PRIOR FILING DATE: 1998-07-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: KopatentIn 1.71  
SEQ ID NO 6  
LENGTH: 24  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-508-734-6

Query Match 92.9%; Score 65; DB 4; Length 24;  
Best Local Similarity 91.7%; Pred. No. 8.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQNNRKVR 12  
Db 3 CFQWQNNRKVR 14

## RESULT 14

US-07-755-161A-10  
Sequence 10, Application US/07755161A  
Patent No. 5304633  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptides and an  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,161A  
FILING DATE: 19910905  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

Query Match 92.9%; Score 65; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWQNNRKVR 12  
Db 4 CFQWQNNRKVR 15

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY: modified site

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 21"

FEATURE:

NAME/KEY: modified site

LOCATION: 21

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

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RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQNNRKVR 12
Db 4 CFQWQNNRKVR 15
Search completed: February 21, 2003, 07:50:33
Job time : 9.7 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107B-70  
Perfect score: 70  
Sequence: 1 CFQWRNNRKR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31059816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

Published Applications AA.\*  
1: /cgn2\_5/prodata/2/pubpaa/US08\_NEW\_PUB.pdb.\*  
2: /cgn2\_5/prodata/2/pubpaa/PCT\_NEW\_PUB.pdb.\*  
3: /cgn2\_5/prodata/2/pubpaa/US06\_NEW\_PUB.pdb.\*  
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11: /cgn2\_5/prodata/2/pubpaa/US10\_NEW\_PUB.pdb.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	43	61.4	15	9	US-09-798-869-4
8	43	61.4	25	9	US-09-798-869-22
9	40	57.1	15	9	US-09-798-869-7
10	40	57.1	15	9	US-09-798-869-8
11	40	57.1	15	9	US-09-798-869-29
12	40	57.1	15	9	US-09-798-869-30
13	38	54.3	338	9	US-09-978-285A-119
14	38	54.3	338	9	US-09-978-697-119
15	38	54.3	338	9	US-09-978-192A-119
16	38	54.3	338	9	US-09-999-832A-119
17	38	54.3	338	9	US-09-978-185-119
18	38	54.3	553	9	US-09-796-753-14
19	38	54.3	553	10	US-09-981-649A-6

20	38	54.3	553	10	US-09-981-649A-24	Sequence 24, Appl
21	38	54.3	554	10	US-09-981-649A-30	Sequence 30, Appl
22	38	54.3	554	10	US-09-981-649A-32	Sequence 32, Appl
23	38	54.3	559	10	US-09-981-649A-28	Sequence 28, Appl
24	38	54.3	2273	10	US-09-995-542-12	Sequence 12, Appl
25	38	54.3	2310	10	US-09-995-542-10	Sequence 10, Appl
26	37	52.9	34	9	US-09-510-332-68	Sequence 68, Appl
27	37	52.9	333	9	US-09-796-753-26	Sequence 26, Appl
28	37	52.9	607	9	US-09-881-579-10	Sequence 10, Appl
29	37	52.9	688	9	US-09-881-579-15	Sequence 15, Appl
30	36	51.4	210	9	US-09-738-626-4884	Sequence 4884, Ap
31	36	51.4	301	9	US-10-080-960-11	Sequence 11, Appl
32	36	51.4	302	10	US-09-948-078-2	Sequence 2, Appl
33	36	51.4	489	9	US-09-888-320-2	Sequence 2, Appl
34	35	50.0	97	9	US-09-738-626-5597	Sequence 5597, Ap
35	35	50.0	747	9	US-10-066-500-58	Sequence 58, Appl
36	35	50.0	747	9	US-10-002-796-58	Sequence 58, Appl
37	35	50.0	747	9	US-10-066-273-58	Sequence 58, Appl
38	35	50.0	747	9	US-10-066-494-58	Sequence 58, Appl
39	34	48.6	46	10	US-09-864-761-35744	Sequence 35744, A
40	34	48.6	69	10	US-09-804-969-17	Sequence 17, Appl
41	34	48.6	71	10	US-09-925-297-872	Sequence 872, App
42	34	48.6	77	10	US-09-864-761-41002	Sequence 41002, A
43	34	48.6	183	10	US-09-925-301-1013	Sequence 1013, Ap
44	34	48.6	209	10	US-09-904-536-8	Sequence 8, Appl
45	34	48.6	209	10	US-09-904-536-9	Sequence 9, Appl

#### ALIGNMENTS

RESULT 1  
US-09-798-869-2  
; Sequence 2, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;  
Best Local Similarity 91.7%; Pred. No. 3.8e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRNNRKR 12  
DB 3 CFQWRNNRKR 14

RESULT 2  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON

```
/ APPLICANT: LARS VORLAND
/ TITLE OF INVENTION: BIOACTIVE PEPTIDES
/ FILE REFERENCE: A34049-PCT-USA-A
/ CURRENT APPLICATION NUMBER: US/09/798,869
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: PCT/GB99/02851
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: GB9818938.4
/ PRIOR FILING DATE: 1998-08-28
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match          92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CFAWQNNRKVR 12
      |||||
Db      3 CFQWQNNRKVR 14

RESULT 3
US-10-023-096-2
/ Sequence 2, Application US/10023096
/ Patent No. US20020160941A1
/ GENERAL INFORMATION:
/ APPLICANT: Krugel, Marian L.
/ APPLICANT: Kurecki, Tomasz
/ APPLICANT: Gollnick, Paul D.
/ APPLICANT: Doyle, Darrell J.
/ TITLE OF INVENTION: Cloning, Expression, and Uses of Human
/ TITLE OF INVENTION: Lactoferrin
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jacobson, Price, Holman & Stern
/ STREET: 400 Seventh St. N.W.
/ CITY: Washington D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,096
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/724,586
/ FILING DATE: 30-SEPT-1996
/ APPLICATION NUMBER: US 08/238,445
/ FILING DATE: 05-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10505/P58185C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 638-6666
/ TELEFAX: (202) 393-5350
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 694 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-10-023-096-2

Query Match          92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CFAWQNNRKVR 12
      |||||
Db      3 CFQWQNNRKVR 14

Query Match          92.9%; Score 65; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CFAWQNNRKVR 12
      |||||
Db      22 CFQWQNNRKVR 33

RESULT 4
US-09-798-869-6
/ Sequence 6, Application US/09798869
/ Publication No. US20030022821A1
/ GENERAL INFORMATION:
/ APPLICANT: JOHN SIGURD SVENDSEN
/ APPLICANT: (YSTEIN REKDAL)
/ APPLICANT: BALDUR SVEINBJ (RNSSON)
/ APPLICANT: LARS VORLAND
/ TITLE OF INVENTION: BIOACTIVE PEPTIDES
/ FILE REFERENCE: A34049-PCT-USA-A
/ CURRENT APPLICATION NUMBER: US/09/798,869
/ CURRENT FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: PCT/GB99/02851
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: GB9818938.4
/ PRIOR FILING DATE: 1998-08-28
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
/ OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match          81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CFAWQNNRKVR 12
      |||||
Db      3 CFQWQNNRKVR 14

RESULT 5
US-09-798-869-3
/ Sequence 3, Application US/09798869
/ Publication No. US20030022821A1
/ GENERAL INFORMATION:
/ APPLICANT: JOHN SIGURD SVENDSEN
/ APPLICANT: (YSTEIN REKDAL)
/ APPLICANT: BALDUR SVEINBJ (RNSSON)
/ APPLICANT: LARS VORLAND
/ TITLE OF INVENTION: BIOACTIVE PEPTIDES
/ FILE REFERENCE: A34049-PCT-USA-A
/ CURRENT APPLICATION NUMBER: US/09/798,869
/ CURRENT FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: PCT/GB99/02851
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: GB9818938.4
/ PRIOR FILING DATE: 1998-08-28
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: CAPRINE
US-09-798-869-3

Query Match          68.6%; Score 48; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.029;
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Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11  
 Db 3 CYQWQRMKRL 13

## RESULT 6

US-09-798-869-23  
 ; Sequence 23, Application US/09798869  
 ; Publication No. US20030022821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN SIGURD SVENDSEN  
 ; APPLICANT: (YSTEIN REKDAL  
 ; APPLICANT: BALDUR SVEINBJ (RNSSON  
 ; APPLICANT: LARS VORLAND  
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
 ; FILE REFERENCE: A34049-PCT-USA-A  
 ; CURRENT APPLICATION NUMBER: US/09/798,869  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: GB9818938.4  
 ; PRIOR FILING DATE: 1998-08-28  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 23  
 ; LENGTH: 25  
 ; TYPE: PRT  
 ; ORGANISM: CAPRINE  
 US-09-798-869-23

Query Match 58.6%; Score 48; DB 9; Length 25;  
 Best Local Similarity 63.6%; Pred. No. 0.046;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11  
 Db 3 CYQWQRMKRL 13

## RESULT 7

US-09-798-869-4  
 ; Sequence 4, Application US/09798869  
 ; Publication No. US20030022821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN SIGURD SVENDSEN  
 ; APPLICANT: (YSTEIN REKDAL  
 ; APPLICANT: BALDUR SVEINBJ (RNSSON  
 ; APPLICANT: LARS VORLAND  
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
 ; FILE REFERENCE: A34049-PCT-USA-A  
 ; CURRENT APPLICATION NUMBER: US/09/798,869  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: GB9818938.4  
 ; PRIOR FILING DATE: 1998-08-28  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: MURINE  
 US-09-798-869-4

Query Match 61.4%; Score 43; DB 9; Length 15;  
 Best Local Similarity 63.6%; Pred. No. 0.2;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11  
 Db 3 CLRQWQRMKRV 13

## RESULT 8

US-09-798-869-22  
 ; Sequence 22, Application US/09798869  
 ; Publication No. US20030022821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN SIGURD SVENDSEN  
 ; APPLICANT: (YSTEIN REKDAL  
 ; APPLICANT: BALDUR SVEINBJ (RNSSON  
 ; APPLICANT: LARS VORLAND  
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
 ; FILE REFERENCE: A34049-PCT-USA-A  
 ; CURRENT APPLICATION NUMBER: US/09/798,869  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: GB9818938.4  
 ; PRIOR FILING DATE: 1998-08-28  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 25  
 ; TYPE: PRT  
 ; ORGANISM: MURINE  
 US-09-798-869-22

Query Match 61.4%; Score 43; DB 9; Length 25;  
 Best Local Similarity 63.6%; Pred. No. 0.32;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11  
 Db 3 CLRQWQRMKRV 13

## RESULT 9

US-09-798-869-7  
 ; Sequence 7, Application US/09798869  
 ; Publication No. US20030022821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN SIGURD SVENDSEN  
 ; APPLICANT: (YSTEIN REKDAL  
 ; APPLICANT: BALDUR SVEINBJ (RNSSON  
 ; APPLICANT: LARS VORLAND  
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
 ; FILE REFERENCE: A34049-PCT-USA-A  
 ; CURRENT APPLICATION NUMBER: US/09/798,869  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: GB9818938.4  
 ; PRIOR FILING DATE: 1998-08-28  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
 ; OTHER INFORMATION: sequence)  
 US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;  
 Best Local Similarity 54.5%; Pred. No. 0.64;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11  
 Db 3 CYQWQRMKRL 13

RESULT 10  
US-09-798-869-8  
; Sequence 8, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: US/09/798,869  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine  
; OTHER INFORMATION: sequence)  
US-09-798-869-8

Query Match 57.1%; Score 40; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.64;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11  
| | | | |  
Db 3 CLRQWEMRKV 13

RESULT 11  
US-09-798-869-29  
; Sequence 29, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: US/09/798,869  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-29

Query Match 57.1%; Score 40; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.64;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11  
| | | | |  
Db 3 CLRQWEMRKV 13

RESULT 12  
US-09-798-869-30

; Sequence 30, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: US/09/798,869  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-30

Query Match 57.1%; Score 40; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.64;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQRMNRKV 11  
| | | | |  
Db 3 CLRQWEMRKV 13

RESULT 13  
US-09-978-295A-119  
; Sequence 119, Application US/09978295A  
; Patent No. US2002015606A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC11  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US/09/978,295A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17

1 PRIOR APPLICATION NUMBER: 60/064249  
2 PRIOR FILING DATE: 1997-11-03  
3 PRIOR APPLICATION NUMBER: 60/065311  
4 PRIOR FILING DATE: 1997-11-13  
5 PRIOR APPLICATION NUMBER: 60/066364  
6 PRIOR FILING DATE: 1997-11-21  
7 PRIOR APPLICATION NUMBER: 60/077450  
8 PRIOR FILING DATE: 1998-03-10  
9 PRIOR APPLICATION NUMBER: 60/077632  
10 PRIOR FILING DATE: 1998-03-11  
11 PRIOR APPLICATION NUMBER: 60/077641  
12 PRIOR FILING DATE: 1998-03-11  
13 PRIOR APPLICATION NUMBER: 60/077649  
14 PRIOR FILING DATE: 1998-03-11  
15 PRIOR APPLICATION NUMBER: 60/077791  
16 PRIOR FILING DATE: 1998-03-12  
17 PRIOR APPLICATION NUMBER: 60/078004  
18 PRIOR FILING DATE: 1998-03-13  
19 PRIOR APPLICATION NUMBER: 60/078886  
20 PRIOR FILING DATE: 1998-03-20  
21 PRIOR APPLICATION NUMBER: 60/078936  
22 PRIOR FILING DATE: 1998-03-20  
23 PRIOR APPLICATION NUMBER: 60/078910  
24 PRIOR FILING DATE: 1998-03-20  
25 PRIOR APPLICATION NUMBER: 60/078939  
26 PRIOR FILING DATE: 1998-03-20  
27 PRIOR APPLICATION NUMBER: 60/079294  
28 PRIOR FILING DATE: 1998-03-25  
29 PRIOR APPLICATION NUMBER: 60/079656  
30 PRIOR FILING DATE: 1998-03-26  
31 PRIOR APPLICATION NUMBER: 60/079664  
32 PRIOR FILING DATE: 1998-03-27  
33 PRIOR APPLICATION NUMBER: 60/079689  
34 PRIOR FILING DATE: 1998-03-27  
35 PRIOR APPLICATION NUMBER: 60/079663  
36 PRIOR FILING DATE: 1998-03-27  
37 PRIOR APPLICATION NUMBER: 60/079728  
38 PRIOR FILING DATE: 1998-03-27  
39 PRIOR APPLICATION NUMBER: 60/079786  
40 PRIOR FILING DATE: 1998-03-27  
41 PRIOR APPLICATION NUMBER: 60/079920  
42 PRIOR FILING DATE: 1998-03-30  
43 PRIOR APPLICATION NUMBER: 60/079923  
44 PRIOR FILING DATE: 1998-03-30  
45 PRIOR APPLICATION NUMBER: 60/080105  
46 PRIOR FILING DATE: 1998-03-31  
47 PRIOR APPLICATION NUMBER: 60/080107  
48 PRIOR FILING DATE: 1998-03-31  
49 PRIOR APPLICATION NUMBER: 60/080165  
50 PRIOR FILING DATE: 1998-03-31  
51 PRIOR APPLICATION NUMBER: 60/080194  
52 PRIOR FILING DATE: 1998-03-31  
53 PRIOR APPLICATION NUMBER: 60/080327  
54 PRIOR FILING DATE: 1998-04-01  
55 PRIOR APPLICATION NUMBER: 60/080328  
56 PRIOR FILING DATE: 1998-04-01  
57 PRIOR APPLICATION NUMBER: 60/080333  
58 PRIOR FILING DATE: 1998-04-01  
59 PRIOR APPLICATION NUMBER: 60/080334  
60 PRIOR FILING DATE: 1998-04-01  
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62 PRIOR FILING DATE: 1998-04-08  
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Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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US-09-978-697-119

; Sequence 119, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
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 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desncoyze, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
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 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630PIC27  
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, APPLICANT: Baker Kevin P.
, APPLICANT: Botstein, David
, APPLICANT: Desnucys, Luc
, APPLICANT: Eaton, Dan
, APPLICANT: Ferrara, Napoleon
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, TITLE OF INVENTION: Acids Encoding the
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Query Match 54.3%; Score 38; DB 9; Length 338;  
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds  
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Title: US-09-743-107b-70

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*\*

2: PIR2:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 JC2323	lactoferrin - goat
3	47	67.1	511	2 AB0858	hypothetical prote
4	45	64.3	33	2 S52107	lactoferrin - shee
5	43	61.4	121	2 AH3147	hypothetical prote
6	43	61.4	282	2 F90580	hypothetical prote
7	43	61.4	707	1 A28438	lactoferrin precu
8	41	58.6	306	1 A39654	cell cycle arrest
9	40	57.1	134	2 D33876	carcinoembryonic a
10	40	57.1	298	2 AD2346	hypothetical prote
11	40	57.1	393	2 D71876	3-deoxy-manno-octu
12	40	57.1	584	2 C84325	hypothetical prote
13	40	57.1	720	2 A96907	hypothetical prote
14	39	55.7	205	2 B90094	26S proteasome SU
15	39	55.7	274	2 B60950	apolipoprotein B-1
16	39	55.7	393	2 B64639	3-deoxy-manno-octu
17	39	55.7	681	2 T19429	hypothetical prote
18	38	54.3	196	2 T00702	hypothetical prote
19	38	54.3	275	1 JC1113	interleukin-2 rece
20	38	54.3	275	1 S07442	interleukin-2 rece
21	38	54.3	289	2 G86403	33.3K hypothetical
22	38	54.3	558	2 T17324	hypothetical prote
23	38	54.3	749	2 A45687	outer capsid prote
24	38	54.3	4568	2 T08030	dynamin beta heavy
25	37	52.9	236	2 A84686	hypothetical prote
26	37	52.9	365	2 I37477	MHC class I histoc
27	37	52.9	500	2 S42867	protein kinase (EC
28	37	52.9	500	2 G71633	ADP-ATP carrier pr
29	37	52.9	2700	2 D88450	protein F21H11.2 [

30 36 51.4 267 2 S77802  
31 36 51.4 283 2 D72378  
32 36 51.4 346 2 F95315  
33 36 51.4 372 2 S76885  
34 36 51.4 386 2 B82921  
35 36 51.4 415 2 H82095  
36 36 51.4 428 2 F81660  
37 36 51.4 431 2 S50977  
38 36 51.4 489 2 C70655  
39 36 51.4 502 2 T01179  
40 36 51.4 1432 2 B85431  
41 35 50.0 61 2 B90853  
42 35 50.0 61 2 E90875  
43 35 50.0 61 2 A30910  
44 35 50.0 206 2 H97451  
45 35 50.0 206 2 AB2670

#### ALIGNMENTS

##### RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text\_change 08-Dec-2000

A:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:REV. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A>Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148 'T', 150-422 'C', 424-711 <REV>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A>Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A>Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:12374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

```

Query Match          68.6%; Score 48; DB 2; Length 708;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 2; Indels

Qy 1 CFAWQNRNRKV 11
   |:|:|:|:|:|
Db 38 CYQWQNRNRKL 48

RESULT 3
AB0858
hypothetical protein STY3070 [imported] - Salmonella enterica s
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C:Accession: AB0858
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard,
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dow
, S.; Moulie, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A:Title: Complete genome sequence of a multiple drug resistant
A:Reference number: AB0502; PMID:11677608
A:Accession: AB0858
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <PAR>
A:Cross-references: GB:AL513382; PID:CAD06049.1; PID:gl6504016
C:Genetics:
A:Gene: STY3070

Query Match          67.1%; Score 47; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 4; Indels

Qy 1 CFAWQNRNRKV 12
   |:|:|:|:|:|
Db 350 CFAWQNRNRKV 361

RESULT 4
SS2107
lactoferrin - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sh
C:Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change
C:Accession: SS2107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A:Title: Isolation and characterization of sheep lactoferrin, a
A:Reference number: SS2107; MUID:95127729; PMID:7827104
A:Accession: SS2107
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-33 <QIA>
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication

Query Match          64.3%; Score 45; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 0.25;
Matches 6; Conservative 3; Mismatches 2; Indels

Qy 1 CFAWQNRNRKV 11
   |:|:|:|:|
Db 19 CYQWQNRNRKL 29

RESULT 5
AH3147
hypothetical protein Atu4804 [imported] - Agrobacterium tumefac
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change
C:Accession: AH3147

```

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
 A;Reference number: AB2577; PMID:11743193  
 A;Accession: AH3147  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-121 <KUR>  
 A;Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187  
 A;Experimental source: strain C58 (Dupont)  
 C;Genetics:  
 A;Gene: Atu4804  
 A;Map position: linear chromosome

Query Match 61.4%; Score 43; DB 2; Length 121;  
 Best Local Similarity 63.6%; Pred. No. 2;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNNRKV 11  
 Db 14 CLAWQNNRV 24  
 ||||| |

RESULT 6  
 F90580  
 A;Title: Hypothetical protein MYPV 5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
 C;Species: Mycoplasma pulmonis  
 C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
 C;Accession: F90580  
 R;Chamoud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
 Nucleic Acids Res. 29, 2145-2153, 2001  
 A;Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*  
 A;Reference number: A99512; MUID:21267165; PMID:11353084  
 A;Accession: F90580  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-282 <KUR>  
 A;Cross-references: GB:AL445566; PID:g14089965; PIDN:CAC13723.1; GSPDB:GN00153  
 A;Experimental source: strain UAB CTIP  
 C;Genetics:  
 A;Gene: MYPV 5500  
 A;Genetic code: SGC3

Query Match 61.4%; Score 43; DB 2; Length 282;  
 Best Local Similarity 60.0%; Pred. No. 4.4;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWQNNRKV 11  
 Db 20 FAWQNNIKKI 29  
 ||||| |

RESULT 7  
 A28438  
 A;Title: Lactoferrin precursor - mouse  
 N;Alternate names: lactotransferrin  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A28438; A41205  
 R;Pentecost, B.T.; Teng, C.T.  
 J. Biol. Chem. 262, 10134-10139, 1987  
 A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre  
 A;Reference number: A92596; MUID:87280033; PMID:3611056  
 A;Accession: A28438  
 A;Molecule type: mRNA  
 A;Residues: 3-707 <PEN>  
 A;Cross-references: EMBL:J03298  
 R;Lin, Y.; Teng, C.T.  
 J. Biol. Chem. 266, 21880-21885, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.  
 A;Reference number: A41205; MUID:92042099; PMID:1939212  
 A;Accession: A41205  
 A;Molecule type: DNA  
 A;Residues: 1-15 <LIU>  
 A;Cross-references: GB:M74778  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-707/Product: lactotransferrin #status predicted <WAT>  
 F;358-695/Domain: transferrin repeat homology <TRH2>  
 F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 1; Length 707;  
 Best Local Similarity 63.6%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQNNRKV 11  
 Db 37 CLRWQNNRKV 47  
 ||||| |

RESULT 8  
 A39654  
 A;Title: cell cycle arrest protein BUB2 - yeast (*Saccharomyces cerevisiae*)  
 N;Alternate names: protein YN9796.08C; protein YNR055C  
 C;Species: *Saccharomyces cerevisiae*  
 C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jul-2000  
 C;Accession: A39654; S54555; S19034  
 R;Hoyt, M.A.; Totlis, L.; Roberts, B.T.  
 Cell 66, 507-517, 1991

A;Title: *Saccharomyces cerevisiae* genes required for cell cycle arrest in response to lor  
 A;Reference number: A39654; MUID:91330299; PMID:1651171  
 A;Accession: A39654  
 A;Molecule type: DNA  
 A;Residues: 1-306 <HOY>  
 A;Cross-references: GB:M64706; NID:g171133; PIDN:AAA16885.1; PID:g171135  
 R;Devlin, K.; Churcher, C.M.  
 submitted to the EMBL Data Library, May 1995  
 A;Reference number: S54558  
 A;Accession: S54555  
 A;Molecule type: DNA  
 A;Residues: 1-306 <DEV>  
 A;Cross-references: EMBL:Z49703; NID:g817880; PIDN:CAA89765.1; PID:g817888; GSPDB:GN00011

Query Match 58.6%; Score 41; DB 1; Length 306;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNNRK 10  
 Db 108 CFAWQNNRK 117  
 ||||| |

RESULT 9  
 D33876  
 A;Title: carcinoembryonic antigen homolog 4 - rat (fragment)  
 C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 23-Jul-1999  
 C;Accession: D33876  
 R;Kodelja, V.; Lucas, K.; Barnet, S.; von Kleist, S.; Thompson, J.A.; Zimmermann, W.  
 J. Biol. Chem. 264, 6906-6912, 1989  
 A;Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis of  
 A;Reference number: A33876; MUID:89214106; PMID:2708349  
 A;Accession: D33876  
 A;Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-114 <KOD>  
A:Cross-references: GB:M60026; NID:9203407; PIDN:AAA40911.1; PID:9554427; GB:J04626; GB:  
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 57.1%; Score 40; DB 2; Length 114;  
Best Local Similarity 60.0%; Pred. No. 6.2;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNRNKKV 11  
|||:|:|:  
Db 42 FAWYGLRKI 51

RESULT 10  
AD2346  
hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AD2346  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AD2346  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA876022.1; PID:gl7133459; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr4323

Query Match 57.1%; Score 40; DB 2; Length 298;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNRNKK 10  
|||:|:|:  
Db 163 FHWQNRK 171

RESULT 11  
D71876  
3-deoxy-manno-octulosonate cytidyltransferase [EC 2.7.7.38] [similarity] - Helicobacte  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 28-Jul-2000  
C:Accession: D71876  
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A:Reference number: A71800; MUID:99120557; PMID:99233682  
A:Accession: D71876  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-393 <ARN>  
A:Cross-references: GB:AE001518; GB:AE001439; NID:G4155454; PIDN:AAD06459.1; PID:G415545  
A:Experimental source: strain J99  
C:Genetics:  
A:Gene: waaA  
C:Superfamily: Chlamydia trachomatis 3-deoxy-manno-octulosonate cytidyltransferase  
C:Keywords: nucleotidyltransferase

Query Match 57.1%; Score 40; DB 2; Length 393;  
Best Local Similarity 36.4%; Pred. No. 21;  
Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 FAWQNRNKKV 12  
|||:|:|:|:  
Db 616 CLAWDRNQR 624

RESULT 14  
E90094  
26S proteasome SU B5 [imported] - Guillardia theta nucleomorph  
C:Species: nucleomorph Guillardia theta  
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

Db 110 FAWKNLKRLK 120

RESULT 12  
C84325  
hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: C84325  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabic  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: C84325  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-584 <STO>  
A:Cross-references: GB:AE004437; NID:gl0581192; PIDN:AAG19967.1; GSPDB:GN00138  
C:Genetics:  
A:Gene: VNG1732C

Query Match 57.1%; Score 40; DB 2; Length 584;  
Best Local Similarity 41.7%; Pred. No. 30;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRNKKV 12  
|||:|:|:|:  
Db 445 CFTWRKQNERK 456

RESULT 13  
A96807  
hypothetical protein T32E8.5 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: A96807  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A96807  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-720 <STO>  
A:Cross-references: GB:AE0051173; NID:G6437532; PIDN:AAF08564.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: T32E8.5  
A:Map position: 1

Query Match 57.1%; Score 40; DB 2; Length 720;  
Best Local Similarity 66.7%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRNKR 9  
|||:|:|:|:  
Db 616 CLAWDRNQR 624

RESULT 14  
E90094  
26S proteasome SU B5 [imported] - Guillardia theta nucleomorph  
C:Species: nucleomorph Guillardia theta  
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
 C;Accession: E90094  
 R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif  
 Nature 410, 1091-1096, 2001  
 A;Title: The highly reduced genome of an enslaved algal nucleus.  
 A;Reference number: A99082; MUID:11323671; PMID:11323671  
 A;Accession: E90094  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-205 <DOU>  
 A;Cross-references: GB:AF165818; NID:gl3794510; PIDN:AAK39885.1; GSPDB:GN00150  
 C;Genetics:  
 A;Gene: prsB5  
 A;Map position: 1  
 A;Genome: nucleomorph  
 C;Keywords: nucleomorph

Query Match 55.7%; Score 39; DB 2; Length 205;  
 Best Local Similarity 62.5%; Pred.No. 16;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQRNM 8  
 |||:  
 Db 63 CFFWERNL 70

## RESULT 15

B60950  
 apolipoprotein B-100 - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Dec-1993 #sequence\_revision 09-Sep-1994 #text\_change 07-Oct-1994  
 C;Accession: B60950  
 R;Law, A.; Scott, J.  
 J. Lipid Res. 31, 1109-1120, 1990  
 A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL  
 A;Reference number: A60950; MUID:90324804; PMID:2373961  
 A;Accession: B60950  
 A;Molecule type: mRNA  
 A;Residues: 1-274 <LAW>  
 A;Note: authors translated the codon ATA for residue 8 as Val  
 C;Superfamily: apolipoprotein B  
 C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 55.7%; Score 39; DB 2; Length 274;  
 Best Local Similarity 60.0%; Pred.No. 22;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 AWQRNMRKVR 12  
 :|||:  
 Db 38 SWDRNLKRF 47

Search completed: February 21, 2003, 07:47:39  
 Job time : 11.65 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107B-70  
Perfect score: 70  
Sequence: 1 CFAWQNMRRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TRFL_HUMAN	P02788 homo sapien
2	48	68.6	708	1 TRFL_CAMDR	Q9tuo0 camelus dro
3	48	68.6	708	1 TRFL_CAPHI	Q29477 capra hircu
4	44	62.9	695	1 TRFL_HORSE	O77811 equus cabal
5	43	61.4	707	1 TRFL_MOUSE	P08071 mus musculu
6	41	58.6	306	1 BUB2_YEAST	P26448 saccharomyc
7	38	54.3	275	1 IL2A_BOVIN	P12342 bos taurus
8	38	54.3	275	1 IL2A_SHEEP	P26898 ovis aries
9	38	54.3	749	1 VP4_ROTGA	Q04916 rotavirus (
10	38	54.3	2273	1 ABCR_HUMAN	P78163 homo sapien
11	38	54.3	4568	1 DYHB_CHLRE	P35630 drosophila
12	37	52.9	267	1 RS3A_DROME	Q39565 chlamydomon
13	37	52.9	365	1 IA34_HUMAN	P30453 homo sapien
14	37	52.9	435	1 DHOM_METGL	P37143 methylcobaci
15	37	52.9	500	1 TLCE_RICPR	O05962 rickettsia
16	36	51.4	62	1 RL28_THETN	Q8x9u1 thermoanaer
17	36	51.4	267	1 Y125_MYCCA	P53661 mycoplasma
18	36	51.4	428	1 SYH_CHLMU	Q991j9 chlamydia m
19	35	50.0	460	1 YQSI_CABEL	Q09309 caenorhabdi
20	35	50.0	685	1 YL14_CABEL	Q11100 caenorhabdi
21	35	50.0	675	1 ZG20_XENLA	P18714 xenopus lae
22	35	50.0	783	1 YNR2_CABEL	Q21988 caenorhabdi
23	35	50.0	1179	1 ATX1_ARATH	O91t02 arabidopsis
24	35	50.0	1574	1 RPOC_AGUAH	O67763 aquifex aeo
25	35	50.0	1576	1 RPOC_AQUFY	Q9xgy2 aquifex pyr
26	35	50.0	1592	1 YH05_YEAST	P38735 saccharomyc
27	35	50.0	1750	1 Y832_METJA	Q58242 methanococc
28	34	48.6	60	1 RL28_BACST	P23374 bacillus st
29	34	48.6	62	1 RL28_LISMO	Q92aj2 listeria mo
30	34	48.6	175	1 PAPI_HUMAN	Q06141 homo sapien
31	34	48.6	227	1 LIPIB_XNYN3	P74519 synecocyst
32	34	48.6	235	1 FL3L_HUMAN	P49771 homo sapien
33	34	48.6	267	1 IL2A_RAT	P26897 rattus norv

34 34 48.6 272 1 IL2A\_HUMAN P01589 homo sapien  
35 34 48.6 334 1 CATL\_MOUSE P06797 mus musculu  
36 34 48.6 334 1 CATL\_RAT P07154 rattus norv  
37 34 48.6 360 1 HISS\_LACLA Q02135 lactococcus  
38 34 48.6 369 1 SP11\_MYXVL P12393 myxoma viru  
39 34 48.6 413 1 CYCL\_DROME O61734 drosophila  
40 34 48.6 428 1 SYH\_CHLTR O84547 chlamydia t  
41 34 48.6 453 1 O83A\_DROME Q9vnb3 drosophila  
42 34 48.6 572 1 MAOX\_HUMAN P48163 homo sapien  
43 34 48.6 572 1 MAOX\_RAT P13697 rattus norv  
44 34 48.6 705 1 FRZ4\_DROME Q9nbw1 drosophila  
45 34 48.6 1293 1 XPC\_DROME Q24595 drosophila

## ALIGNMENTS

RESULT 1  
TRFL\_HUMAN  
ID TRFL\_HUMAN STANDARD; PRT; 711 AA.  
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;  
AC Q96KZ5;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;  
DE Lactoferrin B; Lactoferrin C].  
GN LTF OR LF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90384839; PubMed=2402455;  
RA Rev M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;  
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";  
RL Nucleic Acids Res. 18:5288-5288(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cho Y.Y.;  
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Conneely O.M.;  
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Liang Q., Jimenez-Flores R., Richardson T.;  
RL "Molecular cloning and sequence analysis of human lactoferrin.";  
RN Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Wei X., Han J., Rado T.A.;  
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA  
RN sequences.";  
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cheng H., Chen X., Huan L.;  
RL "cDNA cloning and sequence analysis of human lactoferrin.";  
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Osdan J.E.  
RT "Nucleotide sequence of human lactoferrin cDNA."  
RL Nucleic Acids Res. 18:4013-4013 (1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
RA Legrand D., Spik G., Montreuil J., Jolles P.,  
RT "Human lactoferrin: amino acid sequence and structural  
RT comparisons with other transferrins."  
RL Eur. J. Biochem. 145:659-666 (1984).  
RN [10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
RA Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
RT alignment of the cyanogen bromide fragments and characterization of  
RT N- and C-terminal domains."  
RN Biochim. Biophys. Acta 670:243-254 (1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J.,  
RA Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
RT lactotransferrin."  
RL FEBS Lett. 142:1107-110 (1982).  
RN [12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
RT expression of mRNA during normal and leukemic myelopoiesis."  
RL Blood 70:989-993 (1987).  
RN [13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nhoj L., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnan C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
RA Dragon Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RA Sagripanti J.L.;  
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2585506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
RT and refinement at 2.8-A resolution."  
RL J. Mol. Biol. 209:711-734 (1989).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
RT resolution."  
RL Acta Crystallogr. D 51:629-646 (1995).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
RA Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
RT binding properties and crystal structure of the histidine-  
RT 253-->methionine mutant."  
RL Biochemistry 36:341-346 (1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in *Aspergillus*  
RT *awamori*."  
RL Acta Crystallogr. D 55:403-407 (1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
RT and analysis of ligand-induced conformational change."  
RL Acta Crystallogr. D 54:1319-1335 (1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioid antagonist peptides derived  
RT from human lactoferrin."  
RL Agric. Biol. Chem. 54:1803-1810 (1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
RA Omsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaramanickavel G., Munier P., Schorderet D.F.,  
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejtmanek J.F., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
RT corneal dystrophy): exclusion of linkage to lactoferrin gene."  
RL Mol. Vision 4:31-32 (1998).  
RN [21]  
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
CC OF AN ANION, USUALLY BICARBONATE.  
CC [22]  
RP FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST  
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC [23]  
RP SUBUNIT: MONOMER.  
CC [24]  
RP SUBCELLULAR LOCATION: Secreted.  
CC [25]  
RP DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC [26]  
RP SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC [27]  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC [28]  
RP EMBL; X53961; CAA37914.1; -  
DR EMBL; U07643; AAB60324.1; -  
DR EMBL; M93150; AAA36159.1; -  
DR EMBL; M83202; AAA59511.1; -  
DR EMBL; M83205; AAA58656.1; -  
DR EMBL; M18642; AAA86665.1; -  
DR EMBL; AF332168; AAG48753.1; -  
DR EMBL; BC015822; AAI15822.1; -  
DR EMBL; BC015823; AAI15823.1; -  
DR EMBL; M73700; AAA59479.1; -  
DR EMBL; X52941; CAA37116.1; -  
DR EMBL; U95626; AAB57795.1; -  
DR PIR; S11228; TFHUL.  
DR PDB; 1LCP; 31-AUG-94.  
DR PDB; 1LCT; 31-OCT-93.  
DR PDB; 1LFG; 31-JUL-94.  
DR PDB; 1LFI; 31-OCT-93.  
DR PDB; 1LFT; 31-OCT-93.  
DR PDB; 1LGB; 31-AUG-94.  
DR PDB; 1LGC; 31-AUG-94.  
DR PDB; 1LKA; 08-NOV-96.  
DR PDB; 1LSD; 08-MAR-96.  
DR PDB; 1HSE; 12-MAR-97.  
DR PDB; 1VFD; 21-APR-97.



Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00028;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKKVR 12  
 DB 39 CFQWQNNRKKVR 50

## RESULT 2

TRFL CAMDR  
 ID \_TRFL CAMDR STANDARD; PRT; 708 AA.  
 AC QPTUMQ; Q3MZS5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; AJ131674; CAB53387.1; -  
 EMBL; AF165879; AAF82241.1; -  
 HSP; 077811; IBLX.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SMC0094; TR\_FER.2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW signal.  
 FT CHAIN 1 19 BY SIMILARITY.  
 FT REPEAT 20 708 LACTOTRANSFERRIN.  
 FT REPEAT 20 363 1.  
 FT REPEAT 364 708 2.  
 FT DISULFID 28 64 BY SIMILARITY.  
 FT DISULFID 38 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 080C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;  
 Best Local Similarity 66.7%; Pred. No. 0.34;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNNRKKVR 12  
 DB 38 CAQWQNNRKKVR 49

## RESULT 3

TRFL CAPHI  
 ID \_TRFL CAPHI STANDARD; PRT; 708 AA.  
 AC Q29477; Q29479;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA MEDLINE=94380047; PubMed=8093048;  
 RX le Provost F., Nocard M., Guerin G., Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the  
 RT relevant locus to bovine U12 syntenic group."  
 EL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC  
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 CC  
 CC EMBL; U53857; AAA97958.1; -;  
 CC EMBL; X78902; CAA55517.1; -;  
 CC HSSP; O77698; ICE2.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SM00094; TR\_FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN\_1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 CC PROSITE; PS00207; TRANSFERRIN\_3; 2.  
 CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 CC Signal.  
 CC 1 19 BY SIMILARITY.  
 CC CHAIN 20 708 LACTOTRANSFERRIN.  
 CC REPEAT 20 363 1.  
 CC REPEAT 364 708 2.  
 CC FT DISULFID 28 64 BY SIMILARITY.  
 CC FT DISULFID 38 55 BY SIMILARITY.  
 CC FT DISULFID 134 217 BY SIMILARITY.  
 CC FT DISULFID 176 192 BY SIMILARITY.  
 CC FT DISULFID 189 200 BY SIMILARITY.  
 CC FT DISULFID 250 264 BY SIMILARITY.  
 CC FT DISULFID 367 399 BY SIMILARITY.  
 CC FT DISULFID 377 390 BY SIMILARITY.  
 CC FT DISULFID 424 703 BY SIMILARITY.  
 CC FT DISULFID 444 666 BY SIMILARITY.  
 CC FT DISULFID 476 551 BY SIMILARITY.  
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 CC FT DISULFID 510 524 BY SIMILARITY.  
 CC FT DISULFID 521 534 BY SIMILARITY.  
 CC FT DISULFID 592 606 BY SIMILARITY.  
 CC FT DISULFID 644 649 BY SIMILARITY.  
 CC FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 CC FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 CC FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 CC FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 CC FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 CC FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 CC FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 CC FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 CC FT BINDING 140 140 ANION (BY SIMILARITY).  
 CC FT BINDING 482 482 ANION (BY SIMILARITY).  
 CC FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CONFLICT 56 56 I -> V (IN REF. 2).  
 CC FT CONFLICT 86 86 L -> R (IN REF. 2).  
 CC FT CONFLICT 124 124 Q -> K (IN REF. 2).  
 CC FT CONFLICT 154 154 F -> P (IN REF. 2).  
 CC FT CONFLICT 304 304 S -> R (IN REF. 2).  
 CC FT CONFLICT 414 414 D -> G (IN REF. 2).  
 CC SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;  
 Best Local Similarity 63.6%; Pred. No. 0.34;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFAMQNRVRY 11  
 Db 38 CYQWQRVRY 48

RESULT 4  
 TRFL HORSE  
 ID TRFL HORSE STANDARD; PRT; 695 AA.  
 AC O77811;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).  
 GN LTF.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN (1)  
 RP SEQUENCE FROM N. A.  
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "cDNA sequence of mare lactoferrin";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RC TISSUE=Milk;  
 RX MEDLINE=92296631; PubMed=10366507;  
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "Three-dimensional structure of mare deferic lactoferrin at 2.6-A  
 J. Mol. Biol. 289:303-317(1999).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC  
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 CC  
 CC EMBL; AJ010930; CAA09407.1; -;  
 CC PDB; 1B1X; 02-DEC-98.  
 CC PDB; 1B7U; 02-FEB-99.  
 CC PDB; 1B7Z; 02-FEB-99.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SM00094; TR\_FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN\_1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 CC PROSITE; PS00207; TRANSFERRIN\_3; 1.  
 CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 CC Signal; 3D-structure.  
 CC NON\_TER 1 1  
 CC SIGNAL <1 6 LACTOTRANSFERRIN.  
 CC CHAIN 7 695  
 CC REPEAT 7 350 1.  
 CC REPEAT 351 695 2.  
 CC FT DISULFID 15 51  
 CC FT DISULFID 25 42  
 CC FT DISULFID 121 204  
 CC FT DISULFID 163 179  
 CC FT DISULFID 166 189  
 CC FT DISULFID 176 187  
 CC FT DISULFID 237 251  
 CC FT DISULFID 354 386  
 CC FT DISULFID 364 377  
 CC FT DISULFID 411 690  
 CC FT DISULFID 431 653

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FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 66 66
FT METAL 98 98
FT METAL 198 198
FT METAL 259 259
FT METAL 401 401
FT METAL 439 439
FT METAL 532 532
FT METAL 601 601
FT BINDING 127 127
FT BINDING 469 469
FT CARBOHYD 143 143
FT CARBOHYD 287 287
FT CARBOHYD 482 482
SQ SEQUENCE 695 AA; 75991 MW; 07B84D50E1B165D CRC64;

Query Match 62.9%; Score 44; DB 1; Length 695;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 12
DB 25 CARKFQRMKRV 36

RESULT 5
TRFL_MOUSE STANDARD; PRT: 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T., Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
uterine secretions.";
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishashi K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1939212;
RA Liu Y., Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
RL J. Biol. Chem. 266:21880-21885(1991).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
```

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EMBL; J03298; AAA40525.1; -;  
EMBL; D88510; BAA13633.1; -;  
EMBL; EC006904; AAH06904.1; -;  
EMBL; M74778; AAA39427.1; -;  
PIR; A28438; A28438.  
HSP; P02788; 1CB6.  
MGD; MG1.96837; Itf.  
InterPro; IPR001156; Transferrin.  
Pfam; PF00405; transferrin; 2.  
PRINTS; PR00422; TRANSFERRIN.  
SMART; SMC0094; TR\_FER; 2.  
PROSITE; PS00205; TRANSFERRIN\_1; 1.  
PROSITE; PS00206; TRANSFERRIN\_2; 2.  
PROSITE; PS00207; TRANSFERRIN\_3; 2.  
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
Signal.  
KW SIGNAL.  
FT CHAIN 1 19  
FT REPEAT 20 707  
FT REPEAT 358 707  
FT DISULFID 27 63  
FT DISULFID 37 54  
FT DISULFID 133 216  
FT DISULFID 175 191  
FT DISULFID 188 199  
FT DISULFID 249 263  
FT DISULFID 366 398  
FT DISULFID 376 389  
FT DISULFID 423 702  
FT DISULFID 443 665  
FT DISULFID 475 550  
FT DISULFID 499 693  
FT DISULFID 509 523  
FT DISULFID 520 533  
FT DISULFID 591 605  
FT DISULFID 643 648  
FT METAL 78 78  
FT METAL 110 110  
FT METAL 210 210  
FT METAL 271 271  
FT METAL 413 413  
FT METAL 451 451  
FT METAL 544 544  
FT METAL 613 613  
FT BINDING 139 139  
FT BINDING 481 481  
FT CARBOHYD 118 118  
FT CARBOHYD 494 494  
FT CONFLICT 1 2  
FT CONFLICT 25 25  
FT CONFLICT 82 82  
FT CONFLICT 359 359  
FT CONFLICT 382 382  
FT CONFLICT 449 449  
FT CONFLICT 629 629  
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;

Query Match 61.4%; Score 43; DB 1; Length 707;  
Best Local Similarity 63.6%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11  
DB 37 CLRQWQRMKRV 47

```

RESULT 6
BUB2_YEAST
ID BUB2_YEAST STANDARD; PRT; 306 AA.
AC F25448;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
GN BUB2 OR YNR055C OR YMR996.08C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=91330299; PubMed=1651171;
RA Hoyt M.A., Totis L., Roberts B.T.;
RT "S. cerevisiae genes required for cell cycle arrest in response to
RT loss of microtubule function.";
RL Cell 66:507-517(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21385309; PubMed=11493673;
RA Lee S.B., Jensen S., Frenz L.W., Johnson A.L., Pesquet D.,
RA Johnston L.H.;
RT "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
RT regulates cytokinesis.";
RL J. Cell Sci. 114:2345-2354(2001).
CC -!- FUNCTION: Part of a checkpoint which monitors spindle integrity
CC and prevents premature exit from mitosis. This cell-cycle arrest
CC depends upon inhibition of the G-protein tem1 by the BFA1/BUB2
CC complex.
CC -!- SUBUNIT: Interacts with BFA1.
CC -!- SUBCELLULAR LOCATION: Spindle poles.
CC -!- SIMILARITY: TO S.POMBE CDC16.
CC
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CC
DR EMBL; M64706; AAA16885.1; -.
DR EMBL; 249703; CAA89765.1; -.
DR PIR; A39654; A39654.
DR SGD; S0004659; BUB2.
DR InterPro; IPR000195; RabGAP_TBC.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
KW Cell cycle; Mitosis.
SQ SEQUENCE 306 AA; 35027 MW; A1DDBF548E81EA3 CRC64;

Query Match 58.6%; Score 41; DB 1; Length 306;
Best Local Similarity 60.0%; Pred. No. 2.7; Mismatches 0; Gaps 0;
Matches 6; Conservative 1; Indels 3;

QY 1 CFAWQNRMRK 10
Db 108 CFAWQNRMRK 117

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RESULT 7  
IL2A\_BOVIN

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IL2A_BOVIN STANDARD; PRT; 275 AA.
ID IL2A_BOVIN STANDARD; PRT; 275 AA.
AC P12342;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
DE subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8212503; PubMed=2835311;
RA Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
RA Reeves R., Magnusen J.A.;
RT "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
RL Immunology 63:603-610(1988).
RN [2]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=96116968; PubMed=8563178;
RA Yoo J., de Leon F.A., Stone R.T., Beattie C.W.;
RT "Cloning and chromosomal assignment of the bovine interleukin-2
RT receptor alpha (IL-2R alpha) gene.";
RL Mamm. Genome 6:751-753(1995).
CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC
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CC
DR EMBL; M20818; AAA51414.1; -.
DR EMBL; U24226; AAC48487.1; -.
DR PIR; S07442; S07442.
DR HSP; P01589; IILM.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 2.
DR SMART; SM00032; CCP; 2.
KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
RN SIGNAL 1 21
FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 262 POTENTIAL.
FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 78 SUSHI 1.
FT DOMAIN 122 185 SUSHI 2.
FT DISULFID 24 64 BY SIMILARITY.
FT DISULFID 751 77 BY SIMILARITY.
FT DISULFID 123 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 8.5; Mismatches 0; Gaps 0;
Matches 6; Conservative 1; Indels 5;

QY 1 CFAWQNRMRK 12

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Db 261 CLTWQRKWKQR 272
RESULT 8
IL2A_SHEEP
ID IL2A_SHEEP STANDARD; PRT; 275 AA.
AC P26898;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
DE subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92241682; PubMed=1572550;
RA Bujdosó R., Sargan D.R., Williamson M.L., McConnell I.,
RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
RT protein, CD25."
RL Gene 113,283-284 (1992).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC
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CC
CC EMBL; Z11560; CAA77652.1; -
CC EMBL; X60149; CAA42723.1; -
CC EMBL; A19167; CAA01447.1; -
CC PIR; S18910; S18910.
CC PIR; S18899; S18899.
CC PIR; JC1113; JC1113.
CC HSSP; P01589; IILM.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00084; sushi.2.
CC SMART; SM00032; CCP; 2.
KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 262 POTENTIAL.
FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 78 SUSHI 1.
FT DOMAIN 122 185 SUSHI 2.
FT DISULFID 24 64 BY SIMILARITY.
FT DISULFID 751 77 BY SIMILARITY.
FT DISULFID 123 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 166 186 S -> T (IN REF. 2).
SQ SEQUENCE 275 AA; 30904 MW; 1101A2DE5AC5A088 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CFAMQRNMRKVR 12
DB 261 CLTWQRKWKQR 272

RESULT 9
VP4_ROTGA
ID VP4_ROTGA STANDARD; PRT; 749 AA.
AC Q04316;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
GN S4.
OS Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=12705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93233240; PubMed=8386274;
RA Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;
RT "Identification and baculovirus expression of the VP4 protein of the
RT human group B rotavirus ADRV."
RL J. Virol. 67:2730-2738 (1993).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
CC
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CC
CC EMBL; M91434; AAA47338.1; -
CC InterPro; IPR000416; Cap_VP4.
CC Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 749 AA; 84362 MW; D123527DEAE0P21 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 749;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CFAMQRNMRKVR 12
DB 195 CFTWDMCANVR 206

RESULT 10
ABCR_HUMAN
ID ABCR_HUMAN STANDARD; PRT; 2273 AA.
AC P78363; O60438; O60915; O15112;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Retinal-specific ATP-binding cassette transporter (RIM ABC
DE transporter) (RIM protein) (RMP) (Stargardt disease protein).

```

- GN ABCA4 OR ABCR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., VARIANTS STGD, AND VARIANTS HIS-846 AND GLN-943.  
 RX MEDLINE=97207641; PubMed=9054934;  
 RA Allikmets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,  
 RA Chidambaram A., Gerrard B., Baird L., Stauffer D., Peiffer A.,  
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 RA Nathans J., Leppert M., Dean M., Lupski J.R.;  
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 RL Nat. Genet. 15:236-246(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97345663; PubMed=9202155;  
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 RA "The photoreceptor rim protein is an ABC transporter encoded by the  
 RT gene for recessive Stargardt's disease (ABCR).";  
 RL FEBS Lett. 409:247-252(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.  
 RX MEDLINE=98153759; PubMed=9503029;  
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 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANTS STGD.  
 RX MEDLINE=98141123; PubMed=9490294;  
 RA Nasonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,  
 RA Weber B.H.F.;  
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 RL Hum. Genet. 102:21-26(1998).  
 RN [5]  
 RP CHARACTERIZATION.  
 RX MEDLINE=99175213; PubMed=10075733;  
 RA Sun H., Molday R.S., Nathans J.;  
 RA "Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR,  
 RT the photoreceptor-specific ATP-binding cassette transporter  
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 RL J. Biol. Chem. 274:8269-8281(1999).  
 RN [6]  
 RP DISEASE.  
 RX MEDLINE=98133912; PubMed=9466990;  
 RA Cremers F.P.M., van de Pol D.J.R., van Driel M.A., den Hollander A.I.,  
 RA van Haren F.J.J., Knoers N.V.A.M., Tijmes N., Bergan A.A.B.,  
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 RA "Autosomal recessive retinitis pigmentosa and cone-rod dystrophy  
 RT caused by splice site mutations in the Stargardt's disease gene  
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 RL Hum. Mol. Genet. 7:355-362(1998).  
 RN [7]  
 RP VARIANTS ARMD2, AND VARIANTS.  
 RX MEDLINE=97442530; PubMed=9295269;  
 RA Allikmets R., Shroyer N.F., Singh N., Seddon J.M., Lewis R.A.,  
 RA Bernstein P.S., Peiffer A., Zabriskie N.A., Li Y., Hutchinson A.,  
 RA Dean M., Lupski J.R., Leppert M.;  
 RA "Mutation of the Stargardt disease gene (ABCR) in age-related macular  
 RT degeneration.";  
 RL Science 277:1805-1807(1997).  
 RN [8]  
 RP VARIANTS STGD W-18; C-212; H-636; M-1019; V-1038; C-1108; W-1640;  
 RP S-1977 AND H-2107, AND VARIANTS FFM P-11; P-541; V-1038; E-1091;  
 RP C-1508; F-1970 AND R-1971.  
 RX MEDLINE=98454319; PubMed=9781034;  
 RA Rozet J.-M., Gerber S., Souied E., Perrault I., Chatelain S., Ghazi I.,  
 RA Leowski C., Dufier J.-L., Munnich A., Kaplan J.;  
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 RL Eur. J. Hum. Genet. 6:291-295(1998).  
 RN [9]  
 RP VARIANTS STGD.  
 RX MEDLINE=99138655; PubMed=9973280;  
 RA Lewis R.A., Shroyer N.F., Singh N., Allikmets R., Hutchinson A.,  
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 RA "Genotype/phenotype analysis of a photoreceptor-specific ATP-binding  
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 RN [10]  
 RP VARIANTS STGD, AND VARIANTS.  
 RX MEDLINE=99192348; PubMed=10090887;  
 RA Maugeri A., van Driel M.A., van de Pol D.J.R., Klevering B.J.,  
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 RA "The 2589G->C mutation in the ABCR gene is a mild frequent founder  
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 RT classification of ABCR mutations in patients with Stargardt disease.";  
 RL Am. J. Hum. Genet. 64:1024-1035(1999).  
 RN [11]  
 RP VARIANT STGD TYR-54, AND VARIANT ALA-863.  
 RX MEDLINE=20077755; PubMed=10612508;  
 RA Zhang K., Garibaldi D.C., Khazeva M., Albini T., Chiang M.F.,  
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 RN [12]  
 RP VARIANTS STGD V-60; R-206; N-300; P-541; A-849; P-974; V-1038; C-1108;  
 RP L-1408; R-1488; D-1652; P-1729; E-1961; W-2038; W-2077; H-2107; R-2128  
 RP AND Y-2150.  
 RX MEDLINE=99221420; PubMed=10206579;  
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 RT and sequence variations in the ABCR gene.";  
 RL Arch. Ophthalmol. 117:504-510(1999).  
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 RP VARIANTS GLU-1961 AND ASN-2177.  
 RX MEDLINE=20349288; PubMed=10880298;  
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 RA Dalakishvili K., Lupski J.R., Steiner K., Pauleikhoff D., Holz F.G.,  
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 RA Bergan A.A.B., Maugeri A., van Driel M.A., Hoyng C.B., Cremers F.P.M.,  
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 RA Stanga P., Bhattacharya S.S., Bird A.C.;  
 RA "Further evidence for an association of ABCR alleles with age-related  
 RT macular degeneration.";  
 RL Am. J. Hum. Genet. 67:487-491(2000).  
 RN [14]  
 RP VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247;  
 RP V-288; K-471; P-541; Q-572; R-607; K-635; C-653; Y-764; R-765; A-901;  
 RP I-959; K-1036; P-1038; P-1063; D-1087; C-1097; C-1108; L-1380; K-1399;  
 RP P-1430; V-1440; H-1443; L-1486; M-1537; P-1689; L-1705;  
 RP T-1733; R-1748; P-1763; K-1885; H-1898; R-1961; S-1977; G-2077  
 RP W-2077 AND V-2241, AND VARIANTS Q-152; H-212; R-423; I-552; R-914;  
 RP Q-943; T-1562; I-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND  
 RP V-2216.  
 RX MEDLINE=20442027; PubMed=10959763;  
 RA Rivera A., White K., Stoeckel H., Steiner K., Hemmrich N., Grimm T.,  
 RA Juckli B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,  
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RL Am. J. Hum. Genet. 67:800-813(2000).
RN [15]
RP VARIANTS CORD3 GLU-65; CYS-212; PRO-541; ALA-863; GUY-863 DEL;
RP VAL-1038; LYS-1122; TYR-1490 AND ASP-1598.
RX MEDLINE=20442040; PubMed=10958761;
RA Maugeri A., Klevering B.J., Kohrschneider K., Blankenagel A.,
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RT recessive cone-rod dystrophy."
RL Am. J. Hum. Genet. 67:960-966(2000).
RN [16]
RP VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780
RP AND HIS-1898, AND VARIANT GLN-943.
RX MEDLINE=20208356; PubMed=10746567;
RA Shroyer N.F., Lewis R.A., Lupski J.R.,
RT "Complex inheritance of ABCR mutations in Stargardt disease: linkage
RT disequilibrium, complex alleles, and pseudodominance."
RL Hum. Genet. 106:244-248(2000).
RN [17]
RP VARIANTS STGD.
RX MEDLINE=20098082; PubMed=10634594;
RA Papaiwannou M., Osaka L., Bessant D., Lois N., Bird A.C., Payne A.,
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RT "An analysis of ABCR mutations in British patients with recessive
RT retinal dystrophies."
RL Invest. Ophthalmol. Vis. Sci. 41:16-19(2000).
RN [18]
RP VARIANTS STGD C-212; D-767; I-897; V-1038; K-1087; K-1399; Q-1640 AND
RP E-1961, AND VARIANT HIS-212.
RX MEDLINE=20174852; PubMed=10711710;
RA Simonelli F., Testa F., de Crechcio G., Rinaldi E., Hutchinson A.,
RA Atkinson A., Dean M., D'Urso M., Allikmets R.,
RT "New ABCR mutations and clinical phenotype in Italian patients with
RT Stargardt disease."
RL Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
RN [19]
RP CHARACTERIZATION OF VARIANTS, AND MUTAGENESIS OF GLY-966; LYS-969;
RP GLY-1975 AND LYS-1978.
RX MEDLINE=20472331; PubMed=11017087;
RA Sun H., Smallwood P.M., Nathans J.,
RT "Biochemical defects in ABCR protein variants associated with human
RT retinopathies."
RL Nat. Genet. 26:242-246(2000).
RN [20]
RP VARIANTS STGD ASN-972, AND VARIANTS GLN-943, ILE-1868 AND LEU-1948.
RX MEDLINE=21478761; PubMed=11594993;
RA Eksandh L., Ekstroem U., Abrahamson M., Bauer B., Andreasson S.,
Query Match 54.3%; Score 38; DB 1; Length 2273;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFAWQRNM 8
Db 779 CFAWQDRM 786
RESULT 11
DYHB_CHLRE DTYHB_CHLRE STANDARD; PRT; 4568 AA.
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RN STRAIN=2197;

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RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.,
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
RT chain genes."
RL J. Cell Sci. 107:635-644(1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC -----
CC EMBL; U02963; AAA19956.1;
CC InterPro; IPR004273; Dynein heavy.
CC Pfam; PF03028; Dynein_heavy; 1.
CC Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
CC Coiled coil.
CC FT DOMAIN 277 293 COILED COIL (POTENTIAL).
CC FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
CC FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
CC FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
CC FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
CC FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
CC FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
CC FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
CC FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
CC FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
CC FT NP_BIND 1919 1926 ATP (POTENTIAL).
CC FT NP_BIND 2202 2209 ATP (POTENTIAL).
CC FT NP_BIND 2530 2537 ATP (POTENTIAL).
CC FT NP_BIND 2879 2886 ATP (POTENTIAL).
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QY 1 CFAWQRNMKVR 12
Db 1852 CFQWQSLRYIQ 1863
RESULT 12
RS3A_DROME ID RS3A_DROME STANDARD; PRT; 267 AA.
AC P55830; O44389; Q9V4A9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S3a (C3 protein).
GN RPS3A OR C3 OR M(4)101 OR CG2168.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC STRAIN=Oregon-R; TISSUE=Embryo;
EX MEDLINE=98055162; PubMed=9393444;
RA Reynaud E., Bolshakov V.N., Barajas V.N., Kafatos F.C., Zurita M.,
RT "Antisense suppression of the putative ribosomal protein S3a gene
RT disrupts ovarian development in Drosophila melanogaster."
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RN SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.  
 RP TISSUE=Embryo;  
 RC MEDLINE=98416207; PubMed=9742251;  
 RX van Beest M., Morfin M., Clevers H.;  
 RT "Drosophila Rp3a, a novel minute gene situated between the segment  
 RT polarity genes cubitus interruptus and dTcf.";  
 RL Nucleic Acids Res. 26:4471-4475(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
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 RA Brandon R.C., Rogers J.H., Blazer R.G., Champs M., Pfeiffer B.D.,  
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 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
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 RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
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 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
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 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
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 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
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 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: ESSENTIAL FOR OOOGENESIS; REQUIRED FOR LATE FOLLICLE CELL  
 CC DEVELOPMENT. MAY BIND TO THE 40S RIBOSOMAL SUBUNIT.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED IN STAGE 8 EMBRYOS.  
 CC DURING OOOGENESIS, EXPRESSION IS LOCATED BASALLY IN SOMATIC  
 CC FOLLICULAR EPITHELIUM AND IN THE OOCYTE AT THE LATER STAGES.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY  
 CC THROUGHOUT ALL DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.  
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 CC -----  
 CC EMBL: Y10115; CAA71201.1; -  
 CC DR EMBL: AF034971; AAC62117.1; -  
 CC DR EMBL: AE003845; AAF59372.1; -  
 CC DR FlyBase: FBgn0017545; RPS3A.  
 CC InterPro: IPR001593; Ribosomal\_S3AE.

DR Pfam: PF01015; Ribosomal\_S3AE; 1.  
 DR ProDom: PD003035; Ribosomal\_S3AE; 1.  
 DR PROSITE: PS01191; RIBOSOMAL\_S3AE; 1.  
 KW Ribosomal protein.  
 FT INIT MET 0 0 BY SIMILARITY.  
 FT CONFLICT 61 61 L -> F (IN REF. 1).  
 FT CONFLICT 71 71 A -> VP (IN REF. 1).  
 FT CONFLICT 81 81 R -> H (IN REF. 1).  
 FT CONFLICT 159 160 QQ -> HE (IN REF. 1).  
 FT CONFLICT 168 168 A -> SG (IN REF. 1).  
 FT CONFLICT 252 260 VIDRPGYE -> PKSTALKVK (IN REF. 1).  
 FT CONFLICT 266 266 S -> A (IN REF. 3).  
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 Qy 1 CFANQRNRKVR 12  
 Db 156 CYAQSQSVRKIR 167  
 RESULT 13  
 1A34 HUMAN  
 ID 1A34 HUMAN STANDARD; PET; 365 AA.  
 AC P30453; P30454;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE HLA class I histocompatibility antigen, AW-34(A-10) alpha chain  
 DE precursor.  
 GN HLA-A OR HLA-A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A. (A\*3401/A\*3402).  
 MEDLINE=93056508; PubMed=1431115;  
 RA Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,  
 RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,  
 RA Martell R.W., du Toit E.D., Parham P.;  
 RT "Distinctive HLA-A,B antigens of black populations formed by  
 RT interallelic conversion.";  
 RL J. Immunol. 149:3411-3415(1992).  
 [2]  
 SEQUENCE FROM N.A. (A\*3401/A\*3402).  
 MEDLINE=93235211; PubMed=8475492;  
 RA Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,  
 RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,  
 RA du Toit E.D., Parham P.;  
 RT "Structural diversity in the HLA-A10 family of alleles: correlations  
 RT with serology.";  
 RL Tissue Antigens 41:72-80(1993).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A\*3401  
 CC (AW-34.1) AND A\*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF  
 CC A\*3401.  
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 CC -----  
 CC EMBL: X61704; CAA43873.1; -  
 CC DR EMBL: X61705; CAA43874.1; -





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DR EMBL; AJ235273; CAA15167.1; -;  
DR EMBL; Y11778; CAA72457.1; -;  
DR InterPro; IPR004667; ADP\_ATP\_car.  
DR Pfam; PF03219; TLC; 1.  
DR TIGRFAMs; TIGR00769; AAA; 1.  
KW Transmembrane, Transport; ATP-binding; Multigene family;  
KW Complete proteome.  
FT TRANSMEM 26 46 POTENTIAL.  
FT TRANSMEM 62 82 POTENTIAL.  
FT TRANSMEM 94 114 POTENTIAL.  
FT TRANSMEM 149 169 POTENTIAL.  
FT TRANSMEM 184 204 POTENTIAL.  
FT TRANSMEM 224 244 POTENTIAL.  
FT TRANSMEM 287 307 POTENTIAL.  
FT TRANSMEM 328 348 POTENTIAL.  
FT TRANSMEM 357 377 POTENTIAL.  
FT TRANSMEM 381 401 POTENTIAL.  
FT TRANSMEM 469 489 POTENTIAL.  
SQ SEQUENCE 500 AA; 57073 MW; FE3DB48D08CF5F72 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 500;  
Best Local Similarity 54.5%; Pred. No. 24;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNMVKV 11  
Db 482 CFAWYAVRKI 492

Search completed: February 21, 2003, 07:27:42  
Job time : 5.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107B-70  
Perfect score: 70  
Sequence: 1 CFAMQRMNRKV 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	85.7	711	4 Q8TCD2	Q8TCD2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9UCY5 homo sapien
3	47	67.1	511	16 Q8Z462	Q8Z462 salmonella
4	45	64.3	33	6 Q8TR80	Q8TR80 ovis aries
5	43	61.4	121	16 Q8U6K3	Q8U6K3 agrobacteri
6	43	61.4	282	16 Q8QK19	Q8QK19 mycoplasma
7	40	57.1	114	11 Q63104	Q63104 rattus norv
8	40	57.1	234	11 Q63112	Q63112 rattus norv
9	40	57.1	298	16 Q8YP77	Q8YP77 anabaena sp
10	40	57.1	393	16 Q9ZK94	Q9ZK94 helicobacte
11	40	57.1	469	9 Q38115	Q38115 bacterioph
12	40	57.1	519	10 Q93833	Q93833 arabidopsis
13	40	57.1	584	17 Q9HPA3	Q9HPA3 halobacteri
14	40	57.1	720	10 Q9CA22	Q9CA22 arabidopsis
15	39	55.7	205	8 Q98RR2	Q98RR2 guillardi
16	39	55.7	341	11 Q8R2A4	Q8R2A4 mus musculu

17	39	55.7	393	16	Q25611	helicobacte
18	39	55.7	681	5	Q9XVD1	Q9XVD1 caenorhabdi
19	39	55.7	783	16	Q9FBV4	Q9FBV4 streptomyce
20	39	55.7	886	5	Q9ZV1	Q9ZV1 drosophila
21	38	54.3	196	4	O14557	O14557 homo sapien
22	38	54.3	232	4	Q96H38	Q96H38 homo sapien
23	38	54.3	246	4	Q96GY3	Q96GY3 homo sapien
24	38	54.3	273	2	O31090	O31090 rhizobium 1
25	38	54.3	289	10	Q9C6N2	Q9C6N2 arabidopsis
26	38	54.3	553	4	Q9NZL7	Q9NZL7 homo sapien
27	38	54.3	554	4	Q9NY67	Q9NY67 homo sapien
28	38	54.3	558	4	Q9UFK6	Q9UFK6 homo sapien
29	38	54.3	2310	11	O35600	O35600 mus musculu
30	37	52.9	217	5	Q8SZD2	Q8SZD2 drosophila
31	37	52.9	232	11	Q91W07	Q91W07 mus musculu
32	37	52.9	236	10	Q9SK05	Q9SK05 arabidopsis
33	37	52.9	246	11	Q9D8N6	Q9D8N6 mus musculu
34	37	52.9	294	11	Q9DCU6	Q9DCU6 mus musculu
35	37	52.9	482	10	Q9M5C0	Q9M5C0 volvox cart
36	37	52.9	500	10	Q41383	Q41383 spinacia ol
37	37	52.9	550	11	Q9JUZ5	Q9JUZ5 mus musculu
38	37	52.9	607	4	Q9H8A5	Q9H8A5 homo sapien
39	37	52.9	676	5	Q9K4T5	Q9K4T5 caenorhabdi
40	37	52.9	678	10	Q9FG26	Q9FG26 arabidopsis
41	37	52.9	679	2	Q9SLK8	Q9SLK8 streptover
42	37	52.9	737	5	Q9VQJ8	Q9VQJ8 caenorhabdi
43	37	52.9	2348	5	Q9V346	Q9V346 drosophila
44	37	52.9	2858	5	Q9GYP6	Q9GYP6 caenorhabdi
45	37	52.9	5636	4	Q96RW7	Q96RW7 homo sapien

## ALIGNMENTS

## RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.  
AC Q8TCD2; PRELIMINARY; PRT; 711 AA.  
DT 01-JUN-2002 (TREMREL. 21, Created)  
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)  
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022347; AAH2347.1; -.  
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7E097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;  
Best Local Similarity 90.9%; Pred. No. 0.011;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAMQRMNRKV 11  
Db 39 CFAMQRMNRKV 49

## RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.  
AC Q9UCY5; PRELIMINARY; PRT; 38 AA.  
DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)  
DE Lactoferrin homolog (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato I.; MEDLINE=96081613; PubMed=8551695;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSP; P02788; IBAK.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDEB CRC64;

Query Match 80.08; Score 56; DB 4; Length 38;
Best Local Similarity 90.94; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWQNRNKKVR 12
| | | | |
Db 21 FQWRNKKVR 31

RESULT 3
Q82462
ID Q82462 PRELIMINARY; PRT; 511 AA.
AC Q82462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein STY3070.
GN STY3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham A., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krog A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.; a multiple drug resistant Salmonella
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627276; CAD06049.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match 67.18; Score 47; DB 16; Length 511;
Best Local Similarity 66.78; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAWQNRNKKVR 12
| | | | |
Db 350 FQWRNKKVR 361

RESULT 4
Q9TR80
ID Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O77698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.34; Score 45; DB 6; Length 33;
Best Local Similarity 54.54; Pred. No. 0.23;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAWQNRNKKVR 11
| | | | |
Db 19 CYQWQKQYKRL 29

RESULT 5
Q8U6K3
ID Q8U6K3 PRELIMINARY; PRT; 121 AA.
AC Q8U6K3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein Atu4804.
GN Atu4804.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Okura D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Wood V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyee D. Sr.,
RA Chapman P., Glendinning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tac Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
RA Nester E.W.; The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
DR EMBL; AE009409; AAL45598.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 121 AA; 14085 MW; EBAP41617A3CEA53 CRC64;

Query Match 61.44; Score 43; DB 16; Length 121;
Best Local Similarity 63.64; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAWQNRNKKVR 11
| | | | |
Db 14 CLAWQNRNRRV 24

RESULT 6
Q98Q19
ID Q98Q19 PRELIMINARY; PRT; 282 AA.
AC Q98Q19;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (PSI55

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DE synthase) (Pseudouridylylate synthase) (Uracil hydrolyase)
DN MYPU_5500.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmatadaceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RA MEDLINE=21267165; PubMed=11353084;
RX Chambaud I., Heilig K., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL: AL445565; CAC13723.1; -.
DR Mypulist; MYPU_5500; -.
DR InterPro; IPR004510; TruB.
DR InterPro; IPR002501; TruB_N.
DR Pfam; PF01509; TruB_N; 1.
DR TIGRPFAMs; TIGR00431; TruB; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 282 AA; 31961 MW; A598529F52B1EBEE CRC64;

Query Match 61.4%; Score 43; DB 16; Length 282;
Best Local Similarity 60.0%; Pred. No. 5.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 11
Db |||||:::
20 FAWQNNIKKI 29

RESULT 7
Q63104 PRELIMINARY; PRT; 114 AA.
AC Q63104
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Carcinoembryonic antigen (Fragment).
GN CE4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BD II; TISSUE=LIVER;
RX MEDLINE=8924106; PubMed=2708349;
RA Kodelja V., Lucas K., Barnert S., von Kleist S., Thompson J.A.,
RA Zimmermann W.A.;
RT "Identification of a carcinoembryonic antigen gene family in the rat:
RT Analysis of the N-terminal domains reveals immunoglobulin-like,
RT hypervariable regions.";
RL J. Biol. Chem. 264:6906-6912(1989).
DR EMBL; M60026; AAA40911.1; -.
FT NON TER 1
SQ SEQUENCE 114 AA; 12832 MW; 3AE108689B061686 CRC64;

Query Match 57.1%; Score 40; DB 11; Length 114;
Best Local Similarity 60.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 11
Db |||||:::
42 FAWYGLRKI 51

RESULT 8
Q63112 PRELIMINARY; PRT; 234 AA.
AC Q63112
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Carcinoembryonic antigen-related protein (Fragment).
GN CGM4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX Rebstock S., Lucas K., Thompson J.A., Zimmermann W.A.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=90243655; PubMed=2335509;
RA Rebstock S., Lucas K., Thompson J.A., Zimmermann W.;
RT "cDNA and gene analyses imply a novel structure for a rat
RT carcinoembryonic antigen-related protein.";
RL J. Biol. Chem. 265:7872-7879(1990).
DR EMBL; M32475; AAA66038.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
FT NON TER 1
SQ SEQUENCE 234 AA; 26171 MW; 69BBC9EE0C773F2A CRC64;

Query Match 57.1%; Score 40; DB 11; Length 234;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 11
Db |||||:::
42 FAWYGLRKI 51

RESULT 9
Q8YP77 PRELIMINARY; PRT; 298 AA.
AC Q8YP77
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr4323.
GN ALR4323.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003596; BAB76022.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 34513 MW; 64036E5B52299A9F CRC64;

Query Match 57.1%; Score 40; DB 16; Length 298;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQNNMKV 10

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|

Db 163 FHWQNRXK 171

# RESULT 10

Q2KXK4 ID Q2KXK4 PRELIMINARY; PRT; 393 AA.  
AC Q2KXK4;  
DT 01-MAY-1999 (TREMELrel. 10, Created)  
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)  
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
DE 3-deoxy-D-manno-octulosonic-acid transferase.  
GN WAAA OR JHP0831.  
OS Helicobacter pylori J99 (Campylobacter pylori J99).  
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
OC Helicobacter.  
OX NCBI\_TaxID=85963;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99120557; PubMed=9923682;  
RA Alm R.A., Ling L.-S.B., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
RA Trust T.J.;  
RT "Genomic sequence comparison of two unrelated isolates of the human  
RT gastric pathogen Helicobacter pylori.";  
RL Nature 397:176-180(1999).  
DR EMBL; AB001518; AAD06459.1; -.  
KW Complete proteome.  
SQ SEQUENCE 393 AA; 45442 MW; ADDA88C1EC0C18D CRC64;

Query Match 57.1%; Score 40; DB 16; Length 393;

Best Local Similarity 36.4%; Pred. No. 28; Mismatches 7; Indels 0; Gaps 0;

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|

Qy 2 FAWQNRXKVR 12

Db 110 FAWKXKXK 120

# RESULT 11

Q38115 ID Q38115 PRELIMINARY; PRT; 469 AA.  
AC Q38115;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)  
DE ORF29.  
OS Bacteriophage rlt.  
OC Viruses.  
OX NCBI\_TaxID=43685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96332668; PubMed=8730874;  
RA Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;  
RT "Inducible gene expression mediated by a repressor-operator system  
RT isolated from Lactococcus lactis bacteriophage rlt.";  
RL Mol. Microbiol. 19:1331-1341(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96332669; PubMed=8730875;  
RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Rutgers M.H.,  
RA Venema G., Nauta A.;  
RT "Sequence analysis and molecular characterization of the temperate  
RT lactococcal bacteriophage rlt.";  
RL Mol. Microbiol. 19:1343-1355(1996).  
DR EMBL; U38906; AAB18704.1; -.  
SQ SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;

Query Match 57.1%; Score 40; DB 9; Length 469;

Best Local Similarity 50.0%; Pred. No. 34; Mismatches 5; Indels 2; Gaps 0;

Qy 1 CFAWQNRXK 10  
|:|:|:  
Db 39 CYPWQKNLLK 48

# RESULT 12

P93833 ID P93833 PRELIMINARY; PRT; 519 AA.  
AC P93833;  
DT 01-MAY-1997 (TREMELrel. 03, Created)  
DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
DE Hypothetical 58.5 kDa protein.  
GN PPK1.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsia.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Kwart M., Bucherer T., Frommer W.B.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; Y11930; CAA72680.1; -.

DR InterPro; IPR000719; Euk\_pkinase.

DR InterPro; IPR002230; Ser\_thr\_kinase.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Euk\_pkinase; 1.

DR SMART; SM00220; S\_TKG; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.

DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE-ST; 1.

KW ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;

RW Transferase.

SQ SEQUENCE 519 AA; 58492 MW; 6252EE001B2BC035 CRC64;

Query Match 57.1%; Score 40; DB 10; Length 519;

Best Local Similarity 66.7%; Pred. No. 38; Mismatches 6; Indels 3; Gaps 0;

Qy 1 CFAWQNRXK 9

Db 420 CLAWDRNQR 428

# RESULT 13

Q9HPA3 ID Q9HPA3 PRELIMINARY; PRT; 584 AA.  
AC Q9HPA3;  
DT 01-MAR-2001 (TREMELrel. 16, Created)  
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)  
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
DE Vng1732C.  
GN VNG1732C.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
OX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20504483; PubMed=11016950;  
RA NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,  
RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Maddocks D.G., Jablonaki P.E., Krebs M.P., Angevine C.M., Dale H.,  
RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dasarma S.;  
RT "Genome sequence of Halobacterium species NRC-1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

DR EMEL; AE005078; AAC19967.1; --  
 DR InterPro; IPR001646; Speptide repeat.  
 DR InterPro; IPR001622; X-channel pore.  
 DR Pfam; PF00805; Pentapeptide; 2.  
 SQ Complete proteome.  
 KW SEQUENCE 584 AA; 65151 MW; 21BF5DF0486CCC6 CRC64;  
 Query Match 57.1%; Score 40; DB 17; Length 584;  
 Best Local Similarity 41.7%; Pred. No. 43;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFAWQNRKVR 12  
 |||:::|  
 Db 445 CFTWRKDMERRK 456  
 RESULT 14  
 Q9CA22 Q9CA22 PRELIMINARY; PRT; 720 AA.  
 AC Q9CA22;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 80.0 kDa protein.  
 GN T32E8.5.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Forg B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,  
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana."  
 RL Nature 408:816-820(2000).  
 DR EMEL; AC012193; AAG51619.1; --  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SMO0220; S\_TKc; 1.  
 DR SMART; SMO0219; Tyr\_Kc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
 DR PROSITE; PS00111; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 KW ATP-binding; Hypothetical protein; Transfrase.  
 SQ SEQUENCE 720 AA; 80027 MW; F26A9A031C6D91DE CRC64;

Query Match 57.1%; Score 40; DB 10; Length 720;  
 Best Local Similarity 66.7%; Pred. No. 54;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQNRKVR 9  
 |||:::|

Db 616 C1AWDRNQR 624  
 RESULT 15  
 Q98RR2 Q98RR2 PRELIMINARY; PRT; 205 AA.  
 AC Q98RR2;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE 26S proteasome SU B5.  
 GN PRS85.  
 OS Guillardia theta (Cryptomonas phi).  
 OG Nucleomorph.  
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.  
 OX NCBI\_TaxID=55529;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2122349; PubMed=11333671;  
 RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,  
 RA Wu X., Reith M., Cavalier-Smith T., Maier U.G.;  
 RT "The highly reduced genome of an enslaved algal nucleus."  
 RL Nature 410:1091-1096(2001).  
 DR EMEL; AF165818; AAK39885.1; --  
 DR InterPro; IPR000243; Proteasome\_B.  
 DR InterPro; IPR001353; Proteasome; 1.  
 DR Pfam; PF00227; proteasome; 1.  
 DR PRINTS; PR00141; PROTEASOME.  
 KW Proteasome.  
 SQ SEQUENCE 205 AA; 22691 MW; D30F5289C8C85049 CRC64;  
 Query Match 55.7%; Score 39; DB 8; Length 205;  
 Best Local Similarity 62.5%; Pred. No. 21;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFAWQNRKVR 8  
 |||:::|  
 Db 63 CFFWERNL 70  
 Search completed: February 21, 2003, 07:44:20  
 Job time : 22.8 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107B-71  
Perfect score: 64  
Sequence: 1 CPOAQRNKRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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2: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*  
5: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*  
6: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*  
7: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.\*  
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14: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*  
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22: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	12	21	AAV78071 Human lactoferrin
2	59	92.2	12	21	AAV78080 Human lactoferrin
3	57	89.1	12	21	AAV78038 Human lactoferrin
4	57	89.1	12	21	AAV78046 Human lactoferrin
5	57	89.1	12	21	AAV78047 Human lactoferrin
6	57	89.1	13	21	AAV78037 Human lactoferrin
7	57	89.1	13	21	AAV78048 Human lactoferrin
8	57	89.1	13	21	AAV78049 Human lactoferrin
9	57	89.1	14	21	AAV78036 Human lactoferrin
10	57	89.1	14	21	AAV78050 Human lactoferrin

11	57	89.1	14	21	AAV78051 Human lactoferrin
12	57	89.1	15	17	AAV98554 Peptide for anti-u
13	57	89.1	15	21	AAV78035 Human lactoferrin
14	57	89.1	15	21	AAV78062 Human lactoferrin
15	57	89.1	15	21	AAV78063 Human lactoferrin
16	57	89.1	16	21	AAV78031 Human lactoferrin
17	57	89.1	16	21	AAV78064 Human lactoferrin
18	57	89.1	16	21	AAV78065 Human lactoferrin
19	57	89.1	17	21	AAV78034 Human lactoferrin
20	57	89.1	17	21	AAV78066 Human lactoferrin
21	57	89.1	17	21	AAV78067 Human lactoferrin
22	57	89.1	18	15	AAV69352 Human lactoferrin
23	57	89.1	18	17	AAW13397 Advanced glycosyla
24	57	89.1	18	21	AAV78033 Human lactoferrin
25	57	89.1	19	21	AAV68667 Amino acid sequenc
26	57	89.1	19	21	AAV78032 Human lactoferrin
27	57	89.1	20	13	AAV21810 Anti microbial pep
28	57	89.1	20	14	AAV44841 Lactoferrin-relate
29	57	89.1	20	15	AAV48530 Lactoferrin derive
30	57	89.1	20	15	AAV48531 Lactoferrin derive
31	57	89.1	20	15	AAV57461 Lactoferrin derive
32	57	89.1	20	15	AAV57462 Lactoferrin derive
33	57	89.1	20	16	AAV84498 Bovine lactoferrin
34	57	89.1	20	16	AAV84699 Bovine lactoferrin
35	57	89.1	20	16	AAV80263 Anti-parasitic lac
36	57	89.1	20	16	AAV80264 Anti-parasitic lac
37	57	89.1	20	17	AAV98553 Peptide for anti-u
38	57	89.1	20	17	AAV91852 Lactoferrin-derive
39	57	89.1	20	17	AAV03045 Lactoferrin-derive
40	57	89.1	20	17	AAV90607 Lactoferrin-derive
41	57	89.1	20	17	AAV87821 Lactoferrin-derive
42	57	89.1	20	17	AAV87822 Lactoferrin-derive
43	57	89.1	20	18	AAV26150 Lactoferrin deriva
44	57	89.1	20	18	AAV14036 Anti-parasitic pep
45	57	89.1	20	19	AAV70310 Thrombus formation

#### ALIGNMENTS

RESULT 1  
AAV78071  
ID AAV78071 standard; Peptide; 12 AA.  
XX  
AC AAV78071;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:71.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; candida infection; fungicidal;  
KW bactericidal; preservative.

OS Homo sapiens.  
OS Synthetic.

XX WO200001730-A1.

PD 13-JAN-2000.

PF 06-JUL-1999; 99WO-SEQ01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.



XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX SQ Sequence 12 AA;  
Query Match 100.0%; Score 64; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOAQRNMRKVR 12  
DB 1 CFOAQRNMRKVR 12  
|||||

RESULT 2  
AAY78080  
ID AAY78080 standard; Peptide; 12 AA.  
XX AAY78080;  
AC AAY78080;  
XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:80.  
DE Human, lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX 06-JUL-1999; 99WO-SR01230.  
XX 06-JUL-1998; 98SE-0002441.  
XX 17-JUL-1998; 98SE-0002562.  
XX 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX SQ Sequence 12 AA;  
Query Match 92.2%; Score 59; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.00031;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOAQRNMRKVR 12  
DB 1 CFQLQRNMRKVR 12  
|||||

RESULT 3  
AAY78038  
ID AAY78038 standard; Peptide; 12 AA.  
XX AAY78038;  
AC AAY78038;  
XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:38.  
DE Human, lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX 06-JUL-1999; 99WO-SR01230.  
XX 06-JUL-1998; 98SE-0002441.  
XX 17-JUL-1998; 98SE-0002562.  
XX 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX  
 SQ Sequence 12 AA;

Query Match 89.1%; Score 57; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00071;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFAQQRNKRKVR 12  
 |||||  
 DB 1 CFAQQRNKRKVR 12

## RESULT 4

AAAY78046  
 ID AAY78046 standard; Peptide; 12 AA.

AC AAY78046;

XX  
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:46.

DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SR01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX  
 SQ Sequence 12 AA;

Query Match 89.1%; Score 57; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00071;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFAQQRNKRKVR 12  
 |||||  
 DB 1 CFAQQRNKRKVR 12

## RESULT 5

AAAY78047  
 ID AAY78047 standard; Peptide; 12 AA.

AC AAY78047;

XX  
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:47.

DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SR01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX  
 SQ Sequence 12 AA;

Query Match 89.1%; Score 57; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00071;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12  
 DB 1 CFQQRNMRKVR 12

## RESULT 6

AAAY78037  
 ID AAAY78037 standard; Peptide; 13 AA.

XX AAAY78037;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAAY78001 to AAAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;

Query Match 89.1%; Score 57; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.00077;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12

DB 2 CFQQRNMRKVR 13

## RESULT 7

AAAY78048

ID AAAY78048 standard; Peptide; 13 AA.

XX AAAY78048;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.

XX AAAY78001 to AAAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;

Query Match 89.1%; Score 57; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.00077;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12

DB 2 CFQQRNMRKVR 13

## RESULT 8

AAAY78049

ID AAAY78049 standard; Peptide; 13 AA.

XX AAAY78049;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 DR  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PT  
 XX Claim 18; Page 74; 102pp; English.  
 PS  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 89.1%; Score 57; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 0.00077;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQQRNNRKVR 12  
 DB 2 CFQWRNNRKVR 13  
 RESULT 9  
 AAY78036  
 ID AAY78036 standard; Peptide; 14 AA.  
 AC AAY78036;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT  
 XX Human lactoferrin derived peptide SEQ ID NO:36.  
 DE  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 DR  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PT  
 XX Claim 12; Page 69; 102pp; English.  
 PS  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 89.1%; Score 57; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 0.00083;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQQRNNRKVR 12  
 DB 3 CFQWRNNRKVR 14  
 RESULT 10  
 AAY78050  
 ID AAY78050 standard; Peptide; 14 AA.  
 AC AAY78050;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT  
 XX Human lactoferrin derived peptide SEQ ID NO:50.  
 DE  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections, -  
 PT inflammations and tumors and for use in infant formula food  
 XX Claim 15; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 89.1%; Score 57; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 0.00083;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQAOQNMKVR 12  
 DB ||| |||||  
 3 CFQWQNMKVR 14  
 RESULT 11  
 AAY78051 ID AAY78051 standard; Peptide; 14 AA.  
 XX AC AAY78051;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:51.  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX PD 13-JAN-2000.  
 XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections, -  
 PT inflammations and tumors and for use in infant formula food  
 XX Claim 15; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 89.1%; Score 57; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 0.00083;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQAOQNMKVR 12  
 DB ||| |||||  
 3 CFQWQNMKVR 14  
 RESULT 12  
 AAR98554 ID AAR98554 standard; Peptide; 15 AA.  
 XX AC AAR98554;  
 XX DT 12-NOV-1996 (first entry)  
 XX DE Peptide for anti-ulcer agent.  
 XX KW anti-ulcer agent; low toxicity; stable; heat-resistant.  
 XX OS Synthetic.  
 XX PN JPC8143468-A.  
 XX PD 04-JUN-1996.  
 XX PF 17-NOV-1994; 94JP-0283869.  
 XX PR 17-NOV-1994; 94JP-0283869.  
 XX (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1996-318857/32.  
 XX Anti-ulcer agent contg. peptide - has low toxicity, is  
 PT heat-resistant and water-soluble  
 XX Claim 1; Page 11; 11pp; Japanese.  
 XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low  
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be  
 CC administered orally and be produced in large amounts.  
 XX Sequence 15 AA;  
 SQ

Query Match 89.1%; Score 57; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00089;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
 DB 2 CFQQRNRKVR 13

## RESULT 13

AAV78035  
 ID AAY78035 standard; Peptide; 15 AA.

XX AAY78035;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:35.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 15 AA;

Query Match 89.1%; Score 57; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00089;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
 DB 4 CFQQRNRKVR 15

## RESULT 14

AAV78062  
 ID AAY78062 standard; Peptide; 15 AA.

XX AAY78062;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:62.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 81; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 15 AA;

Query Match 89.1%; Score 57; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00089;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
 DB 4 CFQQRNRKVR 15

## RESULT 15

AAV78063  
 ID AAY78063 standard; Peptide; 15 AA.

XX AAY78063;

Tue Dec 9 06:51:27 2003

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XX 25-APR-2000 (first entry)
DT
XX
DE Human lactoferrin derived peptide SEQ ID NO:63.
DE
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 18; Page 81; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 15 AA;

Query Match 89.1%; Score 57; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAQRNRKVR 12
DB 4 CFQWRNRKVR 15

Search completed: February 21, 2003, 07:37:11
Job time : 28.35 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-71  
Perfect score: 64  
Sequence: 1 CFQAQRNKKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5A COMB pep: \*  
2: /cgn2\_6/prodata/1/iaa/5B COMB pep: \*  
3: /cgn2\_6/prodata/1/iaa/5A COMB pep: \*  
4: /cgn2\_6/prodata/1/iaa/5B COMB pep: \*  
5: /cgn2\_6/prodata/1/iaa/PCUTS COMB pep: \*  
6: /cgn2\_6/prodata/1/iaa/backfiles1 pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	89.1	18	1	US-08-204-487-3
2	57	89.1	18	2	US-08-485-948-8
3	57	89.1	18	2	US-08-628-380-8
4	57	89.1	18	2	US-08-475-055-8
5	57	89.1	20	1	US-07-755-161A-3
6	57	89.1	20	1	US-07-891-174-3
7	57	89.1	20	1	US-08-204-487-1
8	57	89.1	20	1	US-08-256-771-24
9	57	89.1	20	1	US-08-256-771-25
10	57	89.1	20	1	US-08-381-984-24
11	57	89.1	20	1	US-08-381-984-25
12	57	89.1	22	4	US-09-508-734-4
13	57	89.1	24	4	US-09-508-734-6
14	57	89.1	25	1	US-07-755-161A-10
15	57	89.1	25	1	US-07-891-174-10
16	57	89.1	25	1	US-08-204-487-7
17	57	89.1	29	4	US-09-508-734-8
18	57	89.1	36	1	US-07-755-161A-8
19	57	89.1	36	1	US-07-891-174-8
20	57	89.1	36	1	US-08-256-771-30
21	57	89.1	36	1	US-08-381-984-29
22	57	89.1	47	2	US-08-464-182A-6
23	57	89.1	47	2	US-08-406-271-6
24	57	89.1	50	2	US-08-693-274A-7
25	57	89.1	52	4	US-09-017-043A-3
26	57	89.1	53	2	US-08-464-182A-5
27	57	89.1	53	2	US-08-406-271-5

28	57	89.1	54	2	US-08-464-182A-2	Sequence 2, Appli
29	57	89.1	54	2	US-08-406-271-2	Sequence 2, Appli
30	57	89.1	694	3	US-08-724-586-2	Sequence 2, Appli
31	57	89.1	694	4	US-09-421-632-2	Sequence 2, Appli
32	57	89.1	694	4	US-09-332-190-2	Sequence 2, Appli
33	57	89.1	705	2	US-08-655-640-2	Sequence 2, Appli
34	57	89.1	708	2	US-08-655-640-4	Sequence 4, Appli
35	57	89.1	711	1	US-08-154-019-4	Sequence 4, Appli
36	57	89.1	711	1	US-08-461-333-4	Sequence 4, Appli
37	57	89.1	711	3	US-08-464-167-4	Sequence 4, Appli
38	57	89.1	711	3	US-09-158-313-4	Sequence 4, Appli
39	57	89.1	711	4	US-08-476-798-4	Sequence 4, Appli
40	54	84.4	711	1	US-08-145-681-2	Sequence 2, Appli
41	54	84.4	711	1	US-08-250-308-2	Sequence 2, Appli
42	54	84.4	711	1	US-08-453-703-2	Sequence 2, Appli
43	54	84.4	711	2	US-08-456-106-2	Sequence 2, Appli
44	54	84.4	711	3	US-08-456-108-2	Sequence 2, Appli
45	54	84.4	711	4	US-09-265-577-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-204-487-3  
; Sequence 3, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN-ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIYAKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESS: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: RIN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1-18  
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"



OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 89.1%; Score 57; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
||| |||||  
DB 1 CFQQRNRKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/485,948  
; FILING DATE: JUNE 7, 1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-Cl, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; US-08-485-948-8

Query Match 89.1%; Score 57; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
||| |||||  
DB 1 CFQQRNRKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI, YONG MING  
; APPLICANT: VLASSARA, HELEN  
; APPLICANT: CERAMI, ANTHONY  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-Cl, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; US-08-628-380-8

Query Match 89.1%; Score 57; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
||| |||||  
DB 1 CFQQRNRKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Klauber & Jackson  
;; STREET: 411 Hackensack Avenue  
;; CITY: Hackensack  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07601  
;;  
;; COMPUTER READABLE FORM: disk  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/475,055  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/485,948  
;; FILING DATE:  
;; APPLICATION NUMBER: 08/488,217  
;; FILING DATE: JUNE 7, 1995  
;; APPLICATION NUMBER: 08/418,642  
;; FILING DATE: APRIL 7, 1995  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 947-1-008A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201 487-5800  
;; TELEFAX: 201 343-1684  
;; TELEX: 133521  
;;  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; DESCRIPTION: LP-C1, 8-25  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;;  
US-08-475-055-8

Query Match 89.1%; Score 57; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQQRNKRVR 12  
||| |||||  
Db 1 CFQQRNKRVR 12

RESULT 5  
US-07-755-161A-3  
; Sequence 3, Application US/07755161A  
; Patent No. 5304633  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500KB  
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: DisplayWrite  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/755,161A  
;; FILING DATE: 19910905  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX: 202-371-8856  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE:  
;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:  
;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE:  
;; CELL LINE:  
;; ORGANELLE:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:  
;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURE:  
;; NAME/KEY: modified site  
;; LOCATION: 2  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION: /note= "thiol group of  
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
;; OTHER INFORMATION: thiol group of Cys residue at location 19"  
;; FEATURE:  
;; NAME/KEY: modified site  
;; LOCATION: 19  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION: /note= "thiol group of  
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
;; OTHER INFORMATION: thiol group of Cys residue at location 2"  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-755-161A-3

Query Match 89.1%; Score 57; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 0.00021;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNRKVR 12  
DB 2 CFQAOQNRKVR 13

RESULT 6  
US-07-891-174-3  
; Sequence 3, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site

LOCATION: 2  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 19"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 19  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 2"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-3

Query Match 89.1%; Score 57; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00021;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNRKVR 12  
DB 2 CFQAOQNRKVR 13

RESULT 7  
US-08-204-487-1  
; Sequence 1, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIAKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 248-7000

TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE  
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"  
US-08-204-487-1

Query Match 89.1%; Score 57; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00021;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
||| |||||  
DB 2 CFQQRNRKVR 13

RESULT 8  
US-08-256-771-24  
Sequence 24, Application US/08256771  
Patent No. 5656591  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
TITLE OF INVENTION: PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are linked by  
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 89.1%; Score 57; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00021;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
||| |||||  
DB 2 CFQQRNRKVR 13

RESULT 9  
US-08-256-771-25  
Sequence 25, Application US/08256771  
Patent No. 5656591  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
TITLE OF INVENTION: PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are protected to  
OTHER INFORMATION: prevent disulfide bond"  
US-08-256-771-25

Query Match 89.1%; Score 57; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00021;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12  
||| |||||  
DB 2 CFQQRNRKVR 13

RESULT 10  
US-08-381-984-24

Sequence 24, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

## INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

NAME/KEY:  
LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2  
OTHER INFORMATION: and 19 are bonded by disulfide linkage"

FEATURE:

NAME/KEY:  
LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as  
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof

US-08-381-984-24

Query Match 89.1%; Score 57; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00021;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQQRNRKVR 12

Db 2 CFQQRNRKVR 13

## RESULT 11

US-08-381-984-25

Sequence 25, Application US/08381984

Patent No. 5804555

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

## INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

NAME/KEY:

LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as

OTHER INFORMATION: peptides including the specified peptide as a fragment thereof

FEATURE:

NAME/KEY:

LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2

OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"

US-08-381-984-25

Query Match 89.1%; Score 57; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 0.00021;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQQRNRKVR 12

Db 2 CFQQRNRKVR 13

## RESULT 12

US-09-508-734-4

Sequence 4, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
TITLE OF INVENTION: useful microorganism thereof

FILE REFERENCE: FA/SYG/00139

CURRENT FILING DATE: 2000-06-01

CURRENT APPLICATION NUMBER: US/09/508,734

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: PCT/KR99/00373

PRIOR FILING DATE: 1998-07-13

PRIOR APPLICATION NUMBER: KR1998-29351

NUMBER OF SEQ ID NOS: 12

SOFTWARE: KopatentIn 1.71

SEQ ID NO 4

```
/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-508-734-4

Query Match      89.1%; Score 57; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 0.00023;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNNRKVR 12
Db 2 CFQWRNNRKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SVG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match      89.1%; Score 57; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNNRKVR 12
Db 3 CFQWRNNRKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

Query Match      89.1%; Score 57; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNNRKVR 12
Db 4 CFQWRNNRKVR 15
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IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 4"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
PUBLICATION DATE:  
FILING DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-10  
Query Match 89.1%; Score 57; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 0.00027;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFOAQRNMRKVR 12  
Db 4 CFQWQRNMRKVR 15  
Search completed: February 21, 2003, 07:50:33  
Job time : 8.7 secs

RESULT 15  
US-07-891-174-10  
Sequence 10, Application US/07891174  
Patent No. 5317084  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptides and an  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/891,174  
FILING DATE: 29-MAY-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/755,161  
FILING DATE: 05-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 4  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 21"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 21

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)

35.508 Million cell updates/sec

Title: US-09-743-107b-71  
Perfect score: 64  
Sequence: 1 CFQQRNMRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	89.1	15	9	US-09-798-869-2
2	57	89.1	25	9	US-09-798-869-20
3	57	89.1	694	9	US-10-023-096-2
4	49	76.6	15	9	US-09-798-869-6
5	40	62.5	15	9	US-09-798-869-3
6	40	62.5	25	9	US-09-798-869-23
7	37	57.8	97	9	US-09-738-626-5597
8	35	54.7	184	10	US-09-925-301-1248
9	34	53.1	596	9	US-10-093-766-29
10	34	53.1	700	9	US-10-013-310-5
11	34	53.1	882	9	US-10-174-590-574
12	34	53.1	882	9	US-10-176-758-574
13	34	53.1	882	9	US-10-175-737-574
14	34	53.1	882	9	US-10-173-706-574
15	34	53.1	882	9	US-10-175-738-574
16	34	53.1	882	9	US-10-175-752-574
17	34	53.1	882	9	US-10-176-482-574
18	34	53.1	882	9	US-10-176-757-574
19	34	53.1	882	9	US-10-176-913-574

20	34	53.1	882	9	US-10-180-552-574	Sequence 574, App
21	34	53.1	882	9	US-10-180-557-574	Sequence 574, App
22	34	53.1	882	9	US-10-173-700-574	Sequence 574, App
23	34	53.1	882	9	US-10-174-572-574	Sequence 574, App
24	34	53.1	882	9	US-10-174-579-574	Sequence 574, App
25	34	53.1	882	9	US-10-174-582-574	Sequence 574, App
26	34	53.1	882	9	US-10-174-588-574	Sequence 574, App
27	34	53.1	882	9	US-10-175-739-574	Sequence 574, App
28	34	53.1	882	9	US-10-175-740-574	Sequence 574, App
29	34	53.1	882	9	US-10-175-743-574	Sequence 574, App
30	34	53.1	882	9	US-10-176-488-574	Sequence 574, App
31	34	53.1	882	9	US-10-176-492-574	Sequence 574, App
32	34	53.1	882	9	US-10-176-747-574	Sequence 574, App
33	34	53.1	882	9	US-10-176-750-574	Sequence 574, App
34	34	53.1	882	9	US-10-176-985-574	Sequence 574, App
35	34	53.1	882	9	US-10-176-987-574	Sequence 574, App
36	34	53.1	882	9	US-10-176-991-574	Sequence 574, App
37	34	53.1	882	9	US-10-176-992-574	Sequence 574, App
38	34	53.1	882	9	US-10-176-993-574	Sequence 574, App
39	34	53.1	882	9	US-10-184-658-574	Sequence 574, App
40	34	53.1	882	9	US-10-173-695-574	Sequence 574, App
41	34	53.1	882	9	US-10-173-697-574	Sequence 574, App
42	34	53.1	882	9	US-10-173-705-574	Sequence 574, App
43	34	53.1	882	9	US-10-174-576-574	Sequence 574, App
44	34	53.1	882	9	US-10-174-585-574	Sequence 574, App
45	34	53.1	882	9	US-10-174-586-574	Sequence 574, App

## ALIGNMENTS

RESULT 1  
US-09-798-869-2 ; Sequence 2, Application US/09798869  
; Publication No. US2003002821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: BALDUR SVEINBJ (RNSON)  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 89.1% ; Score 57 ; DB 9 ; Length 15 ;  
Best Local Similarity 91.7% ; Pred. No. 4.3e-05 ;  
Matches 11 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

QY 1 CFQQRNMRKVR 12  
DB 3 CFQQRNMRKVR 14

RESULT 2  
US-09-798-869-20 ; Sequence 20, Application US/09798869  
; Publication No. US2003002821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (VSTEIN REKDAL)  
; APPLICANT: BALDUR SVEINBJ (RNSON)



APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-798-869-20

Query Match 89.1%; Score 57; DB 9; Length 25;  
Best Local Similarity 91.7%; Pred. No. 7.4e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNNMKVR 12  
||| |||||  
DB 3 CFQAOQNNMKVR 14

## RESULT 3

US-10-023-096-2  
; Sequence 2, Application US/10023096  
; Patent No. US20020160941A1  
; GENERAL INFORMATION:  
; APPLICANT: Kruzel, Marian L.  
; APPLICANT: Kurecki, Tomasz  
; APPLICANT: Gollnick, Paul D.  
; APPLICANT: Doyle, Darrell J.

; TITLE OF INVENTION: Cloning, Expression, and Uses of Human  
; TITLE OF INVENTION: Lactoferrin  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.125  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/023,096  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,586  
; FILING DATE: 30-SEPT-1996  
; APPLICATION NUMBER: US 08/238,445  
; FILING DATE: 05-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10505/P58185C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-5350

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 694 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-10-023-096-2

Query Match 89.1%; Score 57; DB 9; Length 694;  
Best Local Similarity 91.7%; Pred. No. 0.0027;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQAOQNNMKVR 12  
||| |||||  
DB 22 CFQAOQNNMKVR 33

## RESULT 4

US-09-798-869-6  
; Sequence 6, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ(RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-6

Query Match 76.6%; Score 49; DB 9; Length 15;  
Best Local Similarity 83.3%; Pred. No. 0.0015;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQAOQNNMKVR 12  
||| |||||  
DB 3 CFQAOQNNMKVR 14

## RESULT 5

US-09-798-869-3  
; Sequence 3, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ(RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-3

Query Match 62.5%; Score 40; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.084;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 11  
|:|:|:|:|:|:|:  
Db 3 CYQWQRMRKL 13

## RESULT 6

US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (VSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJARNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 62.5%; Score 40; DB 9; Length 25;  
Best Local Similarity 63.6%; Pred. No. 0.15;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 11  
|:|:|:|:|:|:|:  
Db 3 CYQWQRMRKL 13

## RESULT 7

US-09-738-626-5597  
; Sequence 5597, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 5597  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-5597

Query Match 57.8%; Score 37; DB 9; Length 97;  
Best Local Similarity 70.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 10  
|:|:|:|:|:|:|:  
Db 73 CFLVQRNRK 82

## RESULT 8

US-09-925-301-1248  
; Sequence 1248, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSEN ET AL.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 1248  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1248

Query Match 54.7%; Score 35; DB 10; Length 184;  
Best Local Similarity 63.6%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOAQRNRKVR 12  
|:|:|:|:|:|:|:  
Db 61 FKXQRNRKVR 71

## RESULT 9

US-10-093-766-29  
; Sequence 29, Application US/10093766  
; Publication No. US20030013099A1  
; GENERAL INFORMATION:  
; APPLICANT: LASEK, AMY W.  
; APPLICANT: JONES, DAVID A.  
; APPLICANT: KARPF, ADAM R.  
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS  
; FILE REFERENCE: PA-0047 US  
; CURRENT APPLICATION NUMBER: US/10/093,766  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PERL Program  
; SEQ ID NO 29  
; LENGTH: 596  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030013099A1 476301CD1  
US-10-093-766-29

Query Match 53.1%; Score 34; DB 9; Length 596;  
Best Local Similarity 54.5%; Pred. No. 65;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQAOQNRK 11  
|:|:|:|:|:|:|:  
Db 336 CFMAEQNRK 346

## RESULT 10

US-10-013-310-5  
 ; Sequence 5, Application US/10013310  
 ; Publication No. US20020192216A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lamb, Jonathon Robert  
 ; APPLICANT: Hoyne, Gerard Francis  
 ; APPLICANT: Dallman, Margaret Jane  
 ; TITLE OF INVENTION: Therapeutic Use  
 ; FILE REFERENCE: 674525-2003  
 ; CURRENT APPLICATION NUMBER: US/10/013,310  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: PCT/GB00/02191  
 ; PRIOR FILING DATE: 2000-06-05  
 ; PRIOR APPLICATION NUMBER: UK 9913350.6  
 ; PRIOR FILING DATE: 1999-06-08  
 ; PRIOR APPLICATION NUMBER: UK 9921953.7  
 ; PRIOR FILING DATE: 1999-09-16  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 700  
 ; TYPE: PRT  
 ; ORGANISM: House Mouse  
 US-10-013-310-5

Query Match 53.1%; Score 34; DB 9; Length 700;  
 Best Local Similarity 54.5%; Pred. No. 77;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQQRNRKV 11

Db 666 CEQVDRNRV 676

## RESULT 11

US-10-174-590-574  
 ; Sequence 574, Application US/10174590  
 ; Publication No. US20030008352A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C42  
 ; CURRENT APPLICATION NUMBER: US/10/174,590  
 ; CURRENT FILING DATE: 2002-06-18  
 ; Prior application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 574  
 ; LENGTH: 882  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-174-590-574

Query Match 53.1%; Score 34; DB 9; Length 882;  
 Best Local Similarity 54.5%; Pred. No. 99;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQQRNRKV 11

Db 848 CEQVDRNRV 858

## RESULT 12

US-10-176-758-574  
 ; Sequence 574, Application US/10176758  
 ; Publication No. US20030008353A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C104  
 ; CURRENT APPLICATION NUMBER: US/10/176,758  
 ; CURRENT FILING DATE: 2002-06-21  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 574  
 ; LENGTH: 882  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-176-758-574

Query Match 53.1%; Score 34; DB 9; Length 882;  
 Best Local Similarity 54.5%; Pred. No. 99;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQQRNRKV 11

Db 848 CEQVDRNRV 858

## RESULT 13

US-10-175-737-574  
 ; Sequence 574, Application US/10175737  
 ; Publication No. US20030013153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C50  
 ; CURRENT APPLICATION NUMBER: US/10/175,737  
 ; CURRENT FILING DATE: 2002-06-19  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 574  
 ; LENGTH: 882  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-175-737-574

Query Match 53.1%; Score 34; DB 9; Length 882;  
 Best Local Similarity 54.5%; Pred. No. 99;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQQRNRKV 11

Db 848 CEQVDRNRV 858

Db 848 CEQVDRNIRRV 858

## RESULT 14

US-10-173-706-574

; Sequence 574, Application US/10173706

; Publication No. US2003002293A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC7

; CURRENT APPLICATION NUMBER: US/10/173,706

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 574

; LENGTH: 882

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-706-574

Query Match

Best Local Similarity 53.1%; Score 34; DB 9; Length 882;

Mismatches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOAQRNMRKV 11

Db 848 CEQVDRNIRRV 858

## RESULT 15

US-10-175-738-574

; Sequence 574, Application US/10175738

; Publication No. US2003002294A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC45

; CURRENT APPLICATION NUMBER: US/10/175,738

; CURRENT FILING DATE: 2002-06-19

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 574

; LENGTH: 882

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-175-738-574

Query Match

Best Local Similarity 53.1%; Score 34; DB 9; Length 882;

Mismatches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-71

Perfect score: 64

Sequence: 1 CFQQRNWKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:\*\*

1: Piri:\*\*

2: Piri:\*\*

3: Piri:\*\*

4: Piri:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	57	89.1	711	1 TFHUL	lactotransferrin p
2	40	62.5	47	2 T29370	hypothetical prote
3	40	62.5	708	2 JC2323	lactoferrin - goat
4	38	59.4	57	2 D81949	hypothetical prote
5	37	57.8	33	2 S52107	lactoferrin - shee
6	37	57.8	664	2 T28952	probable potassium
7	37	57.8	887	2 H96315	hypothetical prote
8	37	57.8	990	1 G46335	env polyprotein pr
9	36	56.2	223	2 T37974	probable peroxisom
10	36	56.2	238	2 T40568	hypothetical prote
11	36	56.2	267	2 S77802	hypothetical prote
12	36	56.2	658	2 B69228	ATP synthase, subu
13	35	54.7	325	2 C96784	hypothetical prote
14	35	54.7	335	2 T33211	hypothetical prote
15	35	54.7	431	2 S50977	hypothetical prote
16	35	54.7	545	2 E97728	DNA repair protein
17	35	54.7	622	2 B86309	Similar to mudra p
18	35	54.7	743	2 T00634	hypothetical prote
19	35	54.7	993	2 D96512	protein Fg9.12 (i
20	34	53.1	81	2 E95172	hypothetical prote
21	34	53.1	81	2 E98038	hypothetical prote
22	34	53.1	104	2 D95003	hypothetical prote
23	34	53.1	114	2 JQ0149	hypothetical 12.6k
24	34	53.1	126	2 AB0119	hypothetical prote
25	34	53.1	151	2 G86760	diacylglycerol kin
26	34	53.1	225	2 A90260	conserved hypothet
27	34	53.1	250	2 S62545	hypothetical prote
28	34	53.1	527	2 C87375	hypothetical prote
29	34	53.1	887	2 A96516	hypothetical prote

30 34 53.1 994 2 T21356  
31 34 53.1 1145 2 A59251  
32 33 51.6 125 2 C71669  
33 33 51.6 125 2 H97822  
34 33 51.6 130 2 C72602  
35 33 51.6 133 2 A97324  
36 33 51.6 178 2 AB2743  
37 33 51.6 185 2 S50094  
38 33 51.6 227 2 I64016  
39 33 51.6 249 2 A13401  
40 33 51.6 351 2 S20078  
41 33 51.6 375 2 C71286  
42 33 51.6 433 2 T37605  
43 33 51.6 516 2 T00974  
44 33 51.6 624 2 T01585  
45 33 51.6 862 2 T38996

#### ALIGNMENTS

##### RESULT 1

TFHUL

Lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence\_revision 21-Nov-1997 #text\_change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74;

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBU

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237

R/Rev. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A/Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferi

A/Reference number: A45401; MUID:93125571; PMID:1450183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:9263311; PIDN:AAB24877.1; PID:9263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POM>

A/Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70, 389-393, 1987  
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A;Reference number: S07160; MUID:88001031; PMID:3477300  
 A;Accession: S07160  
 A;Molecule type: mRNA  
 A;Residues: 436-487, 'A', 489-711 <RAD>  
 A;Cross-references: EMBL:M18642; NID:9186815; PIDN:AAA86665.1; PID:g386855  
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51, 3037-3043, 1991  
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A;Reference number: A61169; MUID:91235214; PMID:1674448  
 A;Accession: A61169  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 3-701, 'SWKPVN' <PAN>  
 A;Experimental source: normal breast tissue  
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, P.; Legrand, D.; Spik, G.;  
 Eur. J. Biochem. 145, 659-666, 1984  
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other  
 A;Reference number: A31000; MUID:85076667; PMID:6510420  
 A;Accession: A31000  
 A;Molecule type: protein  
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4  
 A;Note: this is the final paper in a series  
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.  
 Eur. J. Biochem. 241, 303-308, 1996  
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity  
 A;Reference number: S74119; MUID:97054624; PMID:8898921  
 A;Accession: S74119  
 A;Molecule type: protein  
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A;Experimental source: neutrophil granulocytes  
 C;Genetics:  
 A;Gene: GDB:17F  
 A;Cross-references: GDB:119368; OMIM:150210  
 A;Map position: 3q21-3q23  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein; iron binding; milk  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-71/Product: lactotransferrin #status experimental <MAT>  
 F;21-356/Domain: transferrin repeat homology <TRH1>  
 F;360-699/Domain: transferrin repeat homology <TRH2>  
 F;29-65, 99-56, 135-218, 177-193, 190-201, 251-265, 503-637, 595-609/Disulfide bonds: #status e  
 F;157, 498/Binding site: carbonyl site: carboxylate (Asn) (covalent) #status experimental  
 F;368-400, 378-391, 425-706, 447-665, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 89.1%; Score 57; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.0059;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQAQRNRKVR 12  
 ||| |||||  
 DB 39 CFQWRNRKVR 50

RESULT 2  
 T29970  
 hypothetical protein ZK682.1 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T29970  
 R;Du, Z.; Le, T.  
 submitted to the EMBL Data Library, November 1995  
 A;Description: The sequence of C. elegans cosmid ZK682.  
 A;Reference number: Z20714  
 A;Accession: T29970  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-47 <DUZ>  
 A;Cross-references: EMBL:U41110; PIDN:AAA82417.1; CESP:ZK682.1  
 C;Genetics:  
 A;Gene: CESP:ZK682.1

A;Introns: 33/2  
 Query Match 62.5%; Score 40; DB 2; Length 47;  
 Best Local Similarity 63.6%; Pred. No. 0.77;  
 Matches 7; Conservative 3; Mismatches 0; Gaps 0;  
 QY 1 CFQAQRNRKVR 11  
 ||| |||||  
 DB 26 CNEARRNRKVR 36

RESULT 3  
 JC2323  
 lactoferrin - goat  
 C;Species: Capra aegagrus hircus (domestic goat)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C;Accession: JC2323  
 R;Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.  
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994  
 A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus  
 A;Reference number: JC2323; MUID:94380047; PMID:8093048  
 A;Accession: JC2323  
 A;Molecule type: mRNA  
 A;Residues: 1-708 <LEP>  
 A;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein  
 F;359-696/Domain: transferrin repeat homology <TRH2>  
 F;252,300,387,495,564/Binding site: carbonyl site: carboxylate (Asn) (covalent) #status predicted

Query Match 62.5%; Score 40; DB 2; Length 708;  
 Best Local Similarity 63.6%; Pred. No. 11;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CFQAQRNRKVR 11  
 ||| |||||  
 DB 38 CYQWRNRKVR 48

RESULT 4  
 D81949  
 hypothetical protein NMA1014 [imported] - Neisseria meningitidis (strain Z2491 serogroup  
 C;Species: Neisseria meningitidis  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C;Accession: D81949  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holroyd, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A;Reference number: A81775; MUID:20222556; PMID:10761919  
 A;Accession: D81949  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-57 <PAR>  
 A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84283.1; PID:g737971  
 A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 A;Gene: NMA1014

Query Match 59.4%; Score 38; DB 2; Length 57;  
 Best Local Similarity 58.3%; Pred. No. 2.3;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQAQRNRKVR 12  
 ||| |||||  
 DB 21 CFPSSRRMGKVR 32

RESULT 5  
 S52107  
 lactoferrin - sheep (fragment)  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 14-Jul-1995 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997  
 C;Accession: S52107

R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

Biochim. Biophys. Acta 1243, 25-32, 1995  
A:Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a  
A:Reference number: S52107; MUID:95127729; PMID:7827104

A:Accession: S52107

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-33 <QIA>

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication

Query Match 57.8%; Score 37; DB 2; Length 33;

Best Local Similarity 54.5%; Pred. No. 2.1;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAQORNRKVR 11

Db 19 CYQWQKQKRL 29

RESULT 6

T28852

probable potassium channel - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T28852

R;Stellies, L.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid M60.

A:Reference number: Z20532

A:Accession: T28852

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-664 <STE>

A:Cross-references: EMBL:U93995; PIDN:AAC48062.1; GSPDB:GN00028; CESP:klq-2

C:Experimental source: strain Bristol N2; clone M60

C:Genetics:

A:Gene: CESP:klq-2

A:Map position: X

A:Introns: 72/2; 99/1; 158/1; 201/3; 226/2; 271/1; 328/1; 404/2; 454/3; 520/3; 609/2

Query Match 57.8%; Score 37; DB 2; Length 664;

Best Local Similarity 60.0%; Pred. No. 40;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QAQRNRKVR 12

Db 69 QRQRLRRR 78

RESULT 7

H96515

hypothetical protein F16N3.18 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: H96515

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

xer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: H96515

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-887 <STO>

A:Cross-references: GB:AE005173; NID:95668806; PIDN:AAD46032.1; GSPDB:GN00141

C:Genetics:

A:Gene: F16N3.18

A:Map position: 1

Query Match 57.8%; Score 37; DB 2; Length 887;

Best Local Similarity 56.3%; Pred. No. 53;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAQORNRKVR 12

Db 659 CHQIERNERNVR 670

RESULT 8

G46335

env polyprotein precursor - Maedi/Vienna virus (strain SA-OMV)

N:Alternate names: coat polyprotein

C:Species: Maedi/Vienna virus

C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 16-Jul-1999

C:Accession: G46335

R;Querat, G.; Audoly, G.; Sonigo, P.; Vigne, R.

Virolgy 175, 434-447, 1990

A:Title: Nucleotide sequence analysis of SA-OMV, a visna-related ovine lentivirus: phyl.

A:Reference number: A46335; MUID:90223989; PMID:2158181

A:Accession: G46335

A:Molecule type: DNA

A:Residues: 1-990 <QUE>

A:Cross-references: GB:M31646; NID:9808756; PIDN:AAA66817.1; PID:G332551

C:Genetics:

A:Gene: env

C:Superfamily: visna lentivirus type B retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote

F1-101/Domain: signal sequence #status predicted <SIG>

F102-662/Product: exterior membrane glycoprotein #status predicted <EXT>

F1663-990/Product: transmembrane glycoprotein #status predicted <TM>

F1663-689/Region: hydrophobic

F1842-863/Domain: transmembrane #status predicted <TMN>

F1141,162,207,259,299,363,386,402,413,434,438,469,474,480,490,500,514,526,536,542,550,56

Query Match 57.8%; Score 37; DB 1; Length 990;

Best Local Similarity 50.0%; Pred. No. 60;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAQORNRKVR 12

Db 862 CLQAYRQVREIR 873

RESULT 9

T37974

probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000

C:Accession: T37974

R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z21759

A:Accession: T37974

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-223 <MUR>

A:Cross-references: EMBL:Z69909; PIDN:CAA93785.1; GSPDB:GN00066; SPDB:SPAC19G10.03C

A:Experimental source: strain 972h-; cosmid cl9G10

C:Genetics:

A:Gene: SPDB:SPAC19G10.03C

A:Map position: 1

A:Introns: 10/3; 170/2

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09

C:Keywords: peroxisome

Query Match 56.2%; Score 36; DB 2; Length 223;

Best Local Similarity 33.3%; Pred. No. 21;

Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQOQRNMKVR 12  
 : : : : :  
 Db 140 CYELQNSKKIK 151

## RESULT 10

T40568  
 hypothetical protein SPBC582.09 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
 C:Accession: T40568

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z41937

A:Accession: T40568

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-238 <WOO>

A:Cross-references: EMBL:AL096788; PIDN:CAB46672.1; GSPDB:GN00067; SPDB:SPBC582.09

A:Experimental source: strain 972h; cosmid c582

C:Genetics:

A:Gene: SPDB:SPBC582.09

A:Map position: 2

A:Introns: 15/3; 25/3; 185/2

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09

Query Match 56.2%; Score 36; DB 2; Length 238;  
 Best Local Similarity 33.3%; Pred. No. 23;  
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQOQRNMKVR 12

: : : : :  
 Db 155 CYELQNSKKIK 166

## RESULT 11

S77802  
 hypothetical protein MC003 - Mycoplasma capricolum (fragment)  
 C:Species: Mycoplasma capricolum  
 C>Date: 09-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 07-Dec-1999  
 C:Accession: S77802

R:Bor, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.

Mol. Microbiol. 16, 955-967, 1995

A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology

A:Reference number: S77739; MUID:96059641; PMID:7476192

A:Accession: S77802

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-267 <BOR>

A:Cross-references: EMBL:233006

A:Experimental source: ATCC 27343

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

C:Genetics:

A:Genetic code: SGC3

Query Match 56.2%; Score 36; DB 2; Length 267;  
 Best Local Similarity 50.0%; Pred. No. 25;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQOQRNMKVR 12

: : : : :  
 Db 158 CFGKKNRQWR 169

## RESULT 12

E63228  
 ATP synthase, subunit I - Methanobacterium thermoautotrophicum (strain Delta H)  
 C:Species: Methanobacterium thermoautotrophicum  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
 C:Accession: E69228

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwnani, N.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
 A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: E69228

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-658 <MTH>

A:Cross-references: GB:AE000869; GB:AE000666; NID:g2622042; PIDN:AAB85456.1; PID:g26220;

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH960

A:Start codon: GTG

Query Match 56.2%; Score 36; DB 2; Length 658;  
 Best Local Similarity 54.5%; Pred. No. 62;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOAQRNMKVR 12

: : : : :  
 Db 647 FRAERNFKIR 657

## RESULT 13

C96784  
 hypothetical protein F1B16.9 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: C96784

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: C96784

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-325 <STO>

A:Cross-references: GB:AE005173; NID:g10120446; PIDN:AAG13071.1; GSPDB:GN00141

C:Genetics:

A:Gene: F1B16.9

A:Map position: 1

Query Match 54.7%; Score 35; DB 2; Length 325;  
 Best Local Similarity 66.7%; Pred. No. 48;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FOAQRNMK 10

: : : : :  
 Db 315 FRAKRLRK 323

## RESULT 14

T33211  
 hypothetical protein K10C9.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 08-Dec-2000

C:Accession: T33211

R:Du, Z.; Maggi, L.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid K10C9.

A:Reference number: Z21302

A:Accession: T33211

A:Status: preliminary; translated from GB/EMBL/DDJ

A:Molecule type: DNA

A:Residues: 1-335 <DUZ>

A:Cross-references: EMBL:AF067944; PIDN:AAC17673.1; GSPDB:GN00023; CESP:K10C9.6



A;Experimental source: strain Bristol N2; clone K10C9

C;Genetics:

A;Gene: CESP.K10C9.6

A;Map position: 5

C;Introns: 163/2; 313/1

C;Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12

Query Match 54.7%; Score 35; DB 2; Length 335;  
Best Local Similarity 60.0%; Pred. No. 50;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPOAQRNRK 10

Db 217 CVQMRNRK 226

RESULT 15:

S50977

Hypothetical protein YDL005c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein D2930; hypothetical protein YD8119.02c

C;Species: Saccharomyces cerevisiae

C;Date: 11-Feb-1995 #sequence revision 12-May-1995 #text\_change 19-Apr-2002

C;Accession: S50977; S52514; S67537

R;Murphy, L.; Richards, C.; Gentles, S.; Harris, D.

submitted to the EMBL Data Library, January 1995

A;Reference number: S50976

A;Accession: S50977

A;Molecule type: DNA

A;Residues: 1-431 <MUR>

A;Cross-references: EMBL:Z48008; NID:G642799; PIDN:CAA98056.1; PID:G642801

R;Andrie, B.; Visiers, S.; Urrestarazu, L.

submitted to the EMBL Data Library, February 1995

A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV

A;Reference number: S52492

A;Accession: S52514

A;Molecule type: DNA

A;Residues: 1-431 <AND>

A;Cross-references: EMBL:Z48432; NID:G683669; PIDN:CAA88354.1; PID:G683692

R;Urrestarazu, L.A.; Andre, B.; Visiers, S.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67535

A;Accession: S67537

A;Molecule type: DNA

A;Residues: 1-431 <URR>

A;Cross-references: EMBL:Z74053; NID:G1430962; PIDN:CAA98561.1; PID:E252970; PID:G143096

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:MED2

A;Cross-references: SGD:S0002163

A;Map position: 4L

Query Match 54.7%; Score 35; DB 2; Length 431;

Best Local Similarity 87.5%; Pred. No. 64;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QRNRKVR 12

Db 122 QRNRKVR 129

Search completed: February 21, 2003, 07:47:41

Job time : 11.65 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107b-71

Perfect score: 64

Sequence: 1 CFAQQNRMRKVR 12

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	57	89.1	711	1	TRFL_HUMAN	P02788 homo sapien
2	43	67.2	695	1	TRFL_HORSE	O77811 equus caball
3	40	62.5	708	1	TRFL_CAMD	Q97um0 camelus dro
4	40	62.5	708	1	TRFL_CAPHI	Q29477 capra hircu
5	37	57.8	990	1	ENV_OVVIS	P16899 ovine lenti
6	36	56.2	238	1	YBM9_SCHPO	Q10333 schizosacch
7	36	56.2	267	1	Y125_MYCCA	P53661 mycoplasma
8	36	56.2	658	1	VATI_METH	O27041 methanobact
9	35	54.7	545	1	RECN_RICCN	Q92j40 rickettsia
10	34	53.1	510	1	YAGF_SCHPO	Q09877 schizosacch
11	34	53.1	557	1	TKT2_HUMAN	P51854 homo sapien
12	33	51.6	125	1	RS13_RICCN	Q29gy8 rickettsia
13	33	51.6	125	1	RS13_RICPR	Q29cs7 rickettsia
14	33	51.6	227	1	Y940_HAEIN	P44081 haemophilus
15	33	51.6	267	1	RS3A_DROME	P55830 drosophila
16	33	51.6	351	1	NOV_CHICK	Q28686 gallus gall
17	33	51.6	564	1	ARAB_BAGST	Q98468 bacillus et
18	33	51.6	573	1	UREL_LACFE	P26929 lactobacill
19	32	50.0	226	1	NUKM_NEUCR	O47950 neocospira
20	32	50.0	238	1	AGRA_STRAA	P13131 staphylococ
21	32	50.0	252	1	YGHR_ECOLI	Q16842 escherichia
22	32	50.0	272	1	UL24_HSVB1	P09314 equine herp
23	32	50.0	272	1	UL24_HSVB4	P24432 equine herp
24	32	50.0	272	1	UL24_HSVB4	P28937 equine herp
25	32	50.0	399	1	YGV7_SCHPO	O43021 schizosacch
26	32	50.0	618	1	DNAL_CYACA	Q9tll1 cyanidium c
27	32	50.0	770	1	MAOI_RHIME	O3C807 rhizobium m
28	32	50.0	795	1	DEGY_CABEL	O01635 caenorhabd
29	32	50.0	885	1	LONI_MAIZE	P93647 zea mays (m
30	32	50.0	992	1	FRQ_LEPAU	Q01115 leptosphaer
31	32	50.0	1040	1	RAG1_MOUSE	P15919 mus musculu
32	32	50.0	1132	1	TERF_HUMAN	Q14746 homo sapien
33	31	48.4	137	1	KDGL_STRMU	Q05888 streptococc

## RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LTF OR LTF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 19:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Conneely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RT	sequences.";			
RL	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

34	31	48.4	175	1	HER1_CAERL	P34704 caenorhabdi
35	31	48.4	201	1	MUSC_MOUSE	O89940 mus musculu
36	31	48.4	206	1	MUSC_HUMAN	O60682 homo sapien
37	31	48.4	228	1	YDPH_ECOLI	P77577 esche-ichia
38	31	48.4	253	1	TRUA_LACLA	Q9ci80 lactococcus
39	31	48.4	277	1	XKDB_BACSU	P39781 bacillus su
40	31	48.4	311	1	FMT_MYCPN	P52335 mycoplasma
41	31	48.4	345	1	ESTA_STRSC	P22266 streptomyce
42	31	48.4	379	1	TRMU_XYLFA	Q9pdd9 xylella fas
43	31	48.4	410	1	SECY_CYACA	P46249 cyanidium c
44	31	48.4	427	1	YAAH_BACSU	P37531 bacillus su
45	31	48.4	487	1	C8B1_ESCCA	O64899 eschschoelzi

## ALIGNMENTS

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE=Mammary Gland;  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Ouden J.E.;  
RT "Nucleotide sequence of human lactoferrin cDNA.";  
RL Nucleic Acids Res. 18:4013-4013(1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=9076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
R LeGrand D., Spik G., Montreuil J., Jolles P.;  
RT "Human lactotransferrin: amino acid sequence and structural  
RL comparisons with other transferrins.";  
RN Eur. J. Biochem. 145:659-666(1984).  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
R Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
RL alignment of the cyanogen bromide fragments and characterization of  
RN N- and C-terminal domains.";  
RX Biochim. Biophys. Acta 670:243-254(1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
R Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
RL lactotransferrin.";  
RN FEBS Lett. 142:107-110(1982).  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
RL expression of mRNA during normal and leukemic myelopoiesis.";  
RN Blood 70:989-993(1987).  
RP SEQUENCE OF 237-711 FROM N.A.  
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
R Gnoj L., la Baside M., Kaplan N., Greco T., Touchman J., Muzny D.,  
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
RA Dragan Y., Giacalone J., Fae A., Powell E., Solinsky K.A., Desilva U.,  
RA Diaz-Ferez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
R Sagripanti J.I.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2589506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
RL and refinement at 2.8-A resolution.";  
RN J. Mol. Biol. 209:711-734(1989).  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
RL resolution.";  
RN Acta Crystallogr. D 51:629-646(1995).  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
R Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
RL binding properties and crystal structure of the histidine-  
RN 253->-methionine mutant.";  
RN Biochemistry 36:341-346(1997).  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in Aspergillus  
RL awamori.";  
RN Acta Crystallogr. D 55:403-407(1999).  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
RL and analysis of ligand-induced conformational change.";  
RN Acta Crystallogr. D 54:1319-1335(1998).  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioid antagonist peptides derived  
RL from human lactoferrin.";  
RN Agric. Biol. Chem. 54:1803-1810(1990).  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
R Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaranickavel G., Munier F., Schorderet D.F.,  
R El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejtmanecik J.P., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
RL corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RN Mol. Vision 4:31-32(1998).  
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
CC OF AN ANION, USUALLY BICARBONATE.  
CC FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST  
CC ACTIVITY. LACTOFERRIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERRIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC SUBUNIT: MONOMER.  
CC SUBCELLULAR LOCATION: Secreted.  
CC DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
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CC EMBL; X53961; CAA37914.1; -  
CC EMBL; U07643; AAB60324.1; -  
CC EMBL; M93150; AAA36159.1; -  
CC EMBL; M83202; AAA59511.1; -  
CC EMBL; M83205; AAA58656.1; -  
CC EMBL; M18642; AAA86655.1; -  
CC EMBL; AF332168; AAG48753.1; -  
CC EMBL; BC015822; AAH15822.1; -  
CC EMBL; BC015823; AAH15823.1; -  
CC EMBL; W73700; AAA59479.1; -  
CC EMBL; X52941; CAA37116.1; -  
CC EMBL; U95626; AAB57795.1; -  
CC PIR; S11228; TFHUL.  
CC PDB; 1LFC; 31-AUG-94.  
CC PDB; 1LCT; 31-OCT-93.  
CC PDB; 1LEG; 31-JUL-94.  
CC PDB; 1LEH; 31-OCT-93.  
CC PDB; 1LFI; 31-OCT-93.  
CC PDB; 1LGB; 31-AUG-94.  
CC PDB; 1LGC; 31-AUG-94.  
CC PDB; 1BKA; 08-NOV-96.  
CC PDB; 1DSN; 08-MAR-96.  
CC PDB; 1HSE; 12-MAR-97.  
CC PDB; 1VPD; 21-APR-97.

Query Match 89.1%; Score 57; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.0011;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12  
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 Db 39 CFQQRNMRKVR 50

## RESULT 2

TRFL\_HORSE STANDARD; PRT; 695 AA.  
 AC 077811;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).  
 GN LTF.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "cDNA sequence of mare lactoferrin";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RC TISSUE=Milk;  
 RX MEDLINE=98296631; PubMed=10366507;  
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution.";  
 RL J. Mol. Biol. 289:303-317(1999).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; AJ010930; CAA09407.1; -.  
 DR FDB; IB1X; 02-DEC-98.  
 DR PDB; 1B7U; 02-FEB-99.  
 DR PDB; 1B7Z; 02-FEB-99.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SMO0094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 1.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 FT Signal; 3D-structure.  
 FT NON\_TER 1  
 FT SIGNAL <1 6  
 FT CHAIN 7 695 LACTOTRANSFERRIN.  
 FT REPEAT 7 350 1.  
 FT REPEAT 351 695 2.  
 FT DISULFID 15 51  
 FT DISULFID 25 42  
 FT DISULFID 121 204

FT DISULFID 163 179  
 FT DISULFID 166 189  
 FT DISULFID 176 187  
 FT DISULFID 237 251  
 FT DISULFID 254 286  
 FT DISULFID 364 377  
 FT DISULFID 411 690  
 FT DISULFID 431 653  
 FT DISULFID 463 538  
 FT DISULFID 487 681  
 FT DISULFID 497 511  
 FT DISULFID 508 521  
 FT DISULFID 579 593  
 FT DISULFID 631 636  
 FT METAL 66 66  
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 FT METAL 401 401  
 FT METAL 439 439  
 FT METAL 532 532  
 FT METAL 601 601  
 FT BINDING 127 127  
 FT BINDING 469 469  
 FT CARBOHYD 143 143  
 FT CARBOHYD 287 287  
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 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 67.2%; Score 43; DB 1; Length 695;  
 Best Local Similarity 66.7%; Pred. No. 0.7;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQQRNMRKVR 12  
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 Db 25 CAKQQRNMRKVR 36

## RESULT 3

TRFL\_CAMDR STANDARD; PRT; 708 AA.  
 AC Q9TUM0; Q9MZS5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R., Ackermann M., Farah Z., Fuhan Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 2 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
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 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .)  
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 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .)  
 FT CONFLICT 56 56 I -> V (IN REF. 2).  
 FT CONFLICT 88 88 L -> R (IN REF. 2).  
 FT CONFLICT 124 124 Q -> K (IN REF. 2).  
 FT CONFLICT 154 154 F -> P (IN REF. 2).  
 FT CONFLICT 304 304 S -> R (IN REF. 2).  
 FT CONFLICT 414 414 D -> G (IN REF. 2).  
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Query Match 62.5%; Score 40; DB 1; Length 708;  
 Best Local Similarity 63.6%; Pred. No. 2.8;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQQRNRKV 11  
 Db 38 CYQWRNRKL 48

## RESULT 5

ENV\_OMVVS STANDARD; PRT; 990 AA.  
 AC P16899;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE ENV polypeptide precursor (Coat polypeptide).  
 GN ENV.  
 OS Ovine lentivirus (strain SA-OMV).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90223989; PubMed=2158181;  
 RA Querat G., Audoly G., Sonigo P., Vigne R.;  
 RT "Nucleotide sequence analysis of SA-OMV, a visna-related ovine  
 lentivirus: phylogenetic history of lentiviruses.";  
 RL Virology 175:434-447(1990).  
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 CC -----  
 DR EMBL; M34193; AAA6783.1; -;  
 DR EMBL; M31646; AAA68817.1; -;  
 DR PIR; G46335; G46335.  
 DR HIV; M34193; ENV5OMVSACG.  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR Pfam; PF00517; GP41, 1.  
 KW Glycoprotein; Coat protein; Polyprotein; Transmembrane.  
 FT PEPTIDE 1 101  
 FT CHAIN 102 662  
 FT TRANSMEM 663 990  
 FT CHAIN 842 863  
 FT TRANSMEM 141 141  
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Query Match 57.8%; Score 37; DB 1; Length 990;  
 Best Local Similarity 50.0%; Pred. No. 16;  
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Qy 1 CFQQRNRKV 12  
 Db 862 CLQAYRQVREIR 873

## RESULT 6

YBM9 SCHPO STANDARD; PRT; 238 AA.  
 AC Q10333;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein C582.09 in chromosome II.  
 GN SPBC582.09.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Murgall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

```
RA Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutini L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
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CC -----
DR EMBL: AL096788; CAB46672.1; -
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26479 MW; 58095AA8CD708180 CRC64;
Query Match 56.2%; Score 36; DB 1; Length 238;
Best Local Similarity 33.3%; Pred. No. 5.7;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFAOQNMKVR 12
DB 155 CVELQNSKKIK 166
:::|::|::|
RESULT 7
Y125_MYCCA STANDARD; PRT; 267 AA.
ID Y125_MYCCA
AC F53661;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae.
OX NCBI_TaxID=2095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96059641; PubMed=7476192;
RA Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
RA Dolan M., Gilbert W., Gillevet P.M.;
RA "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
RA its physiology.";
RL Mol. Microbiol. 16:985-987(1995).
CC -1- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH
CC (A.SUBTILIS) FAMILY.
CC -----
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CC -----
DR EMBL: Z33006; CAAB3689.1; -
DR InterPro: IPR001454; Hlgnaase/hydrolase.
DR InterPro: IPR000150; Hypotheset_cof.
DR Pfam: PF00702; Hydrolase; 1.
DR PROSITE: PS01228; COF_1; 1.
DR PROSITE: PS01229; COF_2; 1.
KW Hypothetical protein.
FT NON_TER 267
SQ SEQUENCE 267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
Query Match 56.2%; Score 36; DB 1; Length 267;
Best Local Similarity 50.8%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CFAOQNMKVR 12
DB 158 CPGKKNRQMR 169
:::|::|::|
RESULT 8
VATI_METH STANDARD; PRT; 658 AA.
ID VATI_METH
AC Q27041;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
GN ATP1 OR MTH960.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL: AE000869; AAB85456.1; -
DR InterPro: IPR002490; V_ATPase_sub116.
DR Pfam: PF01496; V_ATPase_sub_a; 1.
KW Hydrolase; Hydrogen ion transport; Transmembrane; Complete proteome.
SQ SEQUENCE 658 AA; 74475 MW; 98E48D62EB43BE81 CRC64;
Query Match 56.2%; Score 36; DB 1; Length 658;
Best Local Similarity 54.8%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 FOAQRNMKVR 12
DB 647 FRAENFKIR 657
:::|::|::|
RESULT 9
REC_N R1CCN STANDARD; PRT; 545 AA.
ID REC_N R1CCN
AC Q92J40;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA repair protein recN (Recombination protein N).
GN REC_N OR RC0229.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
```

OX NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Malish 7;  
 RX MEDLINE=21442074; PubMed=11557893;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";  
 RL Science 293:2093-2098(2001).  
 CC -1- FUNCTION: MAY BE INVOLVED IN RECOMBINATIONAL REPAIR OF DAMAGED  
 CC DNA (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE REC N FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AE008590; AAL02767.1; -;  
 DR InterPro; IPR003439; ABC transporter.  
 DR InterPro; IPR004604; RecN.  
 DR TIGRFAMs; TIGR00634; recN; 1.  
 KW DNA repair; ATP-binding; Complete proteome.  
 FT NP BIND 29 36  
 FT ATP (POTENTIAL).  
 SQ SEQUENCE 545 AA; 61729 MW; 59E02AEC8628E283 CRC64;  
 Query Match 54.7%; Score 35; DB 1; Length 545;  
 Best Local Similarity 60.0%; Pred. No. 22;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CFQQRNMRK 10  
 Db 160 CYQAWQNRK 169  
 RESULT 10  
 YAGF SCHPO STANDARD; PRT; 510 AA.  
 AC Q09877; O94555;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein C12G12.15 in chromosome I.  
 GN SPAC12G12.15.  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Scouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,  
 RA Collins M., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins S., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moutle S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Vackaert G., Aert R., Robben J., Gymnopoulos B.,  
 RA Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hunt S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Uesery D., Barrett B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 CC -1- SIMILARITY: SOME, TO YEAST YFR048W.  
 CC -----  
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 CC -----  
 DR EMBL; Z66568; CAA91510.2; -;  
 DR InterPro; IPR003734; DUF155.  
 DR Pfam; PF02582; DUF155; 1.  
 KW Hypothetical protein: Transmembrane.  
 FT TRANSMEM 238 258  
 FT POTENTIAL.  
 SQ SEQUENCE 510 AA; 58445 MW; 232C7729233861C CRC64;  
 Query Match 53.1%; Score 34; DB 1; Length 510;  
 Best Local Similarity 60.0%; Pred. No. 32;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 FQQRNMRKV 11  
 Db 58 FORRENARKI 67  
 RESULT 11  
 TKT2 HUMAN STANDARD; PRT; 557 AA.  
 AC P51854;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Transketolase-like 1 (EC 2.2.1.1) (Transketolase 2) (TK 2)  
 DE Transketolase related protein).  
 GN TKT1 OR TKT2 OR TKR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=96435907; PubMed=8838793;  
 RA Coy J.P., Duebel S., Kioschis P., Thomas K., Micklem G., Delius H.,  
 RA Pouetka A.;  
 RT "Molecular cloning of tissue-specific transcripts of a transketolase-  
 RT related gene: implications for the evolution of new vertebrate  
 RT genes.";  
 RL Genomics 32:309-316(1996).  
 RN [2]  
 RA Hochgeschwender U.;  
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde  
 CC 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.  
 CC -1- COPACITOR: THIAMINE PYROPHOSPHATE (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS ARE DERIVED BY  
 CC ALTERNATIVE SPLICING; THE HEART-SPECIFIC FORM LACKS THE N-  
 CC TERMINAL COMPARED TO THE BRAIN-SPECIFIC FORM WHICH IS SHOWN HERE.  
 CC -1- TISSUE SPECIFICITY: FETAL AND ADULT HEART, BRAIN, LUNG, LIVER,



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CC KIDNEY, ADULT PLACENTA, SKELETAL MUSCLE, PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
CC -----
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CC -----
DR EMBL; X91817; CAA62925.1; -
DR EMBL; X91818; CAA62925.1; JOINED.
DR EMBL; U14622; AAA21557.1; -
DR Genew; HGNC:11835; TXLL1.
DR MIM; 300044; -
DR InterPro; IPR000360; Transketolase.
DR Pfam; PF00456; transketolase; 2.
DR Pfam; PF02779; transket pyr; 1.
DR Pfam; PF02780; transketolase C; 1.
DR PROSITE; PS00801; TRANSKETOLASE 1; FALSE_NEG.
DR PROSITE; PS00802; TRANSKETOLASE 2; 1.
DR Transferase; Thiamine Pyrophosphate; Alternative splicing.
KW TRANSKETOLASE 1
FT CONFLICT 480 480 I -> N (IN REF. 2).
FT CONFLICT 493 493 T -> S (IN REF. 2).
SQ SEQUENCE 557 AA; 61199 MW; 3F773DB8469447F7 CRC64;

Query Match 53.1%; Score 34; DB 1; Length 557;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQQRNMRKV 11
| | | | |
Db 280 CFNAEQNWVS 290

RESULT 12
RS13_RICCN STANDARD; PRT; 125 AA.
AC Q92GX8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S13.
GN RPSM OR RCO984.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sanson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
CC -1- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE
CC INITIATION OF TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AE008651; AAU03522.1; -
DR InterPro; IPR001892; Ribosomal_S13.
DR Pfam; PF00416; Ribosomal_S13; 1.

Query Match 51.6%; Score 33; DB 1; Length 125;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQQRNMRKV 11
| | | | |
Db 86 CYQGLRHRLK 96

RESULT 14
Y940_HAEIN STANDARD; PRT; 227 AA.
AC P44081;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```

DE Hypothetical protein HI0940.  
GN HI0940.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=rd / KW20 / ATCC 51907;  
RA MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Karlyavev A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
RT rd.";  
RL Science 269:496-512(1995).  
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CC -----  
DR EMBL; U32775; AAC22604.1; -;  
DR IGR; HI0940; -;  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 7 26 POTENTIAL.  
SQ SEQUENCE 227 AA; 25484 MW; 576A870A3160A275 CRC64;  
  
Query Match 51.6%; Score 33; DB 1; Length 227;  
Best Local Similarity 66.7%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 FQAQRNRK 10  
|:|:|:|:  
Db 34 FQAQRNRK 42  
  
RESULT 15  
RS3A DROME STANDARD; PRT; 267 AA.  
AC P55830; O43389; Q9V4A9;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 13-JUN-2002 (Rel. 41, Last annotation update)  
DE 40S ribosomal protein S3a (C3 protein).  
GN RPS3A OR C3 OR M(4)101 OR CG2168.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE  
RP SPECIFICITY.  
RX STRAIN=Oregon-R; TISSUE=Embryo;  
RX MEDLINE=96055162; PubMed=9393444;  
RA Reynaud E., Bolshakov V.N., Barajas V.N., Kafatos F.C., Zurita M.;  
RT "Antisense suppression of the putative ribosomal protein S3a gene  
RT disrupts ovarian development in Drosophila melanogaster.";  
RL Mol. Gen. Genet. 256:462-467(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.  
RX TISSUE=Embryo;  
RX MEDLINE=98416207; PubMed=9742251;

van Beest M., Mortin M., Clevers H.;  
RT "Drosophila Rps3a, a novel minute gene situated between the segment  
RT polarity genes cubitus interruptus and dTCF.";  
RL Nucleic Acids Res. 26:4471-4475(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Berkley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.C., Wortman J.R., Yeung M.D., Zhang Q., Chen L.Y.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,  
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.R., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclik J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
CC -!- FUNCTION: ESSENTIAL FOR OOGENESIS; REQUIRED FOR LATE FOLLICLE CELL  
CC DEVELOPMENT. MAY BIND TO THE 40S RIBOSOMAL SUBUNIT.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN STAGE 8 EMBRYOS.  
CC DURING OOOGENESIS. EXPRESSION IS LOCATED BASALLY IN SOMATIC  
CC FOLLICULAR EPITHELIUM AND IN THE OOCYTE AT THE LATER STAGES.  
CC -!- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY  
CC THROUGHOUT ALL DEVELOPMENT.  
CC -!- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
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CC -----  
DR EMBL; Y10115; CAA71201.1; -;  
DR EMBL; AF034971; AAC62117.1; -;  
DR EMBL; AB03845; AAF59372.1; -;  
DR Flybase; FBgn0017545; Rps3A.  
DR InterPro; IPR001593; Ribosomal\_S3AE.  
DR Pfam; PF01015; Ribosomal\_S3AE; 1.  
DR ProDom; PD003035; Ribosomal\_S3AE; 1.  
DR PROSITE; PS01191; RIBOSOMAL\_S3AE; 1.  
RW Ribosomal protein.

FT INIT MET 0 0 BY SIMILARITY.  
 FT CONFLICT 61 61 L -> F (IN REF. 1).  
 FT CONFLICT 71 71 A -> VP (IN REF. 1).  
 FT CONFLICT 81 81 R -> H (IN REF. 1).  
 FT CONFLICT 139 180 QQ -> HE (IN REF. 1).  
 FT CONFLICT 188 188 A -> SG (IN REF. 1).  
 FT CONFLICT 252 260 VIDRPEGVE -> PKSTALKVK (IN REF. 1).  
 FT CONFLICT 266 266 S -> A (IN REF. 3).  
 SQ SEQUENCE 267 AA; 30225 MW; 3FF51141158455E7 CRC64;

Query Match 51.6%; Score 33; DB 1; Length 267;  
 Best Local Similarity 41.7%; Pred. No. 26;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFOAQNMRKVR 12  
 Db 156 CYAQQSVRKIR 167

Search completed: February 21, 2003, 07:27:44  
 Job time : 6.6 secs

GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107b-71

Perfect score: 64

Sequence: 1 CFAQNRMRKV 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL 21.\*  
2: SP\_ARCHAEA.\*  
3: SP\_BACTERIA.\*  
4: SP\_FUNGI.\*  
5: SP\_INVERTEBRATE.\*  
6: SP\_MAMMAL.\*  
7: SP\_NBC.\*  
8: SP\_ORGANELLE.\*  
9: SP\_PHAGE.\*  
10: SP\_PLANT.\*  
11: SP\_RODENT.\*  
12: SP\_VIRUS.\*  
13: SP\_VERTEBRATE.\*  
14: SP\_UNCLASSIFIED.\*  
15: SP\_VIRUS.\*  
16: SP\_BACTERIAP.\*  
17: SP\_ARCHAEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	81.2	711	4 Q8TCD2	Q8Tcd2 homo sapien
2	48	75.0	38	4 Q9UCY5	Q9ucy5 homo sapien
3	40	62.5	47	5 Q23578	Q23578 caenorhabdi
4	39	60.9	729	12 Q91TW1	Q91tw1 tupaia herp
5	38	59.4	57	16 Q9JY34	Q9jy34 neisseria m
6	37	57.8	33	6 Q9TR80	Q9tr80 ovis aries
7	37	57.8	675	5 Q9GYM8	Q9gym8 caenorhabdi
8	37	57.8	887	10 Q9SX85	Q9sx85 arabidopsis
9	35	54.7	150	4 Q9BS42	Q9bs42 homo sapien
10	35	54.7	163	4 Q96HJ1	Q96hj1 homo sapien
11	35	54.7	163	4 Q96C76	Q96c76 homo sapien
12	35	54.7	163	4 Q96B04	Q96b04 homo sapien
13	35	54.7	163	4 Q9UHA3	Q9uha3 homo sapien
14	35	54.7	163	11 Q99L28	Q99l28 mus musculus
15	35	54.7	170	16 Q98M11	Q98m11 rhizobium 1
16	35	54.7	238	2 Q68L58	Q68l58 staphylococ

17	35	54.7	238	2	Q86862	Q86862 staphylococ
18	35	54.7	239	8	Q9TL13	Q9tl13 nephroselimi
19	35	54.7	253	5	Q9VZ06	Q9vz06 drosophila
20	35	54.7	274	11	Q9CQ47	Q9cq47 mus musculus
21	35	54.7	298	10	Q9AY53	Q9ay53 oryza sativ
22	35	54.7	315	5	Q9SSH7	Q9ssh7 drosophila
23	35	54.7	325	10	Q9FWS6	Q9fws6 arabidopsis
24	35	54.7	335	5	Q61888	Q61888 caenorhabdi
25	35	54.7	431	3	Q12124	Q12124 saccharomyc
26	35	54.7	461	2	Q9AK10	Q9aki0 rickettsia
27	35	54.7	536	5	Q8SUS1	Q8sus1 encephalito
28	35	54.7	622	10	Q9SH16	Q9sh16 arabidopsis
29	35	54.7	740	10	Q9SS87	Q9ss87 arabidopsis
30	35	54.7	993	10	Q9M9F3	Q9m9f3 arabidopsis
31	35	54.7	5147	4	Q9Y6V0	Q9y6v0 homo sapien
32	34	53.9	735	10	Q9LG17	Q9lg17 arabidopsis
33	34	53.1	81	16	Q97FW0	Q97fw0 streptococ
34	34	53.1	104	16	Q97TB1	Q97tb1 streptococ
35	34	53.1	121	10	Q9LTN4	Q9ltn4 arabidopsis
36	34	53.1	126	16	Q8ZHD0	Q8zhd0 yersinia pe
37	34	53.1	129	3	Q59956	Q59956 candida alb
38	34	53.1	130	4	Q9H7E7	Q9h7e7 homo sapien
39	34	53.1	151	16	Q9CGK9	Q9cgk9 lactococcus
40	34	53.1	225	17	Q97Z59	Q97z59 sulfolobus
41	34	53.1	306	12	Q55587	Q55587 avian rotav
42	34	53.1	527	2	Q9AGK0	Q9agk0 caulobacter
43	34	53.1	527	2	Q9RQV0	Q9rqv0 caulobacter
44	34	53.1	527	16	Q9A9H2	Q9a9h2 caulobacter
45	34	53.1	536	4	Q9NVN3	Q9nvn3 homo sapien

#### ALIGNMENTS

RESULT 1  
Q8TCD2  
ID Q8TCD2; PRELIMINARY; PRT; 711 AA.  
AC Q8TCD2;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC022347; AAH22347.1; -- 1B9CTEE097C45PAF CRC64;  
SQ SEQUENCE 711 AA; 78327 MW; 1B9CTEE097C45PAF CRC64;

Query Match 81.2%; Score 52; DB 4; Length 711;  
Best Local Similarity 90.9%; Pred. NO. 0.054;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAQNRMRKV 11  
DB 39 CFAQNRMRKV 49

RESULT 2  
Q9UCY5  
ID Q9UCY5 PRELIMINARY; PRT; 38 AA.  
AC Q9UCY5;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE Lactoferrin homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96081613; PubMed=8551695;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
  seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSP; P02788; IBKA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDBE8 CRC64;

Query Match 75.0%; Score 48; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQQRNRKVR 12
   |||||
Db 21 FQQRNRKVR 31

RESULT 3
Q23578 PRELIMINARY; PRT; 47 AA.
AC Q23578;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ZK682.1 protein.
GN ZK682.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A.,
  Bonfield J., Burton J., Durbin R., Favello A., Fulton L.,
  Craxton M., Dear S., Du Z., Durbin R., Hillier L., Jier M., Johnston L.,
  Gardner A., Green P., Hawkins J., Kistner J., Laister N., Latreille P.,
  Jones M., Kershaw J., Kistner J., Laister N., Laister N., Laister N.,
  Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
  Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
  Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
  Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
  Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
  "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
  elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Du Z., Le T.;
RT "The sequence of C. elegans cosmid ZK682.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Waterston R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41110; AAA82417.1; -.
SQ SEQUENCE 47 AA; 5606 MW; DF5332756A120750 CRC64;

Query Match 62.5%; Score 40; DB 5; Length 47;
Best Local Similarity 63.6%; Pred. No. 0.86;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 11
   |||||
Db 26 CFQQRNRKVR 36

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RESULT 4
Q91TW1 PRELIMINARY; PRT; 729 AA.
AC Q91TW1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to HCMVA US23 and MCMVS M143.
OS Tupaia herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae.
OX NCBI_TaxID=10397;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=2;
RC MEDLINE=21211637; PubMed=11312357;
RA Bahr U., Darai G.;
RT "Analysis and Characterization of the Complete Genome of Tupaia (Tree
  Shrew) Herpesvirus.";
RL J. Virol. 75:4854-4870(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=2;
RA Darai G., Bahr U.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF281817; AAK57026.1; -.
DR InterPro; IPR003360; US22.
DR Pfam; PF02393; US22; 1.
SQ SEQUENCE 729 AA; 81192 MW; D5FDE57AAFE3EAB5 CRC64;

Query Match 60.9%; Score 39; DB 12; Length 729;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQQRNRKVR 12
   |||||
Db 26 FQQRNRKVR 36

RESULT 5
Q9JUV34 PRELIMINARY; PRT; 57 AA.
AC Q9JUV34;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein NMA1014.
GN NMA1014.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RC MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
  Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
  Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
  Jags K., Leather S., Moule S., Mungall K., Quail M.A.,
  Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
  Whitehead S., Spratt B.G., Barrall B.G.;
  "Complete DNA sequence of a serogroup A strain of Neisseria
  meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162754; CAB94283.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 57 AA; 6491 MW; A6D8781C29E212C5 CRC64;

Query Match 59.4%; Score 38; DB 16; Length 57;
Best Local Similarity 58.3%; Pred. No. 2.7;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQQRNRKVR 12

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Db      21 CFSRREMGKVR 32
|||::|||
Query Match      57.8%; Score 37; DB 5; Length 675;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
Q9TR80
ID Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP: O77698; ICE2
DR InterPro; IPR011156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match      57.8%; Score 37; DB 6; Length 33;
Best Local Similarity 54.5%; Pred. No. 2.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAQRMKVR 11
|||::|||
Db      19 CYQWKKVR 29
|||::|||

RESULT 7
Q9GYM8
ID Q9GYM8 PRELIMINARY; PRT; 675 AA.
AC Q9GYM8;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Hypothetical 78.0 kDa protein.
GN M60.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Stellyes L.;
RA "The sequence of C. elegans cosmid M60.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RA "Direct Submission.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U39995; AAF99993.2; -.
KW Hypothetical protein.
SQ SEQUENCE 675 AA; 77981 MW; 3A5E193769BD1FA2 CRC64;

Query Match      54.7%; Score 35; DB 4; Length 150;

QY 3 QAQRNMKVR 12
|||::|||
Db      69 QRQNLREIR 78
|||::|||

RESULT 8
Q9SX85
ID Q9SX85 PRELIMINARY; PRT; 887 AA.
AC Q9SX85;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE F16N3.18 protein.
GN F16N3.18
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vyotskaya V.S., Schwartz J.R., Yu G., Tortumi M., Lenz C., Liu S.,
RA Lee J., Liu A., Li J., Kremenetskaia I., Gonzalez A., Altafi H.,
RA Araujo R., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
RA Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C., Rowley D.,
RA Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.;
RL "Arabidopsis thaliana chromosome 1 BAC F16N3 sequence.";
DR Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007519; AAD46032.1; -.
DR InterPro; IPR02048; EF-hand.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
SQ SEQUENCE 887 AA; 100064 MW; 533510830A4A5099 CRC64;

Query Match      57.8%; Score 37; DB 10; Length 887;
Best Local Similarity 58.3%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAQRNMKVR 12
|||::|||
Db      659 QRQNLREIR 670
|||::|||

RESULT 9
Q9BS42
ID Q9BS42 PRELIMINARY; PRT; 150 AA.
AC Q9BS42;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (T-EMBLrel. 18, Last annotation update)
DE 60S ribosomal protein L30 isolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005344; AAH05344.1; -.
DR InterPro; IPR000988; Ribosomal_L24E.
DR Pfam; PF01246; Ribosomal_L24e; 1.
DR PROSITE; PS01073; RIBOSOMAL_L24E; 1.
KW Ribosomal protein.
SQ SEQUENCE 150 AA; 18121 MW; 764482EBD4F53159 CRC64;

Query Match

```

Query Match	54.7%	Score 35;	DB 4;	Length 163;
Best Local Similarity	63.6%	Pred. No. 32;		
Matches	7;	Conservative	2;	Mismatches
			2;	Indels
			0;	Gaps
			0;	Gaps

RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BLADDER WART;  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF201949; AAF17241.1; -  
 DR EMBL; AF165521; AAF86651.1; -  
 DR EMBL; AF060926; AAG43138.1; -  
 DR EMBL; AP212226; AAK26249.1; -  
 DR EMBL; BC016777; AAH16777.1; -  
 DR EMBL; BC008409; AAH08409.1; -  
 DR EMBL; BC008422; AAH08422.1; -  
 DR EMBL; BC008449; AAH08449.1; -  
 DR EMBL; BC009593; AAH09593.1; -  
 DR EMBL; BC009604; AAH09604.1; -  
 DR EMBL; BC012913; AAH12913.1; -  
 DR EMBL; BC016331; AAH16331.1; -  
 DR EMBL; BC016725; AAH16725.1; -  
 DR EMBL; BC026266; AAH26266.1; -  
 DR EMBL; BC026267; AAH26267.1; -  
 DR InterPro; IPR000988; Ribosomal L24E.  
 DR Pfam; PF01246; Ribosomal L24E; 1.  
 DR PROSITE; PS01073; RIBOSOMAL\_L24E; 1.  
 KW Ribosomal protein.  
 SQ SEQUENCE 163 AA; 19621 MW; 1E5D9ECPFCF678D1 CRC64;

Query Match 54.7%; Score 35; DB 4; Length 163;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FQAQNNMKVR 12  
 | : | | | | |  
 Db 40 FKXKNPKVR 50

## RESULT 14

Q99L28 PRELIMINARY; PRT; 163 AA.

AC Q99L28;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Similar to 60S ribosomal protein L30 isolog.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC003885; AAH03885.1; -.

DR InterPro; IPR000988; Ribosomal L24E.  
 DR Pfam; PF01246; Ribosomal L24E; 1.  
 DR PROSITE; PS01073; RIBOSOMAL\_L24E; 1.  
 KW Ribosomal protein.  
 SQ SEQUENCE 163 AA; 19611 MW; 5393707FEA8CC417 CRC64;

Query Match 54.7%; Score 35; DB 11; Length 163;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FQAQNNMKVR 12  
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 Db 40 FKXKNPKVR 50

## RESULT 15

Q98M11 PRELIMINARY; PRT; 170 AA.

AC Q98M11;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 2-amino-4-hydroxy-6-hydroxymethylidihydropteridin e  
 DE pyrophosphokinase.  
 GN ML00785.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Ideesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti.";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP002995; BAB48302.1; -  
 DR InterPro; IPR000550; Hppk.  
 DR Pfam; PF01288; HPPK; 1.  
 DR PROSITE; PS00794; HPPK; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 170 AA; 18551 MW; 5F6C64AALD1668A7 CRC64;

Query Match 54.7%; Score 35; DB 16; Length 170;  
 Best Local Similarity 41.7%; Pred. No. 33;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFAQNNMKVR 12  
 | : | | | | |  
 Db 78 CLDAERKLRVR 89

Search completed: February 21, 2003, 07:44:23  
 Job time : 23.8 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107B-72

Perfect score: 70

Sequence: 1 CFQWAEENMKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	AAV78072	Human lactoferrin
2	66	94.3	12	AAV78087	Human lactoferrin
3	66	94.3	12	AAV78088	Human lactoferrin
4	65	92.9	12	AAV78038	Human lactoferrin
5	65	92.9	12	AAV78046	Human lactoferrin
6	65	92.9	12	AAV78047	Human lactoferrin
7	65	92.9	12	AAV78084	Human lactoferrin
8	65	92.9	12	AAV78091	Human lactoferrin
9	65	92.9	12	AAV78092	Human lactoferrin
10	65	92.9	13	AAV78037	Human lactoferrin

11	65	92.9	13	21	AAV78048	Human lactoferrin
12	65	92.9	13	21	AAV78049	Human lactoferrin
13	65	92.9	14	21	AAV78036	Human lactoferrin
14	65	92.9	14	21	AAV78050	Human lactoferrin
15	65	92.9	14	21	AAV78051	Human lactoferrin
16	65	92.9	15	17	AAV78054	Peptide for anti-u
17	65	92.9	15	21	AAV78035	Human lactoferrin
18	65	92.9	15	21	AAV78062	Human lactoferrin
19	65	92.9	15	21	AAV78063	Human lactoferrin
20	65	92.9	16	21	AAV78031	Human lactoferrin
21	65	92.9	16	21	AAV78064	Human lactoferrin
22	65	92.9	16	21	AAV78055	Human lactoferrin
23	65	92.9	17	21	AAV78034	Human lactoferrin
24	65	92.9	17	21	AAV78066	Human lactoferrin
25	65	92.9	17	21	AAV78067	Human lactoferrin
26	65	92.9	18	15	AAV69352	Human lactoferrin
27	65	92.9	18	17	AAV13397	Advanced glycosyla
28	65	92.9	18	21	AAV78033	Human lactoferrin
29	65	92.9	19	21	AAV68867	Amino acid sequenc
30	65	92.9	19	21	AAV78032	Human lactoferrin
31	65	92.9	20	13	AAV21810	Anti microbial pep
32	65	92.9	20	14	AAV44841	Lactoferrin-relate
33	65	92.9	20	15	AAV48530	Lactoferrin derive
34	65	92.9	20	15	AAV48531	Lactoferrin derive
35	65	92.9	20	15	AAV57461	Lactoferrin derive
36	65	92.9	20	15	AAV57462	Lactoferrin derive
37	65	92.9	20	16	AAV4698	Bovine lactoferrin
38	65	92.9	20	16	AAV4699	Bovine lactoferrin
39	65	92.9	20	16	AAV80263	Anti-parasitic lac
40	65	92.9	20	16	AAV80264	Anti-parasitic lac
41	65	92.9	20	17	AAV98553	Peptide for anti-u
42	65	92.9	20	17	AAV91852	Lactoferrin-derive
43	65	92.9	20	17	AAV03045	Lactoferrin-derive
44	65	92.9	20	17	AAV06067	Lactoferrin derive
45	65	92.9	20	17	AAV87621	Lactoferrin-derive

#### ALIGNMENTS

```

RESULT 1
AAV78072
ID AAV78072 standard; Peptide; 12 AA.
XX
AC AAV78072;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:72.
XX
DE Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 93WO-SR01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.

```

XX New peptides used for treatment and prevention of infections, -  
PT inflammations and tumors and for use in infant formula food -  
XX  
PS Claim 22; Page 35; 102pp; English.  
XX  
CC AAY78001 to AAY78100 represent peptides having sequences based on human  
lactoferrin. The peptides are taken up in the intestine through  
binding to specific lactoferrin receptors and are then transported  
through the circulation. A medicinal product of the peptide or fragment  
can be used for treating and/or prevention of infections (such as  
urinary tract infections, colitis, and Candida infection on a mucosal  
membrane), inflammations and/or tumours. The peptides can also be used  
in food stuffs such as infant formula food. The peptides are also  
fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
anti-inflammatory anti-infectious and anti-tumoural properties they  
cannot be used clinically on a broad basis because of high production  
costs. Therefore, provision of peptides based on lactoferrin would  
enable them to be used for the same purposes as lactoferrin at lower  
cost.  
XX  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 70; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CFQWARRNRKVR 12  
| | | | | | | | | | | |  
DB 1 CFQWARRNRKVR 12  
RESULT 2  
AAY78087  
ID AAY78087 standard; Peptide; 12 AA.  
XX  
AC AAY78087;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:87.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
XX WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 22; Page 37; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
binding to specific lactoferrin receptors and are then transported  
through the circulation. A medicinal product of the peptide or fragment  
can be used for treating and/or prevention of infections (such as  
urinary tract infections, colitis, and Candida infection on a mucosal  
membrane), inflammations and/or tumours. The peptides can also be used  
in food stuffs such as infant formula food. The peptides are also  
fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
anti-inflammatory anti-infectious and anti-tumoural properties they  
cannot be used clinically on a broad basis because of high production  
costs. Therefore, provision of peptides based on lactoferrin would  
enable them to be used for the same purposes as lactoferrin at lower  
cost.  
XX  
SQ Sequence 12 AA;  
Query Match 94.3%; Score 66; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 5.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWARRNRKVR 12  
| | | | | | | | | | | |  
DB 1 CFQWARRNRKVR 12  
RESULT 3  
AAY78088  
ID AAY78088 standard; Peptide; 12 AA.  
XX  
AC AAY78088;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:88.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
XX WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 22; Page 37; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
lactoferrin. The peptides are taken up in the intestine through  
binding to specific lactoferrin receptors and are then transported  
through the circulation. A medicinal product of the peptide or fragment  
can be used for treating and/or prevention of infections (such as  
urinary tract infections, colitis, and Candida infection on a mucosal  
membrane), inflammations and/or tumours. The peptides can also be used  
in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 5.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CFQWARRNKRVR 12  
 |||||  
 Db 1 CFQWARRNKRVR 12

RESULT 4

AAV78038  
 ID AAY78038 standard; Peptide; 12 AA.

XX AC AAY78038;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:38.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 70; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CFQWARRNKRVR 12  
 |||||  
 Db 1 CFQWARRNKRVR 12

RESULT 5

AAV78046  
 ID AAY78046 standard; Peptide; 12 AA.

XX AC AAY78046;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:46.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 35; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12  
 DB 1 CFQWARRNRKVR 12

## RESULT 6

AAV78047  
 ID AAV78047 standard; Peptide; 12 AA.

AC AAV78047;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:47.

KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 urinary tract infection; colitis; Candida infection; fungicidal;  
 bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

PN WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

PS Claim 18; Page 73; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;

Best Local Similarity 91.7%; Pred. No. 7.9e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12

DB 1 CFQWARRNRKVR 12

## RESULT 7

AAV78084

AAV78084 standard; Peptide; 12 AA.

AAV78084;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:84.

KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 urinary tract infection; colitis; Candida infection; fungicidal;  
 bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

PN WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

PS Claim 22; Page 36; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;

Best Local Similarity 91.7%; Pred. No. 7.9e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12

DB 1 CFQWARRNRKVR 12

## RESULT 8

AAV78091

ID AAV78091 standard; Peptide; 12 AA.

AC AAV78091;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:91.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA  
 XX  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 DR  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PT  
 PS Claim 22; Page 38; 102pp; English.  
 XX  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWARRNKKVR 12  
 DB 1 CFQWARRNKKVR 12  
 RESULT 9  
 ID AAY78092 standard; Peptide; 12 AA.  
 AC AAY78092;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT  
 DE Human lactoferrin derived peptide SEQ ID NO:92.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 XX WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA  
 XX  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 DR  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PT  
 PS Claim 22; Page 38; 102pp; English.  
 XX  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWARRNKKVR 12  
 DB 1 CFQWARRNKKVR 12  
 RESULT 10  
 ID AAY78037 standard; Peptide; 13 AA.  
 AC AAY78037;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT  
 DE Human lactoferrin derived peptide SEQ ID NO:37.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX

XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 XX Claim 12; Page 70; 102pp; English.  
 XX  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 XX Sequence 13 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 8.5e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWARMNRKVR 12  
 DB 2 CFQWARMNRKVR 13  
 RESULT 11  
 AAY78048  
 ID AAY78048 standard; Peptide; 13 AA.  
 AC AAY78048;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:48.  
 DE  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 PD 06-JUL-1999; 99WO-SE01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 XX Claim 15; Page 74; 102pp; English.  
 XX  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 XX Sequence 13 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 8.5e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWARMNRKVR 12  
 DB 2 CFQWARMNRKVR 13  
 RESULT 12  
 AAY78049  
 ID AAY78049 standard; Peptide; 13 AA.  
 AC AAY78049;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:49.  
 DE  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 PD 06-JUL-1999; 99WO-SE01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX

PS Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.5e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARNMKVR 12

DB 2 CFQWQNRMKVR 13

RESULT 13

AAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:36.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX SQ Sequence 14 AA;

Query Match 92.9%; Score 65; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 9.2e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARNMKVR 12

DB 3 CFQWQNRMKVR 14

RESULT 14

AAY78050

ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:50.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
XX cost.

SQ Sequence 14 AA;  
Query Match 92.9%; Score 65; DB 21; Length 14;  
Best Local Similarity 91.7%; Pred. No. 9.2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARNMKVR 12  
Db 3 CFQWQRMNKVR 14  
|||||

RESULT 15  
AAAY78051  
ID AAY78051 standard; Peptide; 14 AA.  
XX  
AC AAY78051;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:51.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
PN WC200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
DR WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
PS Claim 18; Page 75; 102pp; English.  
XX  
CC AAY78001 to AAY78100 represent peptides having sequences based on human  
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CC membrane), inflammations and/or tumours. The peptides can also be used  
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CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

SQ Sequence 14 AA;  
Query Match 92.9%; Score 65; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 9.2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARNMKVR 12  
Db 3 CFQWQRMNKVR 14  
|||||

Search completed: February 21, 2003, 07:37:11  
Job time : 28.35 secs



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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-72  
Perfect score: 70  
Sequence: 1 CFQWARMKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCOTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-09-508-734-4
13	65	92.9	24	4	US-09-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	36	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-633-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

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29	65	92.9	54	2	US-08-406-271-2	Sequence 2, Appli
30	65	92.9	694	3	US-08-724-586-2	Sequence 2, Appli
31	65	92.9	694	4	US-09-421-632-2	Sequence 2, Appli
32	65	92.9	694	4	US-09-932-190-2	Sequence 2, Appli
33	65	92.9	705	2	US-08-655-640-2	Sequence 2, Appli
34	65	92.9	708	2	US-08-655-640-4	Sequence 4, Appli
35	65	92.9	711	1	US-08-154-019-4	Sequence 4, Appli
36	65	92.9	711	1	US-08-461-333-4	Sequence 4, Appli
37	65	92.9	711	3	US-08-464-167-4	Sequence 4, Appli
38	65	92.9	711	3	US-09-158-313-4	Sequence 4, Appli
39	65	92.9	711	4	US-08-476-798-4	Sequence 2, Appli
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44	62	88.6	711	3	US-08-456-108-2	Sequence 2, Appli
45	62	88.6	711	4	US-09-285-577-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-204-487-3  
; Sequence 3, Application US/082044487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN/ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FUN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..18  
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1694
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWARRNRKVR 12
| | | | | | | | | |
Db 1 CFQWARRNRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755.161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12  
||| |||||  
Db 2 CFQWARMRKVR 13

RESULT 6  
US-07-891-174-3  
; Sequence 3, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLER:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site

LOCATION: 2  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 19"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 19  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 2"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12  
||| |||||  
Db 2 CFQWARMRKVR 13

RESULT 7  
US-08-204-487-1  
; Sequence 1, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIAKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE  
DERIVED FROM HUMAN LACTOFERRIN"  
US-08-204-487-1

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWARMRKVR 12  
| | | | |  
Db 2 CFQWQRMNRKVR 13

RESULT 8  
US-08-256-771-24  
; Sequence 24, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,771  
; FILING DATE: July 22, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "Cys residues are linked by  
disulfide bond"

US-08-256-771-24  
Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWARMNRKVR 12  
| | | | |  
Db 2 CFQWQRMNRKVR 13

RESULT 9  
US-08-256-771-25  
; Sequence 25, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,771  
; FILING DATE: July 22, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "Cys residues are protected to  
prevent disulfide bond"  
US-08-256-771-25

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWARMNRKVR 12  
| | | | |  
Db 2 CFQWQRMNRKVR 13

RESULT 10  
US-08-381-984-24

Sequence 24, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

## INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "cysteine residues at positions 2  
and 19 are bonded by disulfide linkage"

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 7.3e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12  
Db 2 CFQWQRMNRKVR 13

## US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 7.3e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12

Db 2 CFQWQRMNRKVR 13

## RESULT 11

US-08-381-984-25  
Sequence 25, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

## INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "the specified peptide as well as  
peptides including the specified peptide as a fragment thereof"

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 7.3e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12  
Db 2 CFQWQRMNRKVR 13

## US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 7.3e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMRKVR 12

Db 2 CFQWQRMNRKVR 13

## RESULT 12

US-09-508-734-4  
Sequence 4, Application US/09508734  
Patent No. 6423509  
GENERAL INFORMATION:  
APPLICANT: Samyang Genex Corporation  
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
useful microorganism thereof  
FILE REFERENCE: PA/SYG/00139  
CURRENT APPLICATION NUMBER: US/09/508,734  
CURRENT FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: PCT/KR99/00373  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: KR1998-29351  
PRIOR FILING DATE: 1998-07-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Kopatentin 1.71  
SEQ ID NO 4

```
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4

Query Match          92.9%; Score 65; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWARNRKVR 12
Db 2 CFQWQNRNKRVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SVG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR93/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match          92.9%; Score 65; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 8.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWARNRKVR 12
Db 3 CFQWQNRNKRVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500KB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
```

RESULT 15  
US-07-891-174-10  
; Sequence 10, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 4  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 21"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 21

; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 4"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
; US-07-891-174-10  
; Query Match 92.9%; Score 65; DB 1; Length 25;  
; Best Local Similarity 91.7%; Pred. No. 9.1e-05;  
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWARRNRKVR 12  
DB 4 CFQWARRNRKVR 15  
Search completed: February 21, 2003, 07:50:33  
Job time : 8.7 secs



GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run On: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107B-72  
Perfect score: 70  
Sequence: 1 CFQWARRMKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	40	57.1	15	9	US-09-798-869-7
8	39	55.7	15	9	US-09-798-869-4
9	39	55.7	25	9	US-09-798-869-22
10	38	54.3	489	9	US-09-888-320-2
11	36	51.4	15	9	US-09-798-869-8
12	36	51.4	15	9	US-09-798-869-29
13	36	51.4	15	9	US-09-798-869-30
14	35	50.0	21	10	US-09-864-761-47985
15	35	50.0	62	10	US-09-764-877-1690
16	35	50.0	292	9	US-10-117-824-1
17	34	48.6	77	10	US-09-764-847-613
18	34	48.6	86	9	US-09-738-626-5715
19	34	48.6	312	10	US-09-935-428A-4

20	34	48.6	338	9	US-09-978-295A-119	Sequence 119, App
21	34	48.6	338	9	US-09-978-697-119	Sequence 119, App
22	34	48.6	338	9	US-09-978-132A-119	Sequence 119, App
23	34	48.6	338	9	US-09-999-832A-119	Sequence 119, App
24	34	48.6	338	9	US-09-978-189-119	Sequence 119, App
25	34	48.6	553	9	US-09-796-753-14	Sequence 14, Appli
26	34	48.6	553	10	US-09-981-649A-6	Sequence 6, Appli
27	34	48.6	553	10	US-09-981-649A-24	Sequence 24, Appli
28	34	48.6	554	10	US-09-981-649A-30	Sequence 30, Appli
29	34	48.6	554	10	US-09-981-649A-32	Sequence 32, Appli
30	34	48.6	556	10	US-09-795-691-2	Sequence 2, Appli
31	34	48.6	559	10	US-09-981-649A-28	Sequence 28, Appli
32	34	48.6	1212	9	US-10-219-248-3	Sequence 3, Appli
33	34	48.6	1212	9	US-10-219-247-3	Sequence 3, Appli
34	34	48.6	1212	10	US-09-855-722-3	Sequence 3, Appli
35	34	48.6	1238	9	US-10-219-248-5	Sequence 5, Appli
36	34	48.6	1238	9	US-10-219-247-5	Sequence 5, Appli
37	34	48.6	1238	10	US-09-855-722-5	Sequence 5, Appli
38	34	48.6	1238	10	US-09-944-849-4	Sequence 4, Appli
39	34	48.6	1258	10	US-09-867-852-107	Sequence 107, App
40	33	47.1	31	9	US-09-956-206A-13	Sequence 13, Appli
41	33	47.1	33	10	US-09-864-761-44211	Sequence 44211, A
42	33	47.1	95	10	US-09-764-864-1031	Sequence 1031, Ap
43	33	47.1	287	10	US-09-925-301-1386	Sequence 1386, Ap
44	33	47.1	309	9	US-09-510-332-93	Sequence 93, Appli
45	33	47.1	333	9	US-09-796-753-26	Sequence 26, Appli

## ALIGNMENTS

RESULT 1  
US-09-798-869-2  
; Sequence 2, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798.869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;  
Best Local Similarity 91.7%; Pred. No. 2.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWARRMKVR 12  
Db 3 CFQWARRMKVR 14

RESULT 2  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-798-869-20

Query Match      92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
   |||||
Db 3 CFQWARMNRKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-023-096-2

; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-798-869-20

Query Match      92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
   |||||
Db 3 CFQWARMNRKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-023-096-2

; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
; US-09-798-869-6

Query Match      81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00067;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWARMNRKVR 12
   |||||
Db 3 CFQWARMNRKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
; US-09-798-869-3

Query Match      68.6%; Score 48; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.023;
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Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

Oy 1 CFOWARNMKV 11  
|:|:|:|:|:  
Db 3 CYQWQRMKRL 13

RESULT 6  
US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 68.6%; Score 48; DB 9; Length 25;  
Best Local Similarity 63.6%; Pred. No. 0.039;  
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

Oy 1 CFOWARNMKV 11  
|:|:|:|:|:  
Db 3 CYQWQRMKRL 13

RESULT 7  
US-09-798-869-7  
; Sequence 7, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.55;  
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Oy 1 CFOWARNMKV 11  
|:|:|:|:|:  
Db 3 CYQWQRMKRL 13

RESULT 8  
US-09-798-869-4  
; Sequence 4, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

Oy 1 CFOWARNMKV 11  
|:|:|:|:|:  
Db 3 CLRWQNMKRV 13

RESULT 9  
US-09-798-869-22  
; Sequence 22, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;  
Best Local Similarity 54.5%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

Oy 1 CFOWARNMKV 11  
|:|:|:|:|:  
Db 3 CLRWQNMKRV 13

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RESULT 10
US-09-888-320-2
; Sequence 2, Application US/09888320
; Publication No. US20030013090A1
; GENERAL INFORMATION:
; APPLICANT: Barry III, Clifton E.
; APPLICANT: DeBarber, Andrea E.
; APPLICANT: Mdullu, Khaisimuizi
; APPLICANT: Bekker, Linda-Gail
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
; FILE REFERENCE: 015280-413100US
; CURRENT APPLICATION NUMBER: US/09/888,320
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/214,187
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type BtaA monooxygenase (RV3854c, EthA)
US-09-888-320-2

Query Match 54.3%; Score 38; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWARMNRKV 11
Db 253 CQKWRMRKVM 263

RESULT 11
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 51.4%; Score 36; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.7;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWARMNRKV 11
Db 3 CLRQWQWEMRKV 13

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-72

Perfect score: 70

Sequence: 1 CFQWARMKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 J22323	lactoferrin - goat
3	45	64.3	33	2 S52107	histidyl-trna synt
4	40	57.1	428	2 F81650	hypothetical prote
5	40	57.1	511	2 AB0558	hypothetical prote
6	39	55.7	275	2 T22597	hypothetical prote
7	39	55.7	536	2 T24218	hypothetical prote
8	39	55.7	707	1 A28438	lactoferrin precu
9	39	55.7	1213	2 T41378	probable helicase
10	38	54.3	428	2 H71500	histidine-trna lig
11	38	54.3	489	2 C70555	probable monooxyge
12	38	54.3	501	2 T39801	hypothetical sh3-c
13	38	54.3	743	2 T00634	hypothetical prote
14	38	54.3	1051	2 T48933	WD repeat domain p
15	38	54.3	4568	2 T08030	dysen beta heavy
16	37	52.9	124	2 C96582	F1511.22 (imported
17	37	52.9	172	2 D64388	hypothetical prote
18	37	52.9	211	1 S40836	formate dehydrogen
19	37	52.9	211	2 A86078	formate dehydrogen
20	37	52.9	211	2 B91231	formate dehydrogen
21	37	52.9	211	2 AD0946	formate dehydrogen
22	37	52.9	531	2 A84471	En/Spm-like transp
23	37	52.9	594	2 C84325	hypothetical prote
24	37	52.9	742	2 T25415	hypothetical prote
25	37	52.9	2150	2 T08165	RNA1 polypeptin -
26	36	51.4	224	2 D89836	hypothetical prote
27	36	51.4	274	2 B60950	apolipoprotein B-1
28	36	51.4	298	2 AD2346	hypothetical prote
29	36	51.4	361	2 A24470	probable proteinase

## ALIGNMENTS

### RESULT 1

#### TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74:

R/Cho. Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:g467236; PIDN:AA660324.1; PID:g467237

R/Rev. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <REN>

A/Cross-references: GB:S52659; NID:g263311; PIDN:AA624877.1; PID:g263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>



R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A;Reference number: AB0502; PMID:11677608

A;Accession: AB0858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-511 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:ig16504016; GSPDB:GN00176

C;Genetics:

A;Gene: STY3070

Query Match

Best Local Similarity 57.1%; Score 40; DB 2; Length 511;

Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWARRNRKVR 12

DB 350 CFQWARRNRKVR 361

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QY 1 CFQWARMK 8  
|:|:|:|:|  
Db 1141 CYEWARGM 1149

## RESULT 10

H71500  
Histidine-tRNA ligase (EC 6.1.1.21) - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 03-Jun-2002  
C:Accession: H71500  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Mazatthe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
A:Reference number: A71570; MUID:99000809; PMID:9784136  
A:Accession: H71500  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-428 <ARN>  
A:Cross-references: GB:AE001325; GB:AE001273; NID:G3328980; PIDN:AAC68145.1; PID:G332898  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: huss  
C:Superfamily: histidine-tRNA ligase; histidine-tRNA ligase homology  
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 54.3%; Score 38; DB 2; Length 428;  
Best Local Similarity 45.5%; Pred. No. 44;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMK 11  
|:|:|:|:|  
Db 348 CFSWANRLRL 358

## RESULT 11

C70655  
probable monooxygenase - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: C70655  
R:Coale, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: C70655  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-489 <COL>  
A:Cross-references: GB:283864; GB:AL123456; NID:G3261687; PIDN:CAB06212.1; PID:e301250;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv3854c

Query Match 54.3%; Score 38; DB 2; Length 489;  
Best Local Similarity 54.5%; Pred. No. 50;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARMK 11  
|:|:|:|:|  
Db 253 CQKFRMRK 263

## RESULT 12

T39801  
Hypothetical sh3-containing protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T39801  
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21880  
A:Accession: T39801  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-501 <MCD>  
A:Cross-references: EMBL:AL109731; PIDN:CAB52037.1; GSPDB:GN00067; SPDB:SPBCL19C2.10  
A:Experimental source: strain 972h-; cosmid c19C2  
C:Genetics:  
A:Gene: SPDB:SPBCL19C2.10  
A:Map position: 2  
A:Introns: 196/3

Query Match 54.3%; Score 38; DB 2; Length 501;  
Best Local Similarity 60.0%; Pred. No. 52;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARMK 10  
|:|:|:|:|  
Db 50 CTRVVRNMDK 59

## RESULT 13

T00634  
Hypothetical protein H\_DJ0897G10.1 - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 05-Nov-1999  
C:Accession: T00634  
R:Kalicki, J.; Elliott, G.  
submitted to the EMBL Data Library, January 1998  
A:Description: The sequence of Homo sapiens PAC clone DJ0897G10.  
A:Reference number: Z14194  
A:Accession: T00634  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-743 <KAL>  
A:Cross-references: EMBL:AC004082; NID:G2822160; PIDN:AAB97937.1; PID:G2822161

Query Match 54.3%; Score 38; DB 2; Length 743;  
Best Local Similarity 50.0%; Pred. No. 76;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWARMK 12  
|:|:|:|:|  
Db 498 CFLGRNWK 509

## RESULT 14

T48933  
WD repeat domain protein - Arabidopsis thaliana  
N:Alternate names: protein F14L2.80  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T48933  
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z25008  
A:Accession: T48933  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1051 <JOR>  
A:Cross-references: EMBL:AL353818; GSPDB:GN00061; ATSP:F14L2.80  
A:Experimental source: cultivar Columbia; BAC clone F14L2  
C:Genetics:  
A:Gene: ATSP:F14L2.80  
A:Map position: 3  
A:Introns: 36/3; 121/3; 205/3; 336/2; 668/3; 739/1; 773/1; 853/2; 894/2; 932/3

```

Query Match
Best Local Similarity 54.3%; Score 38; DB 2; Length 1051;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARNRKV 11
   | : | : | : |
Db 64 CWRWAKNSRYV 74

RESULT 15
T08030
dynein beta heavy chain - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C:Accession: T08030
R/Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes
A:Reference number: Z16302; MUID:94274778; PMID:8006077
A:Accession: T08030
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4568 xMIT>
A:Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
A:Experimental source: strain 21gr
C:Genetics:
A:Gene: ODA4
A:Map position: IX
A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
C:Superfamily: dynein heavy chain, ciliary
C:Keywords: Nucleotide binding; P-loop
P:1919-1926/Region: nucleotide-binding motif A (P-loop)
P:2202-2209/Region: nucleotide-binding motif A (P-loop)
P:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match
Best Local Similarity 54.3%; Score 38; DB 2; Length 4568;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARNRKVR 12
   | | | | : | : |
Db 1852 CFQWSQLRYIQ 1863

Search completed: February 21, 2003, 07:47:42
Job time : 10.65 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107B-72  
Perfect score: 70  
Sequence: 1 CFQWARMKRV 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	65	92.9	711	1	TRFL_HUMAN
2	48	68.6	708	1	TRFL_CAMDR
3	48	68.6	708	1	TRFL_CAPHI
4	40	57.1	292	1	NLA_DROME
5	40	57.1	428	1	SYH_CHLMU
6	40	57.1	695	1	TRFL_HORSE
7	39	55.7	146	1	RPOB_LIBAF
8	39	55.7	707	1	TRFL_MOUSE
9	39	55.7	783	1	YNR2_CAEEL
10	38	54.3	422	1	PAFA_CHICK
11	38	54.3	428	1	SYH_CHLTR
12	38	54.3	989	1	T100_HUMAN
13	38	54.3	4568	1	DYHB_CHLRE
14	37	52.9	172	1	Y708_METJA
15	37	52.9	211	1	PDOI_ECOLI
16	37	52.9	573	1	UREI_LACPE
17	36	51.4	369	1	SP11_MXVL
18	36	51.4	435	1	SNXP_HUMAN
19	36	51.4	451	1	YGH9_DROME
20	36	51.4	585	1	XHD9_YEAST
21	35	50.0	62	1	RL28_THETN
22	35	50.0	292	1	CNT8_HUMAN
23	35	50.0	355	1	MURG_NEIMA
24	35	50.0	355	1	MURG_NEIMB
25	35	50.0	365	1	1A34_HUMAN
26	35	50.0	372	1	AR1B_MOUSE
27	35	50.0	430	1	SYH_CHLPN
28	35	50.0	480	1	YQSI_CAEEL
29	35	50.0	749	1	VP4_ROTGA
30	35	50.0	851	1	EF2_CAEEL
31	35	50.0	857	1	EF2_CHICK
32	35	50.0	857	1	EF2_CRICK
33	35	50.0	857	1	EF2_HUMAN

34 35 50.0 857 1 EF2\_MESAU  
35 35 50.0 857 1 EF2\_MOUSE  
36 35 50.0 857 1 EF2\_RAT  
37 35 50.0 966 1 VIA\_BBMV  
38 35 50.0 4568 1 DYHC\_CAEEL  
39 34.5 49.3 727 1 KDGA\_RAT  
40 34.5 49.3 730 1 KDGA\_MOUSE  
41 34 48.6 198 1 PGD2\_HUMAN  
42 34 48.6 214 1 VIF\_SIVS4  
43 34 48.6 224 1 GTXA\_ARATH  
44 34 48.6 238 1 CCDA\_BACHD  
45 34 48.6 246 1 Y495\_SNYF3

P05086 mesocricetu  
P58252 mus musculus  
P05197 rattus norv  
Q00020 broad bean  
Q19020 caenorhabdi  
P15556 rattus norv  
O86733 mus musculus  
O60760 homo sapien  
P12505 simian immu  
P46421 arabidopsis  
Q9kdl8 bacillus ha  
Q55185 synechocyst

## ALIGNMENTS

RESULT 1  
TRFL\_HUMAN  
ID TRFL\_HUMAN STANDARD; PRT; 711 AA.  
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;  
AC Q96KZ5;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Lactoferrin precursor (lactoferrin) [Contains: Lactoferrin A;  
DE Lactoferrin B; Lactoferrin C].  
GN LTF OR LF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90384839; PubMed=2402455;  
RA Rev M.W., Woloshuk S.L., de Boer H.A., Pieper P.R.;  
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cho Y.Y.;  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Connely O.M.;  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Liang Q., Jimenez-Flores R., Richardson T.;  
RT "Molecular cloning and sequence analysis of human lactoferrin.";  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Wei X., Han J., Rado T.A.;  
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cheng H., Chen X., Huan L.;  
RT "cDNA cloning and sequence analysis of human lactoferrin.";  
RN [7]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RN [8]  
RP Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.



Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARRMKVR 12  
 |||||  
 DB 39 CFQWARRMKVR 50

## RESULT 2

TRFL\_CAMDR STANDARD; PRT; 708 AA.  
 AC Q9TUM0; Q9MZS5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R., Ackermann M., Fazah Z., Puhan Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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DR EMBL; AJ31674; CAB53387.1; -  
 DR EMBL; AF165879; AAF82241.1; -  
 DR HSP; O77811; 1B1X.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN\_1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN\_3; 2.  
 DR KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 708 BY SIMILARITY.  
 FT REPEAT 20 363 LACTOTRANSFERRIN.  
 FT REPEAT 364 708 1.  
 FT REPEAT 64 2.  
 FT DISULFID 28 64 BY SIMILARITY.  
 FT DISULFID 38 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLP (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 080C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;  
 Best Local Similarity 66.7%; Pred. No. 0.39;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARRMKVR 12  
 |||||  
 DB 38 CAQWQRRMKVR 49

## RESULT 3

TRFL\_CAPHI STANDARD; PRT; 708 AA.  
 ID TRFL\_CAPHI  
 AC Q29477; Q29479;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary Gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=94380047; PubMed=8093048;  
 RA Le Provost F., Nocart M., Guerin G., Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntenic group.";  
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; U53857; AAA97958.1; -;  
 CC EMBL; X78902; CAA55517.1; -;  
 CC HSP; 077698; 1CE2.  
 CC Inter-Pro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SM00094; TR\_FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN\_1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 CC PROSITE; PS00207; TRANSFERRIN\_3; 2.  
 CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 CC Signal.  
 CC -----  
 CC SIGNAL 1 19 BY SIMILARITY.  
 CC CHAIN 20 708 LACTOTRANSFERRIN.  
 CC REPEAT 20 363 1.  
 CC REPEAT 364 708 2.  
 CC DISULFID 28 64 BY SIMILARITY.  
 CC DISULFID 38 55 BY SIMILARITY.  
 CC DISULFID 134 217 BY SIMILARITY.  
 CC DISULFID 176 192 BY SIMILARITY.  
 CC DISULFID 189 200 BY SIMILARITY.  
 CC DISULFID 250 264 BY SIMILARITY.  
 CC DISULFID 367 399 BY SIMILARITY.  
 CC DISULFID 377 390 BY SIMILARITY.  
 CC DISULFID 424 703 BY SIMILARITY.  
 CC DISULFID 444 666 BY SIMILARITY.  
 CC DISULFID 476 551 BY SIMILARITY.  
 CC DISULFID 500 694 BY SIMILARITY.  
 CC DISULFID 510 524 BY SIMILARITY.  
 CC DISULFID 521 534 BY SIMILARITY.  
 CC DISULFID 592 606 BY SIMILARITY.  
 CC DISULFID 644 649 BY SIMILARITY.  
 CC METAL 79 IRON 1 (BY SIMILARITY).  
 CC METAL 111 IRON 1 (BY SIMILARITY).  
 CC METAL 211 IRON 1 (BY SIMILARITY).  
 CC METAL 272 IRON 1 (BY SIMILARITY).  
 CC METAL 414 IRON 2 (BY SIMILARITY).  
 CC METAL 452 IRON 2 (BY SIMILARITY).  
 CC METAL 545 IRON 2 (BY SIMILARITY).  
 CC METAL 614 IRON 2 (BY SIMILARITY).  
 CC BINDING 140 ANION (BY SIMILARITY).  
 CC BINDING 482 ANION (BY SIMILARITY).  
 CC CARBOHYD 252 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 300 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 387 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 495 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 564 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CONFLICT 56 I -> V (IN REF. 2).  
 CC CONFLICT 88 L -> R (IN REF. 2).  
 CC CONFLICT 124 Q -> K (IN REF. 2).  
 CC CONFLICT 154 F -> P (IN REF. 2).  
 CC CONFLICT 304 S -> R (IN REF. 2).  
 CC CONFLICT 414 D -> G (IN REF. 2).  
 CC SEQUENCE 708 AA; 77358 MW; F2ED3C83539960D CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;  
 Best Local Similarity 63.6%; Pred. No. 0.39;  
 Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 1 CFQWARMRKV 11

Db 38 CYQWQRMRLK 48

RESULT 4  
 NLA\_DROME  
 ID NLA\_DROME STANDARD; PRT; 292 AA.  
 AC Q9XZL8; Q9V391;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Nebula protein.  
 GN NLA OR CG6072.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McCormick A.V., Goldberg M.L.;  
 RT "Gene required for elongation of meiosis I spindle in Drosophila  
 RT females.";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.D.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lambo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.  
 CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.  
 CC -----  
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 CC -----

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF147700; AAD33987.1; -.
CC DR EMBL; AE003712; AAF55285.1; -.
CC DR FLYBase; FBgn0026629; nla.
CC SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F5EA6CF9 CRC64;

Query Match
Best Local Similarity 57.1%; Score 40; DB 1; Length 292;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 F0WANNMKVR 12
DB 150 F0WLRSPRLR 160

RESULT 5
SYN_CHLMU
ID_SYN_CHLMU STANDARD; PRT; 428 AA.
AC Q9FJ09;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hstidy1-trna synthetase (EC 6.1.1.21) (Histidine--trna ligase)
DE (HIS5)
DE HISS OR TC0830.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mopn / Nig9;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brubham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson M., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406 (2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
CC phosphate + L-histidyl-tRNA(His).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AE002349; AAF39630.1; -.
CC DR HSSP; Q32422; 1QE0.
CC DR TIGR; TC0830; -.
CC InterPro; IPR002106; AaRNA_ligaseII.
CC InterPro; IPR004154; HGTP_anticodon.
CC InterPro; IPR004516; Hiss.
CC InterPro; IPR002314; tRNA-synt 2b.
CC Pfam; PF00587; tRNA-synt 2b; 1.
CC DR TIGRFAMs; TIGR00442; Hiss; 1.
CC DR PROSITE; PS00862; AA_tRNA_LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 428 AA; 48939 MW; 9CF859ED05689DDF CRC64;

Query Match
Best Local Similarity 57.1%; Score 40; DB 1; Length 428;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CF0WANNVR 9
DB 348 CFSWAKHLR 356

RESULT 6
TRFL_HORSE
ID_TRFL_HORSE STANDARD; PRT; 695 AA.
AC Q778L1;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) (Fragment).
DE LTF.
GN LTF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RX "cDNA sequence of mare lactoferrin";
RX Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX TISSUE=Milk;
RX MEDLINE=99296631; PubMed=10366507;
RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
RT resolution."
RL J. Mol. Biol. 289:303-317 (1999).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC -----
CC EMBL; AJ010930; CAA09407.1; -.
CC DR PDB; 1B1X; 02-DEC-98.
CC DR PDB; 1B70; 02-FEB-99.
CC DR PDB; 1B72; 02-FEB-99.
CC DR InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC DR PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN 1; 2.
CC PROSITE; PS00206; TRANSFERRIN 2; 2.
CC PROSITE; PS00207; TRANSFERRIN 3; 1.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; 3D-structure.
FT NON TER 1 1
FT SIGNAL <1 6
FT CHAIN 7 695 LACTOTRANSFERRIN.
FT REPEAT 7 350 1.
FT REPEAT 351 695 2.
FT DISULFID 15 51
FT DISULFID 25 42
FT DISULFID 121 204
FT DISULFID 163 179
FT DISULFID 166 189
FT DISULFID 176 187
FT DISULFID 237 251
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PT DISULFID 354 386
PT DISULFID 364 377
PT DISULFID 411 690
PT DISULFID 431 653
PT DISULFID 463 638
PT DISULFID 487 681
PT DISULFID 497 511
PT DISULFID 508 521
PT DISULFID 579 593
PT DISULFID 631 636
PT METAL 66 66
PT METAL 98 98
PT METAL 198 198
PT METAL 259 259
PT METAL 401 401
PT METAL 439 439
PT METAL 532 532
PT METAL 601 601
PT METAL 127 127
PT BINDING 469 469
PT CARBOHYD 143 143
PT CARBOHYD 287 287
PT CARBOHYD 482 482
SQ SEQUENCE 695 AA; 75991 MW; 07B84D50E1B165D CRC64;

Query Match 57.1%; Score 40; DB 1; Length 695;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWARMNRK 12
   |::|::|::|
DB 25 CAKFORNMKVR 36

RESULT 7
RPOB LIBAF
ID _RPOB LIBAF STANDARD; PRT; 146 AA.
AC P41187;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
beta chain) (RNA polymerase beta subunit) (Fragment).
GN RPOB.
OS Liberibacter africanus (Liberibacter africanus).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Candidatus Liberibacter.
CX NCBI_TaxID=34020;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Nelspruit;
RA Planet P., Jagoueix S., Bove J.M., Garnier M.;
RT "Detection and characterization of the African Citrus Greening
Rt Liberobacter by amplification, cloning and sequencing of the rplKJL-
rpoCB operon.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
{RNA}(N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
-----
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DR EMBL; J03298; AAA40525.1; -
DR EMBL; D88510; BAA13633.1; -
DR EMBL; BC006904; AAH06904.1; -

CC EMBL; U09675; AAA19557.1; -
DR InterPro; IPR001572; RNA_pol_B.
DR Pfam; PF00562; RNA_pol_B; 1.
DR PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
KW Transferase; Transcription; DNA-directed RNA polymerase.
PT NON_TER 146 146
SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;

Query Match 55.7%; Score 39; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARMNRK 10
   |::|::|
DB 10 CVQWSEKRGARK 19

RESULT 8
TRFL MOUSE
ID TRFL_MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T., Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
uterine secretions.";
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morlishi K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1939212;
RA Liu Y., Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
RL J. Biol. Chem. 266:21880-21885(1991).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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DR EMBL; J03298; AAA40525.1; -
DR EMBL; D88510; BAA13633.1; -
DR EMBL; BC006904; AAH06904.1; -

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DR EMBL; M74778; AAA39427.1; --  
 DR PIR; A28438; A28438.  
 DR HSP; P02788; 1CB6.  
 DR MGD; MGI:96837; Lcf.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 1.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 FT SIGNAL.  
 FT SIGNAL 1 19 BY SIMILARITY.  
 FT CHAIN 20 707 LACTOTRANSFERRIN.  
 FT REPEAT 20 357 1.  
 FT REPEAT 358 707 2.  
 FT DISULFID 27 63 BY SIMILARITY.  
 FT DISULFID 37 54 BY SIMILARITY.  
 FT DISULFID 133 216 BY SIMILARITY.  
 FT DISULFID 175 191 BY SIMILARITY.  
 FT DISULFID 188 199 BY SIMILARITY.  
 FT DISULFID 249 263 BY SIMILARITY.  
 FT DISULFID 366 398 BY SIMILARITY.  
 FT DISULFID 375 389 BY SIMILARITY.  
 FT DISULFID 423 702 BY SIMILARITY.  
 FT DISULFID 443 665 BY SIMILARITY.  
 FT DISULFID 475 550 BY SIMILARITY.  
 FT DISULFID 499 693 BY SIMILARITY.  
 FT DISULFID 509 523 BY SIMILARITY.  
 FT DISULFID 520 533 BY SIMILARITY.  
 FT DISULFID 591 605 BY SIMILARITY.  
 FT DISULFID 643 648 BY SIMILARITY.  
 FT METAL 78 78 IRON 1 (BY SIMILARITY).  
 FT METAL 110 110 IRON 1 (BY SIMILARITY).  
 FT METAL 210 210 IRON 1 (BY SIMILARITY).  
 FT METAL 271 271 IRON 1 (BY SIMILARITY).  
 FT METAL 413 413 IRON 2 (BY SIMILARITY).  
 FT METAL 451 451 IRON 2 (BY SIMILARITY).  
 FT METAL 544 544 IRON 2 (BY SIMILARITY).  
 FT METAL 613 613 IRON 2 (BY SIMILARITY).  
 FT BINDING 139 139 ANION (POTENTIAL).  
 FT BINDING 481 481 ANION (POTENTIAL).  
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 494 494 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 1 2 MR -> IQG (IN REF. 1).  
 FT CONFLICT 25 25 R -> Q (IN REF. 2).  
 FT CONFLICT 82 82 M -> L (IN REF. 2).  
 FT CONFLICT 359 359 S -> T (IN REF. 2).  
 FT CONFLICT 382 382 A -> D (IN REF. 1).  
 FT CONFLICT 449 449 E -> G (IN REF. 2).  
 FT CONFLICT 629 629 L -> V (IN REF. 1).  
 SQ SEQUENCE 707 AA; 77865 MW; F26AE03404C19A8 CRC64;  
 Query Match 55.7%; Score 39; DB 1; Length 707;  
 Best Local Similarity 54.5%; Pred. No. 17;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CFQWARMNRKV 11  
 Db 37 CLRQWNRKV 47  
 RESULT 9  
 YNR2\_CABEL STANDARD; PRT; 783 AA.  
 AC Q21988;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Hypothetical protein R13G10.2 in chromosome III.  
 GN R13G10.2.  
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Gardner A.E.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP REVISIONS.  
 RA Durbin R.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: FAD (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; Z35602; CAA84671.2; --  
 CC WormPep; R13G10.2; CE35088.  
 DR InterPro; IPR002937; Amino\_oxidase.  
 DR Pfam; PF01593; Amino\_oxidase; 1.  
 KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.  
 FT NP\_BIND 311 366 FAD (ADP PART) (POTENTIAL).  
 FT SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;  
 SQ  
 Query Match 55.7%; Score 39; DB 1; Length 783;  
 Best Local Similarity 50.0%; Pred. No. 18;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CFQWARMNRKV 12  
 Db 540 CIDWGRDQRKV 551  
 RESULT 10  
 ID PAFA\_CHICK STANDARD; PRT; 422 AA.  
 AC Q90678;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)  
 DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated  
 DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine  
 DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).  
 GN PLA2G7.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W.; Eberhardt C.; Unger J.; Trong H.L.; Zimmerman G.A.;  
 RA McIntyre T.M.; Stafforini D.M.; Prescott S.M.; Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 RT phospholipase A2 with a catalytic triad.";  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-acetyl-1-alkyl-sn-glycero-3-phosphocholine +  
 CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: PLASMA.  
 CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
 CC  
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 CC  
 CC EMBL: U34278; AAC59717.1; --  
 CC InterPro: IPR000734; Lipase.  
 CC InterPro: IPR005065; PAF-AH\_P\_II.  
 CC InterPro: IPR000379; Serestrase\_site.  
 CC Pfam: PF03403; PAF-AH\_P\_II; 1.  
 CC PROSITE: PS00120; LIPASE\_SER; 1.  
 CC HydroLase; Lipid degradation; Glycoprotein; Signal.  
 CC  
 CC SIGNAL 1 21 BY SIMILARITY.  
 CC CHAIN 22 422 PLATELET-ACTIVATING FACTOR  
 CC  
 CC FT ACT SITE 266 266 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC FT ACT SITE 289 289 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC FT ACT SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC FT CARBOHYD 331 331 N-LINKED (GLCNAC.. ) (POTENTIAL).  
 CC  
 CC SQ SEQUENCE 422 AA; 47046 MW; 15A5C794376B9141 CRC64;  
 CC  
 CC Query Match 54.3%; Score 38; DB 1; Length 422;  
 CC Best Local Similarity 54.5%; Pred. No. 15;  
 CC Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 CC  
 CC QY 2 FQWARMNRKV 12  
 CC  
 CC DB 316 FQWARMNRKV 326  
 CC  
 CC  
 CC RESULT 11  
 CC SYH CHLTR  
 CC ID SYH CHLTR STANDARD; PRT; 428 AA.  
 CC AC O84547;  
 CC DT 30-MAY-2000 (Rel. 39, Created)  
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)  
 CC (HISRS).  
 CC OS HISS OR CT543.  
 CC OS Chlamydia trachomatis.  
 CC OS Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 CC NCBI\_TaxID=813;  
 CC  
 CC RN SEQUENCE FROM N.A.  
 CC RC STRAIN=D/WW-3/Cx;  
 CC RX MEDLINE=99000809; PubMed=9784136;  
 CC RA Stephens R.S., Kallman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
 CC Mitchell W.P., Olinger L., Tatusov R.I., Zhao Q., Koonin E.V.,  
 CC Davis R.W.;  
 CC RA "Genome sequence of an obligate intracellular pathogen of humans:  
 CC Chlamydia trachomatis.";  
 CC RL Science 282:754-759(1998).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +  
 CC dihydrophosphate + L-histidyl-tRNA(His).  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.  
 CC  
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CC EMBL: AE001325; AAC68145.1; --  
 CC HSP: G32422; IQ50.  
 CC InterPro: IPR002106; AACRNA\_ligaseII.  
 CC InterPro: IPR004154; HGTP\_anticonodon.  
 CC InterPro: IPR004516; HisS.  
 CC InterPro: IPR002314; tRNA-synt 2b.  
 CC Pfam: PF00587; tRNA-synt 2b; 1.  
 CC Pfam: PF03129; HGTP\_anticonodon; 1.  
 CC TIGRFAMs: TIGR00442; hisS; 1.  
 CC PROSITE: PS0862; AA\_tRNA\_LIGASE\_II; 1.  
 CC KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 CC Complete proteome.  
 CC SQ SEQUENCE 428 AA; 49189 MW; 9B9F59A096BD958 CRC64;  
 CC  
 CC Query Match 54.3%; Score 38; DB 1; Length 428;  
 CC Best Local Similarity 45.5%; Pred. No. 15;  
 CC Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 CC  
 CC QY 1 CFQWARMNRKV 11  
 CC  
 CC DB 348 CFSWANRLRL 358  
 CC  
 CC RESULT 12  
 CC T100\_HUMAN  
 CC ID T100\_HUMAN STANDARD; PRT; 989 AA.  
 CC AC O75448; Q14143;  
 CC DT 15-JUN-2002 (Rel. 41, Created)  
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Thyroid hormone receptor-associated protein complex 100 kDa component  
 CC (Trap100).  
 CC GN TRAP100 OR KIAA0130.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 CC  
 CC RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.  
 CC RP MEDLINE=98318590; PubMed=9653119;  
 CC RA Yuan C.-X., Ito M., Pondell J.D., Fu Z.-Y., Roeder R.G.;  
 CC RT "The TRAP220 component of a thyroid hormone receptor-associated  
 CC protein (TRAP) coactivator complex interacts directly with nuclear  
 CC receptors in a ligand-dependent fashion.";  
 CC RL Proc. Natl. Acad. Sci. U.S.A. 95:7939-7944(1998).  
 CC [2]  
 CC RN SEQUENCE FROM N.A.  
 CC RP TISSUE=Bone marrow;  
 CC RX MEDLINE=96127530; PubMed=8590280;  
 CC RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;  
 CC RT "Prediction of the coding sequences of unidentified human genes. IV.  
 CC The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by  
 CC analysis of cDNA clones from human cell line KG-1.";  
 CC RL DNA Res. 2:167-174(1995).  
 CC [3]  
 CC RN SEQUENCE FROM N.A.  
 CC RP TISSUE=Eye;  
 CC RA Strausberg R.;  
 CC RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC CC -!- FUNCTION: Plays a role in nuclear hormone receptor-mediated  
 CC transactivation.  
 CC CC -!- SUBUNIT: Does not directly bind nuclear hormone receptors.  
 CC CC Interacts and coprecipitates with Trap220.  
 CC CC -!- TISSUE SPECIFICITY: Ubiquitous. Abundant in skeletal  
 CC muscle, heart and placenta.  
 CC  
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CC EMBL; AF055995; AAC39855.1; -.
CC EMBL; D50920; BAA09479.1; -.
CC EMBL; BC011375; AAH11375.1; -.
CC MIM; 607000; -.
KW Transcription regulation; Zinc-finger; Repeat; ATP-binding.
FT DOMAIN 128 861 6 X REPEATS OF L-X-X-L-L.
FT REPEAT 128 132 1.
FT REPEAT 344 348 2.
FT REPEAT 448 452 3.
FT REPEAT 557 561 4.
FT REPEAT 788 792 5.
FT REPEAT 857 861 6.
FT ZN_FING 93 117 POTENTIAL.
FT NP_BIND 436 448 ATP (POTENTIAL).
FT CONFLICT 20 20 D -> Y (IN REF. 2).
FT CONFLICT 204 204 A -> T (IN REF. 2).
SQ SEQUENCE 989 AA; 110304 MW; CCEDE7D4E74DB90C CRC64;

Query Match 54.3%; Score 38; DB 1; Length 989;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWARMK 10
DB 21 YQWAINMK 29

RESULT 13
DYHB CHLRE STANDARD; PRT; 4568 AA.
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21gr;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes.";
RL J. Cell Sci. 107:635-644 (1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA). 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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DR EMBL; U02963; AAA19956.1; -.
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).

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FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 17e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMKVR 12
DB 1852 CFQWQSLRYIQ 1863

RESULT 14
Y708 METUA STANDARD; PRT; 172 AA.
AC Q58118;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0708.
GN MJ0708.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.B., Geoghegan N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: TO S.POMBE SPAC1F3.04C AND S.CEREVISIAE YOR006C.
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-----
DR EMBL; U67517; AAB98703.1; -.
DR TIGR; MJ0708; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 172 AA; 20025 MW; 01CF25475AD10B2A CRC64;

Query Match 52.9%; Score 37; DB 1; Length 172;
Best Local Similarity 54.5%; Pred. No. 8.9;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWARMKVR 11
DB 135 CFKWAFTFKV 145

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RESULT 15
PDOI_ECOLI
ID_PDOI_ECOLI STANDARD; PRT; 211 AA.
AC P32174;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Formate dehydrogenase, cytochrome b556(FDO) subunit (Formate
DE dehydrogenase-O gamma subunit) (FDO-Z gamma subunit) (Aerobic formate
DE dehydrogenase cytochrome b556 subunit).
GN FDOI OR B3892 OR Z5434 OR ECS4818.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93347969; PubMed=8346018;
RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes.";
RL Nucleic Acids Res. 21:3391-3398(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimailanta E.F., Potamocousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RN Nature 409:529-533(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [4]
RP CHARACTERIZATION.
RC STRAIN=K12.
RX MEDLINE=9609298; PubMed=8522521;
RA Abaibou H., Pommer J., Giordano G., Mandrand-Berthelot M.-A.;
RT "Expression and characterization of the Escherichia coli fdo locus
RT and a possible physiological role for aerobic formate
RT dehydrogenase.";
RL J. Bacteriol. 177:7141-7149(1995).
RN [5]
RP TOPOLOGY.
RX MEDLINE=99069338; PubMed=9852007;
RA Benoit S., Abaibou H., Mandrand-Berthelot M.-A.;
RT "Topological analysis of the aerobic membrane-bound formate
RT dehydrogenase of Escherichia coli.";
RL J. Bacteriol. 180:6625-6634(1998).
CC -1- FUNCTION: ALLOWS TO USE FORMATE AS MAJOR ELECTRON DONOR DURING
CC AEROBIC RESPIRATION. SUBUNIT GAMMA IS PROBABLY THE CYTOCHROME
CC B556(FDO) COMPONENT OF THE FORMATE DEHYDROGENASE.
CC -1- SUBUNIT: FORMATE DEHYDROGENASE IS A MEMBRANE-BOUND COMPLEX, FORMED
CC BY SUBUNITS ALPHA, BETA AND GAMMA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: STRONG, TO FDOI.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
CC EMBL; LI9201; AAB03025.1; -
CC EMBL; AB000464; AAD13454.1; -
CC EMBL; AF005620; AAG59085.1; -
CC EMBL; AP002567; BAB38241.1; -
CC FIR; S40836; S40836.
CC EcoGene; Ecol1856; fdoI.
KW Electron transport; Heme; Iron; Transmembrane; Complete proteome.
FT DOMAIN 1 17 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 18 32 PROBABLE.
FT DOMAIN 33 53 PERIPLASMIC (PROBABLE).
FT TRANSMEM 54 72 PROBABLE.
FT DOMAIN 73 112 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 113 130 PROBABLE.
FT DOMAIN 131 151 PERIPLASMIC (PROBABLE).
FT TRANSMEM 152 170 PROBABLE.
FT DOMAIN 171 211 CYTOPLASMIC (PROBABLE).
SQ SEQUENCE 211 AA; 24606 MW; 166ACSA661C738D5 CRC64;
Query Match 52.9%; Score 37; DB 1; Length 211;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 WARMNRKV 11
Db 88 WAKNIRKI 95
Search completed: February 21, 2003, 07:27:46
Job time : 6.6 secs
```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107B-72  
Perfect score: 70  
Sequence: 1 CFQWARMKRV 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPTEMBL 21.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	85.7	711	4 Q8TCD2	Q8tcd2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9ucys homo sapien
3	45	64.3	33	6 Q9TR80	Q9tr80 ovis aries
4	40	57.1	148	10 Q9XHP1	Q9xhp1 sesamum ind
5	40	57.1	273	2 O31090	O31090 rhizobium l
6	40	57.1	511	16 Q8Z462	Q8z462 salmonella
7	39	55.7	275	5 Q93780	Q93780 caenorhabdi
8	39	55.7	341	11 Q8R2A4	Q8r2a4 mus musculu
9	39	55.7	544	10 Q949E1	Q949e1 oryza sativ
10	39	55.7	866	10 Q9FHI9	Q9fhi9 arabidopsis
11	39	55.7	1213	3 Q59801	Q59801 schizosacch
12	38	54.3	108	9 Q8SC55	Q8sc55 stx2 conver
13	38	54.3	120	4 Q9BTB8	Q9btb8 homo sapien
14	38	54.3	415	5 Q9U4M9	Q9u4m9 leishmania
15	38	54.3	489	16 P96223	P96223 mycobacteri
16	38	54.3	501	3 Q9UUD0	Q9uud0 schizosacch

Q9n457 caenorhabdi  
Q8s487 zea mays (m  
Q99k74 mus musculu  
Q8nys homo sapien  
Q75448 homo sapien  
Q9lxn4 arabidopsis  
Q9v346 drosophila  
Q9y6v0 homo sapien  
Q8xgq3 arabidopsis  
Q8xgq3 salmoneilla  
Q8xm21 homo sapien  
Q8xs21 ralsconia s  
Q9qb73 yaba monkey  
Q81653 hemerocalli  
Q91mq5 lumpy skin  
Q9dhk5 yaba-like d  
Q9vil8 drosophila  
Q9sio0 arabidopsis  
Q9x330 drosophila  
Q9e6f6 lactobacill  
Q8rgt4 fusobacteri  
Q8rgt4 fusobacteri  
Q8151 caenorhabdi  
Q8tfz2 aspergillus  
Q37086 peach roset  
Q77855 human immun  
Q77856 human immun  
Q9xf45 oryza sativ  
Q9h3k8 homo sapien

## ALIGNMENTS

## RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.  
ID Q8TCD2  
AC Q8TCD2, 550 5 Q9N457  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (FE8-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC023347; AAH23347.1; -- 1B9CTEE097C45FAF CRC64;  
SQ SEQUENCE 711 AA; 78327 MW; 1B9CTEE097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;  
Best Local Similarity 90.9%; Pred. No. 0.0055;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWARMKRV 11  
Db 39 CFQWARMKRV 49

## RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.  
ID Q9UCY5  
AC Q9UCY5, 550 5 Q9N457  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE Lactoferrin homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96081613; PubMed=8551695;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSP; P02788; IBA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F4905EBDDDB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWNRNRKVR 12
DB 21 FQWNRNRKVR 31
||| |||||
||| |||||

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
ID Q9TR80;
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samou D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O77698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;
Best Local Similarity 54.5%; Pred. No. 0.15;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWNRNRKVR 11
DB 19 CYQWQKMRKL 29
||| : |||
||| : |||

RESULT 4
Q9XHP1 PRELIMINARY; PRT; 148 AA.
ID Q9XHP1;
AC Q9XHP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TAINAN 1;
RX MEDLINE=20074970; PubMed=10606554;
RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;

"molecular cloning of 11S globulin and 2S albumin, the two major seed
storage proteins in sesame.";
J. Agric. Food Chem. 47:4932-4938(1999).
EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR00617; Napin.
DR InterPro; IPR001768; Try/amyL inhbr.
DR Pfam; PF00234; tryp_alpha_aml; 1.
DR PRINTS; PR00496; NAFIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13B3DE CRC64;

Query Match 57.1%; Score 40; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 6.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWNRNRKVR 9
DB 54 CMQWNRNRKVR 62
||| |||||
||| |||||

RESULT 5
O31090 PRELIMINARY; PRT; 273 AA.
ID O31090;
AC O31090;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical 31.0 kDa protein.
OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VF39;
RA Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=VF39;
RX MEDLINE=99113394; PubMed=9914965;
RA Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
Ksenzenko V.N.;
RT Structural and functional organization of the exopolysaccharide
RT biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39.";
RL Mol. Biol. (Mosk) 32:797-804(1998).
DR EMBL; AF028810; AAB8891.1; -.
KW Hypothetical protein.
SQ SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;

Query Match 57.1%; Score 40; DB 2; Length 273;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWNRNRKVR 12
DB 245 RWLRNRKVR 254
||| |||||
||| |||||

RESULT 6
Q8Z462 PRELIMINARY; PRT; 511 AA.
ID Q8Z462;
AC Q8Z462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein STY3070.
GN STY3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;

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RN SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churche C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RW EMBL; AL627276; CAD06049.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match 57.1%; Score 40; DB 16; Length 511;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWARMKVR 12
||| |||
Db 350 CFQWDMKAKVR 361

RESULT 7
Q93780 PRELIMINARY; PRT; 275 AA.
AC Q93780;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F53H4.4 protein.
GN F53H4.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z81089; CAB03137.1; --
SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 55.7%; Score 39; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FQWARMKVR 12
||| |||
Db 262 FQWKSMKTR 272

RESULT 8
Q8R2A4 PRELIMINARY; PRT; 341 AA.
AC Q8R2A4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vomeronasal receptor VIRE6.
GN VIRE6.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129X1/SVJ;
RX MEDLINE=21676859; PubMed=11802169;
RT Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;
RT "Multiple new and isolated families within the mouse superfamily of
RT V1r vomeronasal receptors."
RT Nat. Neurosci. 5:134-140(2002).
RL EMBL; AY065506; AAL47911.1; --
KW Receptor.
SQ SEQUENCE 341 AA; 39632 MW; B3D8259F7AD11130 CRC64;

Query Match 55.7%; Score 39; DB 11; Length 341;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWARMNR 9
||| |||
Db 331 CFTWTRNIK 339

RESULT 9
Q949E1 PRELIMINARY; PRT; 544 AA.
AC Q949E1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Lipase-like protein.
GN W485ERIPDM.
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21329048; PubMed=11435398;
RA Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,
RA Duesterhoeft A., Stiekema W., Entian K.D., Terry N., Lemcke K.,
RA Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,
RA Bevan M., Bancroft I.;
RT "Conservation of microstructure between a sequenced region of the
RT genome of rice and multiple segments of the genome of Arabidopsis
RT thaliana."
RL Genome Res. 11:1167-1174(2001).
DR EMBL; AJ307652; CAC39051.1; --
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR002921; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF01764; Lipase_3; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN 1.
SQ SEQUENCE 544 AA; 58895 MW; CF42105BFEC29A5B CRC64;

Query Match 55.7%; Score 39; DB 10; Length 544;
Best Local Similarity 55.8%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWARMNR 9
||| |||
Db 290 CLEWAENLR 298

RESULT 10
Q9FHI9 PRELIMINARY; PRT; 866 AA.
AC Q9FHI9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

```

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Genomic DNA, chromosome 5, pl clone:MPC19.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eumids 11; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=99397451; PubMed=10470850;  
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,  
 RA Miyajima N., Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.  
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen  
 RT pl and TAC clones."  
 RL DNA Res. 6:183-195(1999).  
 DR EMBL: AB018113; EMB0175.1; -;  
 SQ SEQUENCE 866 AA; 100187 MW; 164FAB9B4976D27D CRC64;

Query Match 55.7%; Score 39; DB 10; Length 866;  
 Best Local Similarity 50.0%; Pred. No. 70;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWARMKVR 12  
 |||  
 Db 389 CFNWLKFKLR 400

RESULT 11  
 O59801 PRELIMINARY; PRT; 1213 AA.  
 ID C59801  
 AC C59801  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Putative DEAD/DEAH box helicase.  
 GN SPC550.03C.  
 OS Schizosaccharomyces pombe (Pission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL023592; CAA19107.1; -;  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR Pfam: PF00270; DEAD; 1.  
 DR Pfam: PF00271; Helicase\_C; 1.  
 DR SMART: SM00487; DEXDC; 1.  
 DR SMART: SM00490; HELIC; 1.  
 KW ATP-binding; Helicase.  
 SQ SEQUENCE 1213 AA; 138027 MW; 2F9B2ABF8068A37 CRC64;

Query Match 55.7%; Score 39; DB 3; Length 1213;  
 Best Local Similarity 62.5%; Pred. No. 18+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWARMKVR 8  
 |||  
 Db 1141 CYEWARGM 1148

RESULT 12  
 Q8SC55 PRELIMINARY; PRT; 108 AA.  
 ID Q8SC55  
 AC Q8SC55  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 12.3 kDa protein.  
 OS Stx2 converting bacteriophage I.  
 OC Viruses.  
 OX NCBI\_TaxID=180816;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=STX2 PHAGE-I;  
 RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,  
 RA Yanasaki S., Takeda Y.;  
 RT "Genomic sequence of Shiga toxin 2-converting phage isolated from  
 RT Escherichia coli O157:H7 Okayama strain and comparison with other  
 RT Shiga toxin 2-converting phages."  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP004402; BAB87947.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 108 AA; 12279 MW; 2FF2E76690C78BA7 CRC64;

Query Match 54.3%; Score 38; DB 9; Length 108;  
 Best Local Similarity 60.0%; Pred. No. 12;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWARMKVR 10  
 |||  
 Db 31 CFQWISDNK 40

RESULT 13  
 Q9BTB8 PRELIMINARY; PRT; 120 AA.  
 ID Q9BTB8  
 AC Q9BTB8  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Similar to laminin, alpha 4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PANCREAS;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC004241; AAH04241.1; -;  
 SQ SEQUENCE 120 AA; 12818 MW; 6ABF63CBA663BF3F CRC64;

Query Match 54.3%; Score 38; DB 4; Length 120;  
 Best Local Similarity 60.0%; Pred. No. 13;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CFQWARMKVR 11  
 |||  
 Db 104 FTWARSVKL 113

RESULT 14  
 Q9U4M9 PRELIMINARY; PRT; 415 AA.  
 ID Q9U4M9  
 AC Q9U4M9  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE 7138-2.  
 GN 7138-2.  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIEDLIN;  
 RA Ravel C., Dubessay P., Blaineau C., Lignon M.-F., Bastien P.,  
 RA Dedet J.-P., Pages M.;



Job time : 21.8 secs

RT "Leishmania major chromosome 5 complete sequence."  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF163772; AAP14642.1; -  
DR InterPro; IPR003409; MORN.  
DR Pfam; PF02493; MORN; 4.  
SQ SEQUENCE 415 AA; 46701 MW; 3E3AD710BF23691E CRC64;

Query Match 54.3%; Score 38; DB 5; Length 415;  
Best Local Similarity 66.7%; Pred. No. 49;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWARMNR 9  
| : | | | |  
Db 272 CGEWFRRNR 280

## RESULT 15

P96223 PRELIMINARY; PRT; 489 AA.  
AC P96223;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 55.3 kDa protein (Monooxygenase, flavin-binding family).  
DE RV3854C OR MTCY01A6.14 OR MT3969.  
GN Mycobacterium tuberculosis.  
OS Bacteria; Firmicutes; Actinobacteriia; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
CX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."  
RL Nature 393:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 1551 / OSHKOSH;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Emdolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;  
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z83864; CAB06212.1; -  
DR EMBL; AE007188; AAK48336.1; -  
DR TIGR; MT3969; -  
DR TubercuList; RV3854c; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 489 AA; 55326 MW; 844611B7E831180D CRC64;

Query Match 54.3%; Score 38; DB 16; Length 489;  
Best Local Similarity 54.5%; Pred. No. 59;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWARMNRKV 11  
| : | | | |  
Db 253 CQKWFRRMRKM 263

Search completed: February 21, 2003, 07:44:24

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107b-73

Perfect score: 70

Sequence: 1 CFQWQANRKR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78073 Human lactoferrin
2	65	92.9	12	21	AAV78038 Human lactoferrin
3	65	92.9	12	21	AAV78046 Human lactoferrin
4	65	92.9	12	21	AAV78047 Human lactoferrin
5	65	92.9	12	21	AAV78081 Human lactoferrin
6	65	92.9	12	21	AAV78085 Human lactoferrin
7	65	92.9	13	21	AAV78037 Human lactoferrin
8	65	92.9	13	21	AAV78048 Human lactoferrin
9	65	92.9	13	21	AAV78049 Human lactoferrin
10	65	92.9	14	21	AAV78036 Human lactoferrin

11	65	92.9	14	21	AAV78050 Human lactoferrin
12	65	92.9	14	21	AAV78051 Human lactoferrin
13	65	92.9	15	17	AAV78054 Peptide for anti-u
14	65	92.9	15	21	AAV78035 Human lactoferrin
15	65	92.9	15	21	AAV78062 Human lactoferrin
16	65	92.9	15	21	AAV78063 Human lactoferrin
17	65	92.9	16	21	AAV78031 Human lactoferrin
18	65	92.9	16	21	AAV78064 Human lactoferrin
19	65	92.9	16	21	AAV78065 Human lactoferrin
20	65	92.9	17	21	AAV78034 Human lactoferrin
21	65	92.9	17	21	AAV78066 Human lactoferrin
22	65	92.9	17	21	AAV78067 Human lactoferrin
23	65	92.9	18	15	AAV78032 Human lactoferrin
24	65	92.9	18	17	AAV78033 Advanced glycosyla
25	65	92.9	18	21	AAV78037 Amino acid sequenc
26	65	92.9	19	21	AAV78067 Human lactoferrin
27	65	92.9	19	21	AAV78032 Anti microbial pep
28	65	92.9	20	13	AAV78032 Lactoferrin-relate
29	65	92.9	20	14	AAV78032 Lactoferrin-derive
30	65	92.9	20	15	AAV78032 Lactoferrin-derive
31	65	92.9	20	15	AAV78032 Lactoferrin-derive
32	65	92.9	20	15	AAV78032 Lactoferrin-derive
33	65	92.9	20	15	AAV78032 Lactoferrin-derive
34	65	92.9	20	16	AAV78032 Bovine lactoferrin
35	65	92.9	20	16	AAV78032 Bovine lactoferrin
36	65	92.9	20	16	AAV78032 Anti-parasitic lac
37	65	92.9	20	16	AAV78032 Anti-parasitic lac
38	65	92.9	20	17	AAV78032 Peptide for anti-u
39	65	92.9	20	17	AAV78032 Lactoferrin-derive
40	65	92.9	20	17	AAV78032 Lactoferrin-derive
41	65	92.9	20	17	AAV78032 Lactoferrin-derive
42	65	92.9	20	17	AAV78032 Lactoferrin-derive
43	65	92.9	20	17	AAV78032 Lactoferrin-derive
44	65	92.9	20	18	AAV78032 Lactoferrin-derive
45	65	92.9	20	18	AAV78032 Anti-parasitic pep

#### ALIGNMENTS

RESULT 1  
AAV78073  
ID AAV78073 standard; Peptide; 12 AA.  
XX AAV78073;  
AC AAV78073;  
XX 25-APR-2000 (first entry)  
DT Human lactoferrin derived peptide SEQ ID NO:73.  
DE Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX 06-JUL-1999; 99WO-SE01230.  
XX 06-JUL-1998; 98SE-0002441.  
XX 17-JUL-1998; 98SE-0002562.  
XX 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
XX Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
PS Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 70; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQANMKVR 12  
| | | | | | | | | | | |  
DB 1 CFQWQANMKVR 12  
| | | | | | | | | | | |

RESULT 2  
AAY78038  
ID AAY78038 standard; Peptide; 12 AA.  
XX  
AC AAY78038;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:38.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
DR WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 12; Page 70; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX  
SQ Sequence 12 AA;  
Query Match 92.9%; Score 65; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 7.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQANMKVR 12  
| | | | | | | | | | | |  
DB 1 CFQWQANMKVR 12  
| | | | | | | | | | | |

RESULT 3  
AAY78046  
ID AAY78046 standard; Peptide; 12 AA.  
XX  
AC AAY78046;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:46.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
DR WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 15; Page 35; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7.6e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQANMKVR 12  
 |||||  
 DB 1 CFQWQANMKVR 12

RESULT 4

AAAY78047  
 ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:47.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 73; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane, inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7.6e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQANMKVR 12  
 |||||  
 DB 1 CFQWQANMKVR 12

RESULT 5

AAAY78081  
 ID AAY78081 standard; Peptide; 12 AA.

XX AC AAY78081;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:81.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 22; Page 36; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane, inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 7.6e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12  
 |||||  
 Db 1 CFQWQANMKVR 12

## RESULT 6

AAV78085  
 ID AAY78085 standard; Peptide; 12 AA.

XX AAY78085;  
 AC  
 DT 25-APR-2000 (first entry)  
 XX Human lactoferrin derived peptide SEQ ID NO:85.  
 DE  
 XX Human, lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 FN  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SF01230.  
 PF  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.2%; Pred. NO. 7.6e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12  
 |||||  
 Db 1 CFQWQANMKVR 12

## RESULT 7

AAV78037

AAV78037 standard; Peptide; 13 AA.

AAV78037;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:37.

Human, lactoferrin; modification; infection; inflammation; tumour;  
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 urinary tract infection; colitis; Candida infection; fungicidal;  
 bactericidal; preservative.

Homo sapiens.

Synthetic.

WO200001730-A1.

13-JAN-2000.

06-JUL-1999; 99WO-SF01230.

06-JUL-1998; 98SE-0002441.

17-JUL-1998; 98SE-0002562.

29-DEC-1998; 98SE-0004614.

(ASCI-) A+ SCI INVEST AB.

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections,  
 inflammations and tumors and for use in infant formula food -

Claim 12; Page 70; 102pp; English.

AAV78001 to AAY78100 represent peptides having sequences based on human  
 lactoferrin. The peptides are taken up in the intestine through  
 binding to specific lactoferrin receptors and are then transported  
 through the circulation. A medicinal product of the peptide or fragment  
 can be used for treating and/or prevention of infections (such as  
 urinary tract infections, colitis, and Candida infection on a mucosal  
 membrane), inflammations and/or tumors. The peptides can also be used  
 in food stuffs such as infant formula food. The peptides are also  
 fungicidal and bactericidal and may also be used as preservatives.  
 Even though native human lactoferrin have been shown to have desired  
 anti-inflammatory anti-infectious and anti-tumoural properties they  
 cannot be used clinically on a broad basis because of high production  
 costs. Therefore, provision of peptides based on lactoferrin would  
 enable them to be used for the same purposes as lactoferrin at lower  
 cost.

Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. NO. 8.2e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12

|||||

Db 2 CFQWQANMKVR 13

## RESULT 8

AAV78048

ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

DT 25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 74; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 13 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 8-2e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNNRKVR 12  
 DB 2 CFQWQNNRKVR 13  
 RESULT 9  
 AAY78049  
 ID AAY78049 standard; Peptide; 13 AA.  
 AC AAY78049;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:49.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS

OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 74; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 13 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 8-2e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNNRKVR 12  
 DB 2 CFQWQNNRKVR 13  
 RESULT 10  
 AAY78036  
 ID AAY78036 standard; Peptide; 14 AA.  
 AC AAY78036;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:36.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 PF

XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 69; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX SQ Sequence 14 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CFQWQANMKVR 12  
 DB ||||| |||||  
 3 CFQWQANMKVR 14  
 RESULT 11  
 AAY78050  
 ID AAY78050 standard; Peptide; 14 AA.  
 AC AAY78050;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:50.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 PD 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX SQ Sequence 14 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 8.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CFQWQANMKVR 12  
 DB ||||| |||||  
 3 CFQWQANMKVR 14  
 RESULT 12  
 AAY78051  
 ID AAY78051 standard; Peptide; 14 AA.  
 AC AAY78051;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:51.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 PD 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

PS Claim 18; Page 75; 102pp; English.

CC AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX

SQ Sequence 14 AA;

Query Match 92.9%; Score 65; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 8.9e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12

Db ||||| |||||

3 CFQWQANMKVR 14

RESULT 13

AAR98554

ID AAR98554 standard; Peptide; 15 AA.

AC AAR98554;

XX

XX 12-NOV-1996 (first entry)

DT Peptide for anti-ulcer agent.

DE anti-ulcer agent; low toxicity; stable; heat-resistant.

XX

XX Synthetic.

XX

XX JP08143468-A.

PN

XX 04-JUN-1996.

PD

XX 17-NOV-1994; 94JP-0283869.

PF

XX 17-NOV-1994; 94JP-0283869.

PR

XX (MORG ) MORINAGA MILK IND CO LTD.

PA

XX WPI; 1996-318857/32.

DR

XX Anti-ulcer agent contg. peptide - has low toxicity, is

PT heat-resistant and water-soluble

PT

XX Claim 1; Page 11; 11pp; Japanese.

PS

XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low

CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be

CC administered orally and be produced in large amounts.

XX

SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 17; Length 15;

Best Local Similarity 91.7%; Pred. No. 9.5e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12

Db ||||| |||||

2 CFQWQANMKVR 13

RESULT 14

AAY78035

ID AAY78035 standard; Peptide; 15 AA.

XX

AC AAY78035;

XX

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:35.

XX

XX Human; lactoferrin; modification; infection; inflammation; tumour;

XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX urinary tract infection; colitis; Candida infection; fungicidal;

XX bactericidal; preservative.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX WO200001730-A1.

PN

XX 13-JAN-2000.

PD

XX 06-JUL-1999; 99WO-SE01230.

PF

XX 06-JUL-1998; 98SE-0002441.

PR

XX 17-JUL-1998; 98SE-0002562.

PR

XX 29-DEC-1998; 98SE-0004614.

XX

XX (ASCI-) A+ SCI INVEST AB.

PA

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

FI

XX WPI; 2000-147388/13.

DR

XX New peptides used for treatment and prevention of infections,

PT inflammation and tumors and for use in infant formula food -

PT

XX Claim 12; Page 69; 102pp; English.

PS

XX

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX

SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;

Best Local Similarity 91.7%; Pred. No. 9.5e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12

Db ||||| |||||

4 CFQWQANMKVR 15

RESULT 15

AAY78062

ID AAY78062 standard; Peptide; 15 AA.

XX

AC AAY78062;



```

XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:62.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food -
XX
XX Claim 15; Page 81; 102pp; English.
XX
XX AA78001 to AA78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
XX through the circulation. A medicinal product of the peptide or fragment
XX can be used for treating and/or prevention of infections (such as
XX urinary tract infections, colitis, and Candida infection on a mucosal
XX membrane), inflammations and/or tumors. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also
XX fungicidal and bactericidal and may also be used as preservatives.
XX Even though native human lactoferrin have been shown to have desired
XX anti-inflammatory anti-infectious and anti-tumoural properties they
XX cannot be used clinically on a broad basis because of high production
XX costs. Therefore, provision of peptides based on lactoferrin would
XX enable them to be used for the same purposes as lactoferrin at lower
XX cost.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 92.9%; Score 65; DB 21; Length 15;
XX Best Local Similarity 91.7%; Pred. NO. 9.5e-05;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CFQWQNNMKVR 12
XX |||||
XX 4 CFQWQNNMKVR 15
XX
XX Search completed: February 21, 2003, 07:37:12
XX Job time : 29.35 secs

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OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 3.5e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANMRKVR 12  
||| |||||  
Db 1 CFQWQANMRKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,948  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 3.5e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANMRKVR 12  
||| |||||  
Db 1 CFQWQANMRKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI, YONG MING  
; APPLICANT: VLASSARA, HELEN  
; APPLICANT: CERAMI, ANTHONY  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 3.5e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANMRKVR 12  
||| |||||  
Db 1 CFQWQANMRKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE  
; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Klauber & Jackson  
;; STREET: 411 Hackensack Avenue  
;; CITY: Hackensack  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07601  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: PC-DOS/MS-DOS  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/475,055  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/485,948  
;; FILING DATE:  
;; APPLICATION NUMBER: 08/488,217  
;; FILING DATE: JUNE 7, 1995  
;; APPLICATION NUMBER: 08/418,642  
;; FILING DATE: APRIL 7, 1995  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 947-1-008A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201 487-5800  
;; TELEFAX: 201 343-1684  
;; TELEX: 133521  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; DESCRIPTION: LF-CI, 8-25  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;; US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 3.5e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMKVR 12  
Db 1 CFQWQANMKVR 12

RESULT 5  
US-07-755-161A-3  
; Sequence 3, Application US/07755161A  
; Patent No. 5304633  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: DisplayWrite  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/755.161A  
;; FILING DATE: 19910905  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX: 202-371-8856  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE:  
;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:  
;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE:  
;; CELL LINE:  
;; ORGANELLE:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:  
;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURE:  
;; NAME/KEY: modified site  
;; LOCATION: 2  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION: /note= "thiol group of  
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
;; OTHER INFORMATION: thiol group of Cys residue at location 19"  
;; FEATURE:  
;; NAME/KEY: modified site  
;; LOCATION: 19  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION: /note= "thiol group of  
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
;; OTHER INFORMATION: thiol group of Cys residue at location 2"  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO:  
;; US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 3.8e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12  
| | | | | | | | | |  
Db 2 CFQWQNNRKR 13

RESULT 6  
US-07-891-174-3  
; Sequence 3, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 08-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Creek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site

LOCATION: 2  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 19"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 19  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 2"  
PUBLICATION INFORMATION:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 3.8e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKR 12  
| | | | | | | | | |  
Db 2 CFQWQNNRKR 13

RESULT 7  
US-08-204-487-1  
; Sequence 1, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGERAKI  
; APPLICANT: DOSAKO, SHUN-ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIAKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: RUN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE  
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"  
US-08-204-487-1

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 3.8e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12  
Db 2 CFQWQNNRKVR 13

RESULT 8  
US-08-256-771-24  
Sequence 24, Application US/08256771  
Patent No. 5656591  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
TITLE OF INVENTION: PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are linked by  
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 3.8e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12  
Db 2 CFQWQNNRKVR 13

RESULT 9  
US-08-256-771-25  
Sequence 25, Application US/08256771  
Patent No. 5656591  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
TITLE OF INVENTION: PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are protected to  
OTHER INFORMATION: prevent disulfide bond"  
US-08-256-771-25

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 3.8e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNNRKVR 12  
Db 2 CFQWQNNRKVR 13

RESULT 10  
US-08-381-984-24

```

; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
; US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
DB 2 CFQWQANMRKVR 13

RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

```

```

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
; US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12
DB 2 CFQWQANMRKVR 13

RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-299351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4

```

; LENGTH: 22

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;  
Best Local Similarity 91.7%; Pred. No. 4.2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12

Db 2 CFQWQNNRKVR 13

RESULT 13

US-09-508-734-6

; Sequence 6, Application US/09508734

; Patent No. 6423509

; GENERAL INFORMATION:

; APPLICANT: Samyang Genex Corporation

; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and

; FILE REFERENCE: PA/SYG/00139

; CURRENT APPLICATION NUMBER: US/09/508,734

; PRIOR FILING DATE: 2000-06-01

; PRIOR FILING DATE: 1999-07-14

; PRIOR FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: KopatentIn 1.71

; SEQ ID NO 6

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-508-734-6

Query Match 92.9%; Score 65; DB 4; Length 24;  
Best Local Similarity 91.7%; Pred. No. 4.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12

Db 3 CFQWQNNRKVR 14

RESULT 14

US-07-755-161A-10

; Sequence 10, Application US/07755161A

; Patent No. 5304633

; GENERAL INFORMATION:

; APPLICANT: Mamoru TOMITA et al.

; TITLE OF INVENTION: Antimicrobial Peptides and an

; FILE REFERENCE: Antimicrobial Agent

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind &amp; Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500KB

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: DisplayWrite

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/755,161A

; FILING DATE: 19910905

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX: 202-371-8856

; TELEX:

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE:

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE:

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT:

; MAP POSITION:

; UNITS:

; FEATURE:

; NAME/KEY: modified site

; LOCATION: 4

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of

; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with

; OTHER INFORMATION: thiol group of Cys residue at location 21"

; FEATURE:

; NAME/KEY: modified site

; LOCATION: 21

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of

; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with

; OTHER INFORMATION: thiol group of Cys residue at location 4"

; PUBLICATION INFORMATION:

; AUTHORS:

; TITLE:

; JOURNAL:

; VOLUME:

; ISSUE:

; PAGES:

; DATE:

; DOCUMENT NUMBER:

; FILING DATE:

; PUBLICATION DATE:

; RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 92.9%; Score 65; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 4.8e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12

Db 4 CFQWQNNRKVR 15



## RESULT 15

US-07-891-174-10  
; Sequence 10, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891.174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 4  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 21"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 21

; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 4"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
; US-07-891-174-10  
; Query Match 92.9%; Score 65; DB 1; Length 25;  
; Best Local Similarity 91.7%; Pred. No. 4.8e-05;  
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
; QY 1 CFWQANMKVR 12  
; Db 4 CFWQANMKVR 15  
; Search completed: February 21, 2003, 07:50:33  
; Job time : 8.7 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107B-73  
Perfect score: 70 CFQWQANMKVR 12  
Sequence: 1 CFQWQANMKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31059816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

Published Applications AA.\*  
1: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/prodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	63	90.0	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	46	65.7	15	9	US-09-798-869-7
8	43	61.4	15	9	US-09-798-869-4
9	43	61.4	25	9	US-09-798-869-22
10	42	60.0	15	9	US-09-798-869-8
11	42	60.0	15	9	US-09-798-869-29
12	42	60.0	15	9	US-09-798-869-30
13	38	55.7	62	10	US-09-815-242-12129
14	39	55.7	62	10	US-09-815-242-13026
15	39	55.7	747	9	US-10-066-500-58
16	39	55.7	747	9	US-10-002-796-58
17	39	55.7	747	9	US-10-066-273-58
18	39	55.7	747	9	US-10-066-494-58
19	36	51.4	15	9	US-09-798-869-5

20	35	50.0	235	9	US-09-764-868-762	Sequence 762, App
21	34	48.6	49	10	US-09-864-761-47074	Sequence 47074, A
22	34	48.6	239	10	US-09-864-761-37353	Sequence 37353, A
23	34	48.6	484	9	US-10-032-063-27	Sequence 27, Appl
24	34	48.6	1128	10	US-09-888-615-97	Sequence 37, Appl
25	33	47.1	13	9	US-09-798-869-26	Sequence 26, Appl
26	33	47.1	14	9	US-09-798-869-25	Sequence 25, Appl
27	33	47.1	15	9	US-09-798-869-1	Sequence 1, Appl
28	33	47.1	15	9	US-09-798-869-10	Sequence 10, Appl
29	33	47.1	15	9	US-09-798-869-28	Sequence 28, Appl
30	33	47.1	18	9	US-09-798-869-24	Sequence 24, Appl
31	33	47.1	25	9	US-09-798-869-21	Sequence 21, Appl
32	33	47.1	25	10	US-09-909-652-4	Sequence 4, Appl
33	33	47.1	25	10	US-09-030-619-205	Sequence 205, App
34	33	47.1	25	10	US-09-917-340-16	Sequence 16, Appl
35	33	47.1	81	10	US-09-864-761-41887	Sequence 41887, A
36	33	47.1	190	10	US-09-815-242-10092	Sequence 10092, A
37	33	47.1	257	10	US-09-860-232A-19	Sequence 19, Appl
38	33	47.1	579	10	US-09-824-588-2	Sequence 2, Appl
39	33	47.1	1258	10	US-09-867-852-107	Sequence 107, App
40	33	47.1	2273	10	US-09-995-542-12	Sequence 12, Appl
41	33	47.1	2310	10	US-09-995-542-10	Sequence 10, Appl
42	32	45.7	21	10	US-09-864-761-47985	Sequence 47985, A
43	32	45.7	63	9	US-09-984-245-320	Sequence 320, App
44	32	45.7	103	10	US-09-867-550-2054	Sequence 2054, Ap
45	32	45.7	178	9	US-09-738-626-5420	Sequence 5420, Ap

#### ALIGNMENTS

RESULT 1  
US-09-798-869-2  
; Sequence 2, Application US/09798869  
; Publication No. US2003002821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVEINSEN  
; APPLICANT: (VSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 92.9% Score 65; DB 9; Length 15;  
Best Local Similarity 91.7%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CFQWQANMKVR 12  
Db 3 CFQWQANMKVR 14

RESULT 2  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US2003002821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVEINSEN  
; APPLICANT: (VSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON

; APPLICANT: LARS VORLAND  
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
 ; FILE REFERENCE: A34049-PCT-USA-A  
 ; CURRENT APPLICATION NUMBER: US/09/798,869  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: GB9818938.4  
 ; PRIOR FILING DATE: 1998-08-28  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 20  
 ; LENGTH: 25  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-09-798-869-20

Query Match 92.9%; Score 65; DB 9; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 3.7e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANMKVR 12  
 |||||  
 Db 3 CFQWQANMKVR 14

RESULT 3  
 US-10-023-096-2  
 ; Sequence 2, Application US/10023096  
 ; Patent No. US20020160941A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kruzel, Marian L.  
 ; APPLICANT: Kurecki, Tomasz  
 ; APPLICANT: Gollnick, Paul D.  
 ; APPLICANT: Doyle, Darrell J.  
 ; TITLE OF INVENTION: Cloning, Expression, and Uses of Human  
 ; TITLE OF INVENTION: Lactoferrin  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern  
 ; STREET: 400 Seventh St. N.W.  
 ; CITY: Washington D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/023,096  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/724,586  
 ; FILING DATE: 30-SEPT-1996  
 ; APPLICATION NUMBER: US 08/238,445  
 ; FILING DATE: 05-MAY-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Player, William E.  
 ; REGISTRATION NUMBER: 31,409  
 ; REFERENCE/DOCKET NUMBER: 10505/P58185C  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 638-8666  
 ; TELEFAX: (202) 393-5350  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 694 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-10-023-096-2

Query Match 92.9%; Score 65; DB 9; Length 694;  
 Best Local Similarity 91.7%; Pred. No. 0.00093;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANMKVR 12  
 |||||  
 Db 22 CFQWQANMKVR 33

RESULT 4  
 US-09-798-869-6  
 ; Sequence 6, Application US/09798869  
 ; Publication No. US20030022821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN SIGURD SVENDSEN  
 ; APPLICANT: (YSTEIN REKDAL  
 ; APPLICANT: BALDUR SVEINBJ RNSON  
 ; APPLICANT: LARS VORLAND  
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
 ; FILE REFERENCE: A34049-PCT-USA-A  
 ; CURRENT APPLICATION NUMBER: US/09/798,869  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: GB9818938.4  
 ; PRIOR FILING DATE: 1998-08-28  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens  
 ; OTHER INFORMATION: sequence)  
 US-09-798-869-6

Query Match 90.0%; Score 63; DB 9; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 5.1e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQANMKVR 12  
 |||||  
 Db 3 CFQWQANMKVR 14

RESULT 5  
 US-09-798-869-3  
 ; Sequence 3, Application US/09798869  
 ; Publication No. US20030022821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN SIGURD SVENDSEN  
 ; APPLICANT: (YSTEIN REKDAL  
 ; APPLICANT: BALDUR SVEINBJ RNSON  
 ; APPLICANT: LARS VORLAND  
 ; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
 ; FILE REFERENCE: A34049-PCT-USA-A  
 ; CURRENT APPLICATION NUMBER: US/09/798,869  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: GB9818938.4  
 ; PRIOR FILING DATE: 1998-08-28  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: CAPRINE  
 US-09-798-869-3

Query Match 68.6%; Score 48; DB 9; Length 15;  
 Best Local Similarity 63.6%; Pred. No. 0.02;

	Matches	7: Conservative	2: Mismatches	2: Indels	0: Gaps	0:
QY	1	CFQWQANMRKV	11			
		: : : : :				
Db	3	CYQWQRRMRKL	13			

```

RESULT 6
US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINEJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT

RESULT 8
US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINEJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

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Query Match 61.4%; Score 43; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred.No. 0.15;  
Matches 7; Conservative 1; Mismatches 3; Indels

[illegible]

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RESULT 9
US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US2003002821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTRIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/SB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: G989818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
; US-09-798-869-22

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Query Match 61.4%; Score 43; DB 9; Length 25;  
 Best Local Similarity 63.6%; Pred. No. 0.24;  
 Matches 7; Conservative 1; Mismatches 3; Indels

RESULT 10  
US-09-798-869-8  
; Sequence 8, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine  
; OTHER INFORMATION: sequence)  
US-09-798-869-8

Query Match 60.0%; Score 42; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.22;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANRKY 11  
| : || |||  
Db 3 CLRQWEMKYL 13

RESULT 11  
US-09-798-869-29  
; Sequence 29, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-29

Query Match 60.0%; Score 42; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.22;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANRKY 11  
| : || |||  
Db 3 CFRQWEMKYL 13

RESULT 12  
US-09-798-869-30

; Sequence 30, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-30

Query Match 60.0%; Score 42; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.22;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANRKY 11  
| : || |||  
Db 3 CFRQWEMKYL 13

RESULT 13  
US-09-815-242-12129  
; Sequence 12129, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12129  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-12129

Query Match 55.7%; Score 39; DB 10; Length 62;

Best Local Similarity 60.0%; Pred. No. 2.8;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQANNEKVR 12  
Db 28 RWNANLQKVR 37

## RESULT 14

US-09-815-242-13026  
; Sequence 13026 Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA 011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 1410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13026  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-13026

Query Match 55.7%; Score 39; DB 10; Length 62;  
Best Local Similarity 60.0%; Pred. No. 2.8;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQANNEKVR 12  
Db 28 RWNANLQKVR 37

## RESULT 15

US-10-066-500-58  
; Sequence 58 Application US/10066500  
; Patent No. US20020177165A1  
; GENERAL INFORMATION:  
; APPLICANT: Avi J. Ashkenazi  
; APPLICANT: Kevin P. Baker  
; APPLICANT: David A. Botstein  
; APPLICANT: Luc Desnoyers  
; APPLICANT: Dan L. Eaton  
; APPLICANT: Napoleone Ferrara  
; APPLICANT: Sherman Fong  
; APPLICANT: Wei-Oiang Gao  
; APPLICANT: Hanspeter Gerber  
; APPLICANT: Mary E. Gerritsen  
; APPLICANT: Audrey Goddard

; APPLICANT: Paul J. Godowski  
; APPLICANT: Austin L. Gurney  
; APPLICANT: Ivar J. Kljavin  
; APPLICANT: Jennie P. Macher  
; APPLICANT: Mary A. Napier  
; APPLICANT: James Pan  
; APPLICANT: Nicholas P. Paoni  
; APPLICANT: Margaret Ann Roy  
; APPLICANT: Timothy A. Stewart  
; APPLICANT: Daniel Tumas  
; APPLICANT: Colin K. Watanabe  
; APPLICANT: P. Mickey Williams  
; APPLICANT: William I. Wood  
; APPLICANT: Zemin Zang  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3130R1C7  
; CURRENT APPLICATION NUMBER: US/10/066,500  
; CURRENT FILING DATE: 2002-02-01  
; PRIOR APPLICATION NUMBER: 10/002,796  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062285  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062816  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063082  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/063329  
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; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
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; PRIOR FILING DATE: 1997-11-25  
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; PRIOR FILING DATE: 1997-12-16  
; PRIOR APPLICATION NUMBER: 60/074086  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/074092  
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; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/095998  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/097000  
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; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
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; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101922  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/106032  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: 60/109304  
; PRIOR FILING DATE: 1998-11-20

;; PRIOR APPLICATION NUMBER: 60/125778  
;; PRIOR FILING DATE: 1999-03-23  
;; PRIOR APPLICATION NUMBER: 60/139595  
;; PRIOR FILING DATE: 1999-08-15  
;; PRIOR APPLICATION NUMBER: 60/145070  
;; PRIOR FILING DATE: 1999-07-20  
;; PRIOR APPLICATION NUMBER: 60/145698  
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;; PRIOR APPLICATION NUMBER: 60/149396  
;; PRIOR FILING DATE: 1999-08-17  
;; PRIOR APPLICATION NUMBER: 60/169495  
;; PRIOR FILING DATE: 1999-12-07  
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;; PRIOR FILING DATE: 1997-08-26  
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;; PRIOR FILING DATE: 1997-09-19  
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;; PRIOR FILING DATE: 1999-06-14  
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;; PRIOR FILING DATE: 1999-08-25  
;; PRIOR APPLICATION NUMBER: 09/403296  
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;; PRIOR APPLICATION NUMBER: 09/403297  
;; PRIOR FILING DATE: 1999-10-18  
;; PRIOR APPLICATION NUMBER: 09/423741  
;; PRIOR FILING DATE: 1999-11-10  
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;; PRIOR FILING DATE: 1999-11-12  
;; PRIOR APPLICATION NUMBER: 09/522342  
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;; PRIOR FILING DATE: 2000-04-13  
;; PRIOR APPLICATION NUMBER: 09/664610  
;; PRIOR FILING DATE: 2000-09-18  
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;; PRIOR FILING DATE: 2000-09-18  
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;; PRIOR FILING DATE: 2000-11-08  
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;; PRIOR FILING DATE: 2001-01-22  
;; PRIOR APPLICATION NUMBER: 09/802706  
;; PRIOR FILING DATE: 2001-03-09  
;; PRIOR APPLICATION NUMBER: 09/808689  
;; PRIOR FILING DATE: 2001-03-14  
;; PRIOR APPLICATION NUMBER: 09/866028  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 09/870574  
;; PRIOR FILING DATE: 2001-05-30  
;; PRIOR APPLICATION NUMBER: 09/872035  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: 09/886342  
;; PRIOR FILING DATE: 2001-06-19  
;; PRIOR APPLICATION NUMBER: PCT/US98/14552  
;; PRIOR FILING DATE: 1998-07-14  
;; PRIOR APPLICATION NUMBER: PCT/US98/18824  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: PCT/US98/19093  
;; PRIOR FILING DATE: 1998-09-14  
;; PRIOR APPLICATION NUMBER: PCT/US98/19330  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: PCT/US98/19437  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: PCT/US98/24855  
;; PRIOR FILING DATE: 1998-11-20  
;; PRIOR APPLICATION NUMBER: PCT/US98/25108  
;; PRIOR FILING DATE: 1998-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US98/25190  
;; PRIOR FILING DATE: 1998-11-25  
;; PRIOR APPLICATION NUMBER: PCT/US99/05028  
;; PRIOR FILING DATE: 1999-03-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: 1999-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/20111  
;; PRIOR FILING DATE: 1999-09-01  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 55.7%; Score 39; DB 9; Length 747;  
Best Local Similarity 45.5%; Pred. No. 32;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQANMKV 11  
Db 311 CWRQINSRRI 321

Search completed: February 21, 2003, 08:08:04  
Job time : 10.55 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 / Search time 9.6 Seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-73

Perfect score: 70

Sequence: 1 CFQWQANRRKR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	33	2 S52107	lactoferrin - shee
3	48	68.6	708	2 JC2323	lactoferrin - goat
4	46	65.7	4568	2 T08030	dynain beta heavy
5	43	61.4	275	2 T22597	hypothetical prote
6	43	61.4	707	1 A28438	lactoferrin precu
7	42	60.0	511	2 AB0858	hypothetical prote
8	39	55.7	60	2 A48396	ribosomal protein
9	39	55.7	62	2 AH1301	ribosomal protein
10	39	55.7	62	2 AH1673	ribosomal protein
11	39	55.7	62	2 C89895	50S ribosomal prot
12	39	55.7	206	2 H97451	pyridoxamine 5'-ph
13	39	55.7	206	2 AB2670	probable pyridoxam
14	39	55.7	208	2 AG3441	hypothetical prote
15	39	55.7	570	2 T46261	hypothetical prote
16	38	54.3	361	2 T29571	chromosome segrega
17	38	54.3	1154	2 A13431	protein UNC-89 - C
18	38	54.3	6642	2 T29757	cell cycle arrest
19	37	52.9	306	1 A39654	hypothetical prote
20	37	52.9	349	2 T16882	adenosylmethionine
21	37	52.9	433	2 D81164	probable adenosylm
22	37	52.9	433	2 F81940	hypothetical prote
23	37	52.9	464	2 A12343	hypothetical prote
24	37	52.9	475	2 F64151	probable cytochrom
25	37	52.9	518	2 B84514	cell polarity prot
26	37	52.9	522	2 T19429	hypothetical prote
27	37	52.9	601	2 A45687	outer capsid prote
28	37	52.9	749	2 A45687	hypothetical prote
29	37	52.9	962	2 S67385	hypothetical prote

30	37	52.9	2700	2 D88450	protein F21H11.2 [
31	36.5	52.1	235	2 S91097	hypothetical prote
32	36.5	52.1	235	2 A58943	hypothetical prote
33	36	51.4	62	2 S39862	ribosomal protein
34	36	51.4	62	2 D83962	ribosomal protein
35	36	51.4	282	2 F90580	hypothetical prote
36	36	51.4	289	2 G86403	33.3K hypothetical
37	36	51.4	298	2 AD2346	hypothetical prote
38	36	51.4	346	2 T19980	hypothetical prote
39	36	51.4	513	2 F82216	transcription regu
40	36	51.4	517	2 F71417	cytochrome P450 -
41	36	51.4	572	1 DEM5MX	malate dehydrogena
42	36	51.4	572	2 JC4160	malate dehydrogena
43	36	51.4	584	2 C84325	hypothetical prote
44	36	51.4	649	2 AB2154	hypothetical prote
45	36	51.4	703	2 A45543	lactoferrin precu

## ALIGNMENTS

### RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence\_revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74:

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237

R:Rev. M.M.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A:Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:9263311; PIDN:AAB24877.1; PID:9263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Molecule type: mRNA

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>



R;Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70, 989-993, 1987  
 A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A:Reference number: S07160; MUID:88001031; PMID:3477300  
 A:Accession: S07160  
 A:Molecule type: mRNA  
 A:Residues: 436-487, 'A', 489-711 <RAD>  
 A:Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855  
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51, 3037-3043, 1991  
 A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A:Reference number: A61169; MUID:91235214; PMID:1674448  
 A:Accession: A61169  
 A:Molecule type: mRNA  
 A:Status: not compared with conceptual translation  
 A:Residues: 3-701, 'SWKDPVN' <PAN>  
 A:Experimental source: normal breast tissue  
 R;Metz-Butigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984  
 A:Title: Human lactotransferrin: amino acid sequence and structural comparisons with other  
 A:Reference number: A31000; MUID:85076667; PMID:6510420  
 A:Accession: A31000  
 A:Molecule type: protein  
 A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-400  
 A:Notes: this is the final paper in a series  
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L. Eur. J. Biochem. 241, 303-308, 1996  
 A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity chromatography  
 A:Reference number: S74119; MUID:97054624; PMID:8898921  
 A:Accession: S74119  
 A:Molecule type: protein  
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A:Experimental source: neutrophil granulocytes  
 C:Genetics:  
 A:Gene: GDB:LTF  
 A:Cross-references: GDB:119368; OMIM:150210  
 A:Map position: 3q21-3q23  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein; iron binding; milk  
 F1-19/Domain: signal sequence #status predicted <SIG>  
 F20-711/Product: lactotransferrin #status experimental <MAT>  
 F21-356/Domain: transferrin repeat homology <TRH1>  
 F360-699/Domain: transferrin repeat homology <TRH2>  
 F29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status experimental  
 F157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #status experimental

Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00097;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANRRKV 12  
 DB 39 CFQWQANRRKV 50  
 |||||  
 |||||

RESULT 2  
 S52107  
 lactoferrin - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 14-Jul-1995 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997  
 C:Accession: S52107  
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M. Biochim. Biophys. Acta 1243, 25-32, 1995  
 A:Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet aggregation  
 A:Reference number: S52107; MUID:95127729; PMID:782104  
 A:Accession: S52107  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-33 <QIA>  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication

Query Match 68.6%; Score 48; DB 2; Length 33;  
 Best Local Similarity 63.6%; Pred. No. 0.055;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANRRKV 11  
 DB 19 CYQWQKMRKL 29  
 |||||  
 |||||

RESULT 3  
 JC2323  
 lactoferrin - goat  
 C:Species: Capra aegagrus hircus (domestic goat)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C:Accession: JC2323  
 R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P. Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994  
 A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus  
 A:Reference number: JC2323; MUID:94380047; PMID:8093048  
 A:Accession: JC2323  
 A:Molecule type: mRNA  
 A:Residues: 1-708 <LEP>  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein  
 F359-596/Domain: transferrin repeat homology <TRH2>  
 F252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.6%; Score 48; DB 2; Length 708;  
 Best Local Similarity 63.6%; Pred. No. 1.1;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANRRKV 11  
 DB 38 CYQWQKMRKL 48  
 |||||  
 |||||

RESULT 4  
 T08030  
 dynamin beta heavy chain - Chlamydomonas reinhardtii  
 C:Species: Chlamydomonas reinhardtii  
 C:Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 02-Feb-2001  
 C:Accession: T08030  
 R;Mitchell, D.R.; Brown, K.S. J. Cell Sci. 107, 635-644, 1994  
 A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.  
 A:Reference number: Z16302; MUID:94274778; PMID:8006077  
 A:Accession: T08030  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-4568 <MIT>  
 A:Cross-references: EMBL:U02963; NID:G409965; PIDN:AAA19956.1; PID:G514215  
 A:Experimental source: strain 21gr  
 C:Genetics:  
 A:Gene: ODA4  
 A:Map position: IX  
 A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3  
 C:Superfamily: dynein heavy chain, ciliary  
 C:Keywords: nucleotide binding; P-loop  
 F1919-1926/Region: nucleotide-binding motif A (P-loop)  
 F2202-2209/Region: nucleotide-binding motif A (P-loop)  
 F2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 65.7%; Score 46; DB 2; Length 4568;  
 Best Local Similarity 50.0%; Pred. No. 15;  
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQANRRKV 12  
 DB 1852 CFQWQSLRYIQ 1863  
 |||||  
 |||||

RESULT 5

T22597  
 Hypothetical protein F53H4.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
 C:Accession: T22597  
 R:Dobson, R.  
 Submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19587  
 A:Accession: T22597  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-275 <MIL>  
 A:Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN000028; CESP:F53H4.4  
 A:Experimental source: clone F53H4  
 C:Genetics:  
 A:Gene: CESP:F53H4.4  
 A:Map position: X  
 A:Introns: 67/1; 153/1  
 C:Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 61.4%; Score 43; DB 2; Length 275;  
 Best Local Similarity 63.6%; Pred. No. 3.4;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FQWQANMKVR 12  
 |||:|||||  
 Db 262 FQWKISMRKTR 272

RESULT 6  
 A28438  
 Lactoferrin precursor - mouse  
 N:Alternate names: lactotransferrin  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A28438; A41205  
 R:Pentecost, B.T.; Teng, C.T.  
 J. Biol. Chem. 262, 10134-10139, 1987  
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretory cells  
 A:Reference number: A92596; MUID:87280033; PMID:3611056  
 A:Accession: A28438  
 A:Molecule type: mRNA  
 A:Residues: 3-707 <PEN>  
 A:Cross-references: EMBL:A03298  
 R:Liu, Y.; Teng, C.T.  
 J. Biol. Chem. 266, 21880-21885, 1991  
 A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.  
 A:Reference number: A41205; MUID:92042099; PMID:1939212  
 A:Accession: A41205  
 A:Molecule type: DNA  
 A:Residues: 1-15 <LIU>  
 A:Cross-references: GB:M74778  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-707/Product: lactotransferrin #status predicted <MAT>  
 F:358-695/Domain: transferrin repeat homology <TRH2>  
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 1; Length 707;  
 Best Local Similarity 63.6%; Pred. No. 8.6;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQANMKV 11  
 |||:|||||  
 Db 37 CLRWQNEMKV 47

RESULT 7  
 A80858  
 Hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
 C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
 C:Accession: AB0858  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Paratyphi A  
 A:Reference number: AB0502; PMID:11677608  
 A:Accession: AB0858  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-511 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:G16504016; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STY3070

Query Match 60.0%; Score 42; DB 2; Length 511;  
 Best Local Similarity 58.3%; Pred. No. 9.5;  
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQANMKVR 12  
 |||:|||||  
 Db 350 CFANDMKAKVR 361

RESULT 8  
 A48396  
 ribosomal protein L28 - Bacillus stearothermophilus  
 C:Species: Bacillus stearothermophilus  
 C>Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Aug-1998  
 C:Accession: A48396  
 R:Kruft, V.; Kapp, U.; Wittmann-Liebhold, B.  
 Biochimie 73, 855-860, 1991  
 A:Title: Characterization and primary structure of proteins L28, L33 and L34 from Bacillus stearothermophilus  
 A:Reference number: A48396; MUID:92075758; PMID:1742360  
 A:Accession: A48396  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-60 <KRU>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:69662)  
 C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 60;  
 Best Local Similarity 56.7%; Pred. No. 4.1;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WQANMKVR 12  
 |||:|||||  
 Db 27 WKANLQKVR 35

RESULT 9  
 A1301  
 ribosomal protein L28 [imported] - Listeria monocytogenes (strain EGD-e)  
 C:Species: Listeria monocytogenes  
 C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 17-May-2002  
 C:Accession: A1301  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.  
 A:Reference number: A1077; MUID:21537279; PMID:11679669  
 A:Accession: A1301  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-62 <GLA>  
 A:Cross-references: GB:NC\_003210; PIDN:CAC99894.1; PID:G16411270; GSPDB:GN00177  
 A:Experimental source: strain EGD-e  
 C:Genetics:

A:Gene: rpsB  
C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 62;  
Best Local Similarity 56.7%; Pred. No. 4.2;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WQANMRKVR 12  
|:|:|:|:|

DB 29 WKANLQKVR 37

RESULT 10

AH1673  
ribosomal protein L28 [imported] - Listeria innocua (strain Clip11262)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 17-May-2002  
C:Accession: AH1673  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blocker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Møller, C.; Schluerer, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehlund, O.  
A:Title: Comparative Genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1673  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-62 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC97160.1; PID:gl6414431; GSPDB:GN00178  
A:Experimental source: strain Clip11262  
C:Genetics:  
A:Gene: rpsB  
C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 62;  
Best Local Similarity 56.7%; Pred. No. 4.2;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WQANMRKVR 12  
|:|:|:|:|

DB 29 WKANLQKVR 37

RESULT 11

C89895  
50S ribosomal protein L28 [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 17-May-2002  
C:Accession: C89895  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: C89895  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-62 <KUR>  
A:Cross-references: GB:BA000018; PID:gl3701024; PIDN:BA842319.1; GSPDB:GN00149  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: rpsB  
C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 55.7%; Score 39; DB 2; Length 62;  
Best Local Similarity 56.0%; Pred. No. 4.2;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WQANMRKVR 12  
|:|:|:|:|

DB 28 RMNANLQKVR 37

RESULT 12

H97451  
pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (strain H97451)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C:Accession: H97451  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A:Reference number: A97359; PMID:11743194  
A:Accession: H97451  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-206 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:gl5155733; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C1381  
A:Map position: circular chromosome  
C:Superfamily: pyridoxamine-phosphate oxidase

Query Match 55.7%; Score 39; DB 2; Length 206;

Best Local Similarity 50.0%; Pred. No. 14;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12

DB 88 CFHWKSLRRQVR 99

RESULT 13

AB2670  
pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002  
C:Accession: AB2670  
R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AB2670

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-206 <KUR>

A:Cross-references: GB:AE008698; PIDN:AAL41776.1; PID:gl7739129; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: pdxH

A:Map position: circular chromosome

C:Superfamily: pyridoxamine-phosphate oxidase

Query Match 55.7%; Score 39; DB 2; Length 206;

Best Local Similarity 50.0%; Pred. No. 14;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKVR 12

DB 88 CFHWKSLRRQVR 99

RESULT 14

AG3441  
probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis (strain AG3441)  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 03-May-2002  
C:Accession: AG3441

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, E.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letee, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
 A;Reference number: AD3252; PMID:1175868  
 A;Accession: AC3441  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-208 <KUR>  
 A;Cross-references: GB:AE008917; PIDN:AA152698.1; PID:gl7983525; GSPDB:GNO0190  
 A;Experimental source: strain 16M  
 C;Genetics:  
 A;Gene: BME11517  
 A;Map position: I  
 C;Superfamily: pyridoxamine-phosphate oxidase  
 C;Keywords: oxidoreductase

Query Match 55.7%; Score 39; DB 2; Length 208;  
 Best Local Similarity 50.0%; Pred.No. 14;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWQANMKVR 12  
 |||::|::|::|  
 Db 90 CFHWKSLRRQVR 101

RESULT 15  
 T46261  
 hypothetical protein DKFP761E1824.1 - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C;Accession: T46261  
 R;Boecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, January 2000  
 A;Reference number: Z23032  
 A;Accession: T46261  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-570 <AAA>  
 A;Cross-references: EMBL:AL137432  
 A;Experimental source: adult amygdala; clone DKFP761E1824  
 C;Genetics:  
 A;Note: DKFP761E1824.1

Query Match 55.7%; Score 39; DB 2; Length 570;  
 Best Local Similarity 45.5%; Pred.No. 36;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMKV 11  
 |||::|::|::|  
 Db 134 CVRWQINSRI 144

Search completed: February 21, 2003, 07:47:44  
 Job time : 11.65 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107b-73  
Perfect score: 70  
Sequence: 1 CFQWQANMRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TRFL_HUMAN	P02788 homo sapien
2	48	68.6	708	1 TRFL_CAMDR	Q9tuo0 camelus dro
3	48	68.6	708	1 TRFL_CAPHI	Q29477 capra hircu
4	45	65.7	4568	1 DYHE_CHIRE	Q39565 chlamydomon
5	43	61.4	707	1 TRFL_MOUSE	P08071 mus musculu
6	40	57.1	695	1 TRFL_HORSE	Q77811 equus cabal
7	39	55.7	60	1 RL28_BACST	P23374 bacillus st
8	39	55.7	62	1 RL28_LISMO	Q92aj2 listeria mo
9	39	55.7	62	1 RL28_STAAM	Q99up4 staphylococ
10	38	54.3	62	1 RL28_THETN	Q8r5ul thermoaer
11	38	54.3	422	1 PAFA_CHICK	Q90678 g platelet-
12	38	54.3	435	1 YKYL_CAEEL	Q19910 caenorhabdi
13	37	52.9	306	1 SUB2_YEAST	P26448 saccharomyc
14	37	52.9	475	1 YEB4_HAEIN	P44693 haemophilus
15	37	52.9	522	1 COR1_SCHPO	O13688 schizosacch
16	37	52.9	749	1 VP4_ROTGA	Q04316 rotavirus (
17	37	52.9	982	1 YBX7_SCHPO	Q10201 schizosacch
18	36	51.4	62	1 RL28_BACHD	Q9K924 bacillus ha
19	36	51.4	62	1 RL28_BACSU	P37807 bacillus su
20	36	51.4	572	1 MAOX_MOUSE	P06801 mus musculu
21	36	51.4	704	1 TRFL_PIG	P14632 sus scrofa
22	36	51.4	1131	1 PHY_FINSY	Q41046 pinus sylve
23	35	50.0	133	1 HS90_PLAEP	P20147 plasmodium
24	35	50.0	401	1 PGK_HALVA	P50315 haloarcula
25	35	50.0	441	1 HS82_ASFFU	P40292 aspergillus
26	35	50.0	457	1 SYS_SULSO	O33780 sulfolobus
27	35	50.0	679	1 HS82_AJECA	P33125 ajelomycus
28	35	50.0	701	1 HS90_PODAN	P43109 podospora a
29	35	50.0	704	1 HS83_YEAST	P15108 saccharomyc
30	35	50.0	707	1 HS90_CANAL	P48598 candida alb
31	35	50.0	708	1 TRFL_BUBBU	O77698 bubalus bub
32	35	50.0	709	1 HS82_YEAST	P02829 saccharomyc
33	35	50.0	713	1 HS90_EIMTE	Q44001 elmeria ten

#### RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Theis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RN	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Straubeberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

34	35	50.0	716	1 HS83_DROAV	O02192 drosophila
35	35	50.0	717	1 HS83_DROME	P02828 drosophila
36	35	50.0	721	1 HS90_THERA	P24724 theileria p
37	35	50.0	989	1 TI00_HUMAN	O75448 homo sapien
38	35	50.0	1019	1 VP3_EDVF	Q98630 rice dwarf
39	35	50.0	1072	1 ITA6_CHICK	P26007 gallus gall
40	35	50.0	1173	1 GIGA_ORYSA	Q9awl7 oryza sativ
41	34.5	49.3	256	1 YQEC_ECOLI	Q46809 escherichia
42	34.5	49.3	432	1 TRKI_HUMAN	O15756 homo sapien
43	34	48.6	134	1 YA7B_HAEIN	Q57425 haemophilus
44	34	48.6	213	1 IF4E_XENLA	P48597 xenopus lae
45	34	48.6	217	1 IF4E_HUMAN	P06730 homo sapien

#### ALIGNMENTS

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE-Mammary Gland;  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Oden J.E.;  
RT "Nucleotide sequence of human lactoferrin cDNA.";  
RL Nucleic Acids Res. 18:4013-4013(1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
R LeGrand D., Spik G., Montreuil J., Jolles P.;  
RT "Human lactotransferrin: amino acid sequence and structural  
R comparisons with other transferrins.";  
RL Eur. J. Biochem. 145:659-666(1984).  
RN [10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
R Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
R alignment of the cyanogen bromide fragments and characterization of  
R N- and C-terminal domains.";  
RL Biochim. Biophys. Acta 670:243-254(1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
R Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
R lactotransferrin.";  
RL FEBS Lett. 142:1107-1110(1982).  
RN [12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=8801031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
R expression of mRNA during normal and leukemic myelopoiesis.";  
RL Blood 70:989-993(1987).  
RN [13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
R Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
R Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
R Chen C.N., Evans C., Fitzgerald M., See L.H., Fang M., Porcel B.M.,  
R Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
R Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
R Sagripanti J.L.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2855506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
R and refinement at 2.8-A resolution.";  
RL J. Mol. Biol. 209:711-734(1989).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
R resolution.";  
RL Acta Crystallogr. D 51:629-646(1995).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
R Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
R binding properties and crystal structure of the histidine-  
R 253-->methionine mutant.";  
RL Biochemistry 36:341-346(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in Aspergillus  
R awamori.";  
RL Acta Crystallogr. D 55:403-407(1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
R and analysis of ligand-induced conformational change.";  
RL Acta Crystallogr. D 54:1319-1335(1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioid antagonist peptides derived  
R from human lactoferrin.";  
RL Agric. Biol. Chem. 54:1803-1810(1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
R Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
R Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,  
R El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
R Hejtmancik J.F., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
R corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RL Mol. Vision 4:31-32(1998).  
RN [21]  
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
CC OF AN ANION, USUALLY BICARBONATE.  
CC -I- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST  
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC -I- SUBUNIT: MONOMER.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC -I- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X53961; CAA37914.1; -  
CC EMBL; U07643; AAB60324.1; -  
CC EMBL; M93150; AAA36159.1; -  
CC EMBL; M83202; AAA59511.1; -  
CC EMBL; M83205; AAA58656.1; -  
CC EMBL; M18642; AAA86665.1; -  
CC EMBL; AF332168; AAG48753.1; -  
CC EMBL; BC015822; AAH15822.1; -  
CC EMBL; BC015823; AAH15823.1; -  
CC EMBL; M73700; AAA59479.1; -  
CC EMBL; X52941; CAA37116.1; -  
CC EMBL; U95626; AAB57795.1; -  
CC PIR; S11228; TFHUL.  
CC DR PDB; 1LCP; 31-AUG-94.  
CC DR PDB; 1LCT; 31-OCT-93.  
CC DR PDB; 1LFG; 31-JUL-94.  
CC DR PDB; 1LFI; 31-OCT-93.  
CC DR PDB; 1LGB; 31-AUG-94.  
CC DR PDB; 1LGC; 31-AUG-94.  
CC DR PDB; 1BKA; 08-NOV-96.  
CC DR PDB; 1DSN; 08-MAR-96.  
CC DR PDB; 1HSE; 12-MAR-97.  
CC DR PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00017;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKYR 12  
 DB 39 CFQWQNNRKYR 50

## RESULT 2

TRFL\_CAMDR STANDARD; PRT; 708 AA.  
 AC QSTUN0; Q9MZ55;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhon Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 CC -----

DR EMBL; A131674; CAB53387.1; -;  
 DR EMBL; AF165879; AAF82241.1; -;  
 DR HSP; O77811; 1B1X.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN\_1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN\_3; 2.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW Signal.  
 FT CHAIN 1 19 BY SIMILARITY.  
 FT REPEAT 20 708 LACTOTRANSFERRIN.  
 FT REPEAT 20 363 1.  
 FT REPEAT 364 708 2.  
 FT DISULFID 28 64 BY SIMILARITY.  
 FT DISULFID 38 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;  
 Best Local Similarity 66.7%; Pred. No. 0.25;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNNRKYR 12  
 DB 38 CAQWQRRMKYR 49

## RESULT 3

TRFL\_CAMDR STANDARD; PRT; 708 AA.  
 AC Q29477; Q29479;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA MEDLINE=94380047; Pubmed=8093048;  
 RA le Provost F., Nocard M., Guerin G., Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the  
 RT relevant locus to bovine U12 syntenic group."  
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.





DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN Lf.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RX MEDLINE=87280033; PubMed=3611056;  
 RA Pentecost B.T.; Teng C.T.;  
 RT "Lactotransferrin is the major estrogen inducible protein of mouse  
 uterine secretions.";  
 RL J. Biol. Chem. 262:10134-10139(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Moriishi K.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-14 FROM N.A.  
 RX MEDLINE=92042099; PubMed=1939212;  
 RA Liu Y.; Teng C.T.;  
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";  
 RL J. Biol. Chem. 266:21880-21885(1991).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC  
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 CC  
 DR EMBL; J03298; AAA40525.1; -;  
 DR EMBL; D88510; BAA13633.1; -;  
 DR EMBL; BC006904; AAH06904.1; -;  
 DR EMBL; M74778; AAA39427.1; -;  
 DR PIR; A28438; A28438.  
 DR HSP; P02789; ICB6.  
 DR MGD; MGI:96837; Ltf.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN\_1; 1.  
 DR PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN\_3; 2.  
 KW Transferrin; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW Signal.  
 FT CHAIN 1 19 BY SIMILARITY  
 FT REPEAT 20 707 LACTOTRANSFERRIN.  
 FT REPEAT 358 707 1.  
 FT DISULFID 27 63 BY SIMILARITY.  
 FT DISULFID 37 54 BY SIMILARITY.  
 FT DISULFID 133 216 BY SIMILARITY.  
 FT DISULFID 175 191 BY SIMILARITY.  
 FT DISULFID 188 199 BY SIMILARITY.  
 FT DISULFID 249 263 BY SIMILARITY.

FT DISULFID 366 398 BY SIMILARITY.  
 FT DISULFID 376 389 BY SIMILARITY.  
 FT DISULFID 423 702 BY SIMILARITY.  
 FT DISULFID 443 665 BY SIMILARITY.  
 FT DISULFID 475 550 BY SIMILARITY.  
 FT DISULFID 499 693 BY SIMILARITY.  
 FT DISULFID 509 523 BY SIMILARITY.  
 FT DISULFID 520 533 BY SIMILARITY.  
 FT DISULFID 591 605 BY SIMILARITY.  
 FT DISULFID 643 648 BY SIMILARITY.  
 FT METAL 78  
 FT METAL 110  
 FT METAL 210  
 FT METAL 271 271  
 FT METAL 413 413  
 FT METAL 451 451  
 FT METAL 544 544  
 FT METAL 613 613  
 FT BINDING 139 139  
 FT BINDING 481 481  
 FT CARBOHYD 118 118  
 FT CARBOHYD 494 494  
 FT CONFLICT 1 2  
 FT CONFLICT 25 25  
 FT CONFLICT 82 82  
 FT CONFLICT 359 359  
 FT CONFLICT 382 382  
 FT CONFLICT 449 449  
 FT CONFLICT 629 629  
 SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;  
 Query Match 61.4%; Score 43; DB 1; Length 707;  
 Best Local Similarity 63.6%; Pred. No. 2.1;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWQANNRKV 11  
 DB 37 CLRWQNNRKV 47  
 RESULT 6  
 ID TREFL HORSE STANDARD; PRT; 695 AA.  
 AC 077811;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).  
 GN LTF.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Paramasivam M.; Srinivasan A.; Yadav M.P.; Singh T.P.;  
 RT "cDNA sequence of mare lactoferrin.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RC TISSUE=Milk;  
 RX MEDLINE=99296631; PubMed=10366507;  
 RA Sharma A.K.; Paramasivam M.; Srinivasan A.; Yadav M.P.; Singh T.P.;  
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A  
 resolution.";  
 RL J. Mol. Biol. 289:303-317(1999).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.



DR EMBL; AL591981; CAC99894.1; -  
 DR EMBL; AL596170; CAC97160.1; -  
 DR Listlist; LINO1930; -  
 DR Listlist; LMO01816; -  
 DR InterPro; IPRO01383; Ribosomal\_L28.  
 DR Pfam; PF00830; Ribosomal\_L28; 1.  
 DR TIGRFAMs; TIGR00009; L28; 1.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 62 AA; 6991 MW; AA43DE039213C562 CRC64;  
 Query Match 55.7%; Score 39; DB 1; Length 62;  
 Best Local Similarity 66.7%; Pred. No. 0.98;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 YQ 4 WQANNRKYR 12  
 : : : : :  
 Db 29 WKANLQKVR 37  
 : : : : :  
 RESULT 9  
 ID RL28 STAAM STANDARD; PRT; 62 AA.  
 AC Q99UP4;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 50S ribosomal protein L28.  
 GN RPMB OR SAV1224 OR SA1067 OR MW1107.  
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),  
 OS Staphylococcus aureus (strain N315), and  
 OS Staphylococcus aureus (strain MW2).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=158878, 158879, 196620;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mu50 / ATCC 700699, and N315;  
 RX MEDLINE=21311952; PubMed=11418146;  
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,  
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,  
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
 RA Kanehisa M., Yamashita A., Oshina K., Furuya K., Yoshino C., Shiba T.,  
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;  
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
 aureus";  
 RL Lancet 357:1225-1240 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mu50;  
 RX MEDLINE=22040717; PubMed=12044378;  
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,  
 RA Yamamoto K., Hiramatsu K.;  
 RT "Genome and virulence determinants of high virulence community-  
 acquired MRSA";  
 RL Lancet 359:1819-1827 (2002).  
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.  
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 CC EMBL; AP003361; BAB57386.1; -  
 CC EMBL; AP003133; BAB42319.1; -  
 CC EMBL; AP004826; BAB94972.1; -  
 CC InterPro; IPRO01383; Ribosomal\_L28.  
 CC Pfam; PF00830; Ribosomal\_L28; 1.  
 CC TIGRFAMs; TIGR00009; L28; 1.

KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 62 AA; 6977 MW; 20042609E7D9C26A CRC64;  
 Query Match 55.7%; Score 39; DB 1; Length 62;  
 Best Local Similarity 60.0%; Pred. No. 0.98;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 YQ 3 WQANNRKYR 12  
 : : : : :  
 Db 28 RWANLQKVR 37  
 : : : : :  
 RESULT 10  
 ID RL28 THETN STANDARD; PRT; 62 AA.  
 AC Q8R9U1;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 50S ribosomal protein L28.  
 GN RPMB OR TTE1495.  
 OS Thermoanaerobacter tengcongensis.  
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
 OX NCBI\_TaxID=119072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MB4 / JCM 11007;  
 RX MEDLINE=21992816; PubMed=1197336;  
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;  
 RA "A complete sequence of T. tengcongensis genome";  
 RL Genome Res. 12:689-700 (2002).  
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; AE013107; AAM24713.1; -  
 CC Ribosomal protein; Complete proteome.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;  
 Query Match 54.3%; Score 38; DB 1; Length 62;  
 Best Local Similarity 60.0%; Pred. No. 1.5;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 YQ 3 WQANNRKYR 12  
 : : : : :  
 Db 27 RWKPNIRKYR 36  
 : : : : :  
 RESULT 11  
 ID PAPA CHICK STANDARD; PRT; 422 AA.  
 AC Q90678;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)  
 DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (IDL-associated  
 DE phospholipase A2) (IDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine  
 DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).  
 GN P242G.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.

OX NCBI\_TaxID=9031;  
 RN [1] SEQUENCE FROM N.A.  
 RP TISSUE=Splice;  
 RC MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 RT phospholipase A2 with a catalytic triad";  
 RL J. Biol. Chem. 270:25481-25487(1995)  
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -!- CATALYTIC ACTIVITY: 2-acetyl-1-alkyl-sn-glycero-3-phosphocholine +  
 CC H<sub>2</sub>O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: PLASMA.  
 CC -!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.  
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 CC  
 DR EMBL; U34278; AAC59717.1; -;  
 DR InterPro; IPR000734; Lipase.  
 DR InterPro; IPR005065; PAF-AH\_P\_II.  
 DR InterPro; IPR000379; Ser estri\_site.  
 DR Pfam; PF03403; PAF-AH\_P\_II; 1.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY;  
 FT CHAIN 22 422 PLATELET-ACTIVATING FACTOR  
 FT ACT\_SITE 266 266 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 289 289 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 422 AA; 47046 MW; 15A5C794376E9141 CRC64;  
 Query Match 54.3%; Score 38; DB 1; Length 422;  
 Best Local Similarity 54.5%; Pred. No. 11;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 FQWQANRKYR 12  
 DB 316 FQWAAILRMK 326  
 RESULT 12  
 YKYL CAEEL  
 ID YKYL CAEEL STANDARD; PRT; 455 AA.  
 AC Q19910;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein F30B5.4 in chromosome IV.  
 GN F30B5.4  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Miller N., Bradshaw H.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP REVISIONS.  
 RA Waterston R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.  
 CC  
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 CC  
 DR EMBL; U42437; AAA83493.2; -;  
 DR WormPep; F30B5.4; CE28552.  
 KW Hypothetical protein.  
 SQ SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;  
 Query Match 54.3%; Score 38; DB 1; Length 455;  
 Best Local Similarity 50.0%; Pred. No. 12;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWQANMRK 10  
 DB 102 CIQWELNRRR 111  
 RESULT 13  
 BUB2 YEAST  
 ID BUB2 YEAST STANDARD; PRT; 306 AA.  
 AC P26438;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).  
 GN BUB2 OR YMR055C OR YMR9796.08C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 MEDLINE=91330299; PubMed=1651171;  
 RA Hoyt M.A., Totis L., Roberts B.T.;  
 RT "S. cerevisiae genes required for cell cycle arrest in response to  
 RT loss of microtubule function";  
 RL Cell 66:507-517(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP CHARACTERIZATION.  
 MEDLINE=21385309; PubMed=11493673;  
 RA Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fèsquet D.,  
 RA Johnston L.H.;  
 RT "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and  
 RT regulates cytokinesis";  
 RL J. Cell Sci. 114:2345-2354(2001).  
 CC -!- FUNCTION: Part of a checkpoint which monitors spindle integrity  
 CC and prevents premature exit from mitosis. This cell-cycle arrest  
 CC depends upon inhibition of the G-protein Tem1 by the BFA1/BUB2  
 CC complex.  
 CC -!- SUBUNIT: Interacts with BFA1.  
 CC -!- SUBCELLULAR LOCATION: Spindle poles.  
 CC -!- SIMILARITY: TO S.POMBE CDC16.  
 CC  
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DR ENBL; M64706; AAA16885.1; -;  
 DR ENBL; M249703; CAA89765.1; -;  
 DR PIR; A39654; A39654.  
 DR SGD; S0004659; BUR2.  
 DR InterPro; IPR000195; RabGAP\_TBC.  
 DR Pfam; PF00566; TBC; 1.  
 DR SMART; SM00164; TBC; 1.  
 KW Cell cycle; Mitosis.  
 SQ SEQUENCE 306 AA; 35027 MW; A1DBFB548E81EA3 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 306;  
 Best Local Similarity 50.0%; Pred. No. 12;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQANRX 10  
 DB 108 CFQWQANRX 117

RESULT 14  
 YEBB\_HAEIN STANDARD; PRT; 475 AA.  
 AC P44693;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein H10409.  
 GN H10409.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 CC Haemophilus.  
 CC NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Rd / KW20 / ATCC 51907;  
 RX MEDLINE=9530630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kertavagis A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RL Rd";  
 RL Science 269:496-512(1995).

CC -!- FUNCTION: COULD BE INVOLVED IN CELL WALL DEGRADATION OR  
 CC FORMATION (BY SIMILARITY).  
 CC -!- SIMILARITY: STRONG, TO E.COLI YEBB.  
 CC -!- SIMILARITY: TO STAPHYLOCOCCUS LYSOSTAPHIN.  
 CC -----  
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 CC -----  
 CC ENBL; U32724; AAC22068.1; -;  
 CC MEROPS; M37.UFW; -;  
 DR TIGR; H10409; -;  
 DR InterPro; IPR002886; Peptidase M37.  
 DR Pfam; PF01551; Peptidase M37; 1.  
 KW Hypothetical protein; Cell wall; Complete proteome.  
 SQ SEQUENCE 475 AA; 53255 MW; 143C10F92233939D CRC64;

Query Match 52.9%; Score 37; DB 1; Length 475;  
 Best Local Similarity 50.0%; Pred. No. 19;  
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQANRKYR 12  
 DB 251 QWQANRKYR 160

RESULT 15  
 CORL\_SCHPO STANDARD; PRT; 522 AA.  
 AC O13688;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Core protein 1.  
 GN CORL OR SPAC1E3.08C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 CC Schizosaccharomycetes.  
 CC NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Sawin K.E., Hajibagheri M., Nurse P.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds R., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Sipakowski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe";  
 RL Nature 415:871-880(2002).

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 CC -----  
 CC ENBL; AJ002494; CAA05501.1; -;  
 DR ENBL; Z98595; CAB11187.1; -;  
 SQ SEQUENCE 522 AA; 59898 MW; 36CF241DD74AF0F5 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 522;  
 Best Local Similarity 45.5%; Pred. No. 21;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPWOANRKY 11  
| : | : | :  
Db 203 CSEWIANLEKI 213

Search completed: February 21, 2003, 07:27:47  
Job time : 5.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107b-73

Perfect score: 70

Sequence: 1 CFQWQANMRKV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mbc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirois:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	85.7	711	4 Q8TCD2	Q8TCD2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9UCY5 homo sapien
3	48	68.6	33	6 Q9TR80	Q9TR80 ovis aries
4	43	61.4	275	5 Q93780	Q93780 caenorhabdi
5	42	60.0	511	16 Q8Z462	Q8Z462 salmonella
6	42	60.0	514	10 Q9SP27	Q9SP27 callistephu
7	41	58.6	305	4 Q8TAX2	Q8TAX2 homo sapien
8	41	58.6	466	4 Q9NUS2	Q9NUS2 homo sapien
9	39	55.7	205	16 Q986A0	Q986A0 rhizobium l
10	39	55.7	206	16 Q8UHC2	Q8UHC2 agrobacteri
11	39	55.7	206	16 Q92RH8	Q92RH8 rhizobium m
12	39	55.7	208	16 Q8YFK3	Q8YFK3 brucella me
13	39	55.7	274	4 Q96M21	Q96M21 homo sapien
14	39	55.7	570	4 Q9NTA7	Q9NTA7 homo sapien
15	39	55.7	570	4 Q96DM9	Q96DM9 homo sapien
16	39	55.7	620	4 Q8WX60	Q8WX60 homo sapien

17	39	55.7	866	10 Q9FHI9	Q9FHI9 arabidopsis
18	38	54.3	62	16 Q8R9U1	Q8R9U1 thermocanaer
19	38	54.3	108	9 Q8SC55	Q8SC55 stx2 conver
20	38	54.3	333	17 Q975Y9	Q975Y9 sulfobus
21	38	54.3	433	5 Q83A2	Q83A2 ciona intes
22	38	54.3	471	16 Q99Z05	Q99Z05 streptococc
23	38	54.3	513	10 Q9LJY8	Q9LJY8 arabidopsis
24	38	54.3	531	10 Q9LTD4	Q9LTD4 arabidopsis
25	38	54.3	557	10 Q9LOH7	Q9LOH7 arabidopsis
26	38	54.3	1154	16 Q8YFT1	Q8YFT1 brucella me
27	38	54.3	6632	5 Q17362	Q17362 caenorhabdi
28	38	54.3	6632	5 Q01761	Q01761 caenorhabdi
29	37	52.9	279	16 Q8XSE2	Q8XSE2 ralscontia s
30	37	52.9	349	5 Q22512	Q22512 caenorhabdi
31	37	52.9	424	5 Q9VT09	Q9VT09 drosophila
32	37	52.9	433	16 Q9K086	Q9K086 neisseria m
33	37	52.9	433	16 Q8JTV6	Q8JTV6 neisseria m
34	37	52.9	464	16 Q8YPP5	Q8YPP5 anabaena sp
35	37	52.9	469	9 Q38115	Q38115 bacteriophag
36	37	52.9	518	10 Q9SI49	Q9SI49 arabidopsis
37	37	52.9	681	5 Q9XVD1	Q9XVD1 caenorhabdi
38	37	52.9	737	5 Q95QJ8	Q95QJ8 caenorhabdi
39	37	52.9	940	10 Q9AV70	Q9AV70 oryza sativ
40	37	52.9	1121	10 Q9SM56	Q9SM56 lycopersico
41	37	52.9	2858	5 Q9CYP6	Q9CYP6 caenorhabdi
42	36.5	52.1	235	16 Q8XEI9	Q8XEI9 escherichia
43	36	51.4	48	6 Q77558	Q77558 sus scrofa
44	36	51.4	125	5 Q26115	Q26115 pseudalexia
45	36	51.4	134	13 Q98UD4	Q98UD4 xenopus lae

## ALIGNMENTS

### RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.  
ID Q8TCD2  
AC Q8TCD2  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022347; AAH22347.1; --  
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;  
Best Local Similarity 90.9%; Pred. No. 0.0052;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11  
Db 39 CFQWQANMRKV 49

### RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.  
ID Q9UCY5  
AC Q9UCY5  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE Lactoferrin homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96081613; PubMed=8551695;
RX Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
  seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSP; P02788; IBA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EDDEB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNNRKVR 12
Db 21 FQWQNNRKVR 31

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samouri D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O77698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 68.6%; Score 48; DB 6; Length 33;
Best Local Similarity 63.6%; Pred. No. 0.037;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 11
Db 19 CYQWQNNRKVR 29

RESULT 4
Q93780 PRELIMINARY; PRT; 275 AA.
AC Q93780;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F53H4.4 protein.
GN F53H4.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96069613; PubMed=9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81089; CAB03137.1; -.
SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 61.4%; Score 43; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNNRKVR 12
Db 262 FQWQNNRKVR 272

RESULT 5
Q82462 PRELIMINARY; PRT; 511 AA.
AC Q82462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein STY3070.
GN STY3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
  Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
  Baker S., Basham D., Brooks R., Chillingworth T., Connor P.,
  Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
  Felwell T., Hamlin S., Haque A., Hien T.T., Holroyd S., Jagers K.,
  Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
  Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
  Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
  enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627276; CAD06049.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match 60.0%; Score 42; DB 16; Length 511;
Best Local Similarity 56.3%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNNRKVR 12
Db 350 CFQWQNNRKVR 361

RESULT 6
Q9SP27 PRELIMINARY; PRT; 514 AA.
AC Q9SP27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Flavone synthase II.
GN CYP93B5.
OS Callistephus chinensis (China aster).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Astereae; Callistephus.

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OX NCBI\_TaxID=113379;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Martens S., Forkmann G.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
DR EMBL; AF188612; AAF04115.1; -.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
KW Heme; Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 514 AA; 58412 MW; 90B631B28952A5E7 CRC64;

Query Match 60.0%; Score 42; DB 10; Length 514;  
Best Local Similarity 54.5%; Pred. No. 10;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFOWQANMKV 11  
|||:|:|:  
Db 470 CFENANDKEV 480

RESULT 7

Q8TAX2 PRELIMINARY; PRT; 306 AA.  
ID Q8TAX2  
AC Q8TAX2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Similar to hypothetical protein FLJ11175.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PANCREAS;  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC025708; AAH25708.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 306 AA; 43D9AD722566B343 CRC64;

Query Match 58.6%; Score 41; DB 4; Length 306;  
Best Local Similarity 55.6%; Pred. No. 9.1;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOWQANMR 9  
|||:|:|:  
Db 269 CFQWESTLR 277

RESULT 8

Q9NUS2 PRELIMINARY; PRT; 466 AA.  
ID Q9NUS2  
AC Q9NUS2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol ester/diacylglycerol-binding protein UNC-13.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagatsuna M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK002037; BAA92048.1; -.  
DR HSSP; P21707; 1BYN.  
DR InterPro; IPR000008; C2.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00168; C2; 1.  
DR PRINTS; PR00360; C2DOMAIN.  
DR SMART; SM00239; C2; 1.  
DR PROSITE; PS00499; C2\_DOMAIN\_1; UNKNOWN\_1.  
DR PROSITE; PS00004; C2\_DOMAIN\_2; 1.  
DR PROSITE; PS00030; RNP\_RNP\_1; UNKNOWN\_1.  
SQ SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;

Query Match 58.6%; Score 41; DB 4; Length 466;  
Best Local Similarity 55.6%; Pred. No. 14;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOWQANMR 9  
|||:|:|:  
Db 269 CFQWESTLR 277

RESULT 9

Q986A0 PRELIMINARY; PRT; 205 AA.  
ID Q986A0  
AC Q986A0;  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Pyridoxamine 5'-phosphate oxidase.  
GN ML17454.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAFF303099;  
RX MEDLINE=21082930; PubMed=11214969;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";  
RL DNA Res. 7:331-338(2000).  
DR EMBL; AP003011; BAB53553.1; -.  
DR InterPro; IPR000659; Pyridox\_oxidase.  
DR Pfam; PF01243; Pyridox\_oxidase; 1.  
DR ProDom; PD008312; Pyridox\_oxidase; 1.  
DR TIGRFAMs; TIGR00558; pdxH; 1.  
DR PROSITE; PS01064; PYRIDOX\_OXIDASE; 1.  
KW Complete proteome.  
SQ SEQUENCE 205 AA; 23300 MW; 0BADE4CD312327EA CRC64;

Query Match 55.7%; Score 39; DB 16; Length 205;  
Best Local Similarity 50.0%; Pred. No. 14;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFOWQANMRKVR 12  
|||:|:|:  
Db 88 CFHWKSLRQVR 99

RESULT 10

Q8UHC2 PRELIMINARY; PRT; 206 AA.  
ID Q8UHC2  
AC Q8UHC2;

DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Pyridoxamine 5'-phosphate oxidase.  
 GN Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;  
 RT "the genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58.";  
 RL Science 294:2317-2323 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 RA Houmel K., Gordon J., Vaundin D., Iartchouk O., Epp A., Liu F.,  
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328 (2001).  
 DR EMBL; AE009043; AAL41776.1; -;  
 DR EMBL; AE008009; AAK8569.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 206 AA; 23720 MW; 3B8488AE5307C0C1 CRC64;  
 Query Match 55.7%; Score 39; DB 16; Length 206;  
 Best Local Similarity 50.0%; Pred. No. 14;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWQANMKVR 12  
 DB 88 CFHWKSLRRQVR 99  
 RESULT 11  
 Q92RH8 PRELIMINARY; PRT; 206 AA.  
 ID Q92RH8  
 AC Q92RH8  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein  
 DE (EC 1.4.3.5).  
 GN PDHX OR R00895 OR SMC00069.  
 OS Rhizobium meliloti (sinorhizobium meliloti).  
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=1021.  
 RA MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaue V., Masuy D.,  
 RA Pohl T., Portetellette D., Puehler A., Purnelle B., Ramsperger U.,

RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).  
 DR EMBL; AL591785; CAC45467.1; -;  
 DR InterPro; IPR000659; Pyridox oxidase.  
 DR Pfam; PF01243; Pyridox oxidase; 1.  
 DR ProDom; PD006312; Pyridox oxidase; 1.  
 DR TIGRFAMs; TIGR00558; pdxH; 1.  
 DR PROSITE; PS01064; PYRIDOX\_OXIDASE; UNKNOWN\_1.  
 KW Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;  
 Query Match 55.7%; Score 39; DB 16; Length 206;  
 Best Local Similarity 50.0%; Pred. No. 14;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWQANMKVR 12  
 DB 88 CFHWKSLRRQVR 99  
 RESULT 12  
 Q8YFK3 PRELIMINARY; PRT; 208 AA.  
 ID Q8YFK3  
 AC Q8YFK3  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).  
 GN BMEI1517.  
 OS Brucella melitensis.  
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=16M / ATCC 23456 / BIOTYPE 1;  
 RX MEDLINE=20020109; PubMed=11756688;  
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,  
 RA Jablonski L., Larsen N., D'Souza W., Bernal A., Mazur M., Goltzman E.,  
 RA Selkov E., Eizer F.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
 RA Haselkorn R., Kyrides N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 RT Brucella melitensis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
 DR EMBL; AE009587; AAL52698.1; -;  
 DR InterPro; IPR000659; Pyridox oxidase.  
 DR Pfam; PF01243; Pyridox oxidase; 1.  
 DR ProDom; PD006312; Pyridox oxidase; 1.  
 DR TIGRFAMs; TIGR00558; pdxH; 1.  
 DR PROSITE; PS01064; PYRIDOX\_OXIDASE; 1.  
 KW Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;  
 Query Match 55.7%; Score 39; DB 16; Length 208;  
 Best Local Similarity 50.0%; Pred. No. 14;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWQANMKVR 12  
 DB 90 CFHWKSLRRQVR 101  
 RESULT 13  
 Q96M21 PRELIMINARY; PRT; 274 AA.  
 ID Q96M21  
 AC Q96M21  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE CDNA FLJ32891 fis, clone TESTI2004929.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057453; BAB71493.1; -;
SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

Query Match 55.7%; Score 39; DB 4; Length 274;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 12
Db |||||:|:|:|
66 CFQWRGVRYLR 77

RESULT 14
ID Q9NTA7 PRELIMINARY; PRT; 570 AA.
AC Q9NTA7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 63.7 kDa protein (Fragment).
GN DKFZP761E1824.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AMYGDALA;
RA Bloembergen H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137432; CAB70735.1; -;
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 2.
DR SMART; SM00032; CCP; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 570 AA; 63713 MW; 66B1A4B4096C3A1B CRC64;

Query Match 55.7%; Score 39; DB 4; Length 570;
Best Local Similarity 45.5%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11
Db |||||:|:|:|
134 CVRWQINSRRI 144

RESULT 15
ID Q96DM9 PRELIMINARY; PRT; 570 AA.
AC Q96DM9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDNA FLJ32142 fis, clone PLACE5000068, weakly similar to C4B-binding
protein precursor (C4BP).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056704; BAB71259.1; -;
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 2.
SQ SEQUENCE 570 AA; 64211 MW; E67489C3A38B868A CRC64;

Query Match 55.7%; Score 39; DB 4; Length 570;
Best Local Similarity 45.5%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQANMRKV 11
Db |||||:|:|:|
159 CVRWQINSRRI 169

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Search completed: February 21, 2003, 07:44:26  
Job time : 22.8 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107B-74  
Perfect score: 69  
Sequence: 1 CFQWRMRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	12	21	AAV78074 Human lactoferrin
2	65	94.2	12	21	AAV78089 Human lactoferrin
3	65	94.2	12	21	AAV78090 Human lactoferrin
4	65	94.2	12	21	AAV78093 Human lactoferrin
5	64	92.8	12	21	AAV78086 Human lactoferrin
6	63	91.3	12	21	AAV78038 Human lactoferrin
7	63	91.3	12	21	AAV78046 Human lactoferrin
8	63	91.3	12	21	AAV78047 Human lactoferrin
9	63	91.3	12	21	AAV78095 Human lactoferrin
10	63	91.3	13	21	AAV78037 Human lactoferrin

11	63	91.3	13	21	AAV78048 Human lactoferrin
12	63	91.3	13	21	AAV78049 Human lactoferrin
13	63	91.3	14	21	AAV78036 Human lactoferrin
14	63	91.3	14	21	AAV78050 Human lactoferrin
15	63	91.3	14	21	AAV78051 Human lactoferrin
16	63	91.3	15	17	AAV78054 Peptide for anti-u
17	63	91.3	15	21	AAV78035 Human lactoferrin
18	63	91.3	15	21	AAV78062 Human lactoferrin
19	63	91.3	15	21	AAV78063 Human lactoferrin
20	63	91.3	16	21	AAV78031 Human lactoferrin
21	63	91.3	16	21	AAV78064 Human lactoferrin
22	63	91.3	16	21	AAV78065 Human lactoferrin
23	63	91.3	17	21	AAV78034 Human lactoferrin
24	63	91.3	17	21	AAV78066 Human lactoferrin
25	63	91.3	17	21	AAV78067 Human lactoferrin
26	63	91.3	18	15	AAV78067 Human lactoferrin
27	63	91.3	18	17	AAV78032 Advanced glycosyla
28	63	91.3	18	21	AAV78033 Human lactoferrin
29	63	91.3	19	21	AAV78067 Amino acid sequenc
30	63	91.3	19	21	AAV78032 Human lactoferrin
31	63	91.3	20	13	AAV78032 Anti microbial pep
32	63	91.3	20	14	AAV78032 Lactoferrin-relate
33	63	91.3	20	15	AAV78032 Lactoferrin-derive
34	63	91.3	20	15	AAV78032 Lactoferrin-derive
35	63	91.3	20	15	AAV78032 Lactoferrin-derive
36	63	91.3	20	15	AAV78032 Lactoferrin-derive
37	63	91.3	20	16	AAV78032 Bovine lactoferrin
38	63	91.3	20	16	AAV78032 Bovine lactoferrin
39	63	91.3	20	16	AAV78032 Anti-parasitic lac
40	63	91.3	20	16	AAV78032 Anti-parasitic lac
41	63	91.3	20	17	AAV78032 Peptide for anti-u
42	63	91.3	20	17	AAV78032 Lactoferrin-derive
43	63	91.3	20	17	AAV78032 Lactoferrin-derive
44	63	91.3	20	17	AAV78032 Lactoferrin-derive
45	63	91.3	20	17	AAV78032 Lactoferrin-derive

## ALIGNMENTS

RESULT 1  
AAV78074

ID AAV78074 standard; Peptide, 12 AA.

XX AAV78074;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:74.

XX Human, lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX Sequence 12 AA;  
SQ

Query Match 100.0%; Score 69; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12  
DB 1 CFQWQRAMRKVR 12  
|||||

RESULT 2  
AAY78089  
ID AAY78089 standard; Peptide; 12 AA.  
XX  
AC AAY78089;  
XX  
DT 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:89.  
DE  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200001730-A1.  
PN  
XX 13-JAN-2000.  
PD  
XX 06-JUL-1999; 99WO-S01230.  
PF  
XX 06-JUL-1998; 98SE-0002441.  
PR  
XX 17-JUL-1998; 98SE-0002562.  
PR  
XX 29-DEC-1998; 98SE-0004614.  
PR  
XX (ASCI-) A+ SCI INVEST AB.  
PA  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
PI  
XX WPI; 2000-147388/13.  
DR  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX Sequence 12 AA;  
SQ

Query Match 94.2%; Score 65; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.00014;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12  
DB 1 CFQWQRAMRKVR 12  
|||||

RESULT 3  
AAY78090  
ID AAY78090 standard; Peptide; 12 AA.  
XX  
AC AAY78090;  
XX  
DT 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:90.  
DE  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200001730-A1.  
PN  
XX 13-JAN-2000.  
PD  
XX 06-JUL-1999; 99WO-S01230.  
PF  
XX 06-JUL-1998; 98SE-0002441.  
PR  
XX 17-JUL-1998; 98SE-0002562.  
PR  
XX 29-DEC-1998; 98SE-0004614.  
PR  
XX (ASCI-) A+ SCI INVEST AB.  
PA  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
PI  
XX WPI; 2000-147388/13.  
DR  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX SQ Sequence 12 AA;

Query Match 94.2%; Score 65; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.00014;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQRAVRKVR 12  
DB 1 CFQWQRAVRKVR 12

RESULT 4  
AAV78093  
ID AAY78093 standard; Peptide; 12 AA.

XX AC AAY78093;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:93.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
XX inflammations and tumors and for use in infant formula food

XX PS Claim 22; Page 38; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
XX lactoferrin. The peptides are taken up in the intestine through  
XX binding to specific lactoferrin receptors and are then transported  
XX through the circulation. A medicinal product of the peptide or fragment  
XX can be used for treating and/or prevention of infections (such as  
XX urinary tract infections, colitis, and Candida infection on a mucosal  
XX membrane), inflammations and/or tumours. The peptides can also be used  
XX in food stuffs such as infant formula food. The peptides are also  
XX fungicidal and bactericidal and may also be used as preservatives.

XX CC Even though native human lactoferrin have been shown to have desired  
XX anti-inflammatory anti-infectious and anti-tumoural properties they  
XX cannot be used clinically on a broad basis because of high production  
XX costs. Therefore, provision of peptides based on lactoferrin would  
XX enable them to be used for the same purposes as lactoferrin at lower  
XX cost.

XX SQ Sequence 12 AA;

Query Match 94.2%; Score 65; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.00014;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQRAVRKVR 12  
DB 1 CFQWQRAVRKVR 12

RESULT 5  
AAV78086  
ID AAY78086 standard; Peptide; 12 AA.

XX AC AAY78086;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:85.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
XX inflammations and tumors and for use in infant formula food

XX PS Claim 22; Page 36; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
XX lactoferrin. The peptides are taken up in the intestine through  
XX binding to specific lactoferrin receptors and are then transported  
XX through the circulation. A medicinal product of the peptide or fragment  
XX can be used for treating and/or prevention of infections (such as  
XX urinary tract infections, colitis, and Candida infection on a mucosal  
XX membrane), inflammations and/or tumours. The peptides can also be used  
XX in food stuffs such as infant formula food. The peptides are also  
XX fungicidal and bactericidal and may also be used as preservatives.

XX CC Even though native human lactoferrin have been shown to have desired  
XX anti-inflammatory anti-infectious and anti-tumoural properties they  
XX cannot be used clinically on a broad basis because of high production  
XX costs. Therefore, provision of peptides based on lactoferrin would  
XX enable them to be used for the same purposes as lactoferrin at lower  
XX cost.

XX SQ Sequence 12 AA;

Query Match 92.8%; Score 64; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.00021;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
 |||||  
 Db 1 CFQWQRMKVR 12

## RESULT 6

AAV78038  
 ID AAY78038 standard; Peptide; 12 AA.

XX AAY78038;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:38.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 12 AA;  
 SQ Query Match 91.3%; Score 63; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00031;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
 |||||  
 Db 1 CFQWQRMKVR 12

## RESULT 7

AAV78046

ID AAY78046 standard; Peptide; 12 AA.

XX AAY78046;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:46.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

SQ Sequence 12 AA;

Query Match 91.3%; Score 63; DB 21; Length 12;

Best Local Similarity 91.7%; Pred. No. 0.00031;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
 |||||  
 Db 1 CFQWQRMKVR 12

## RESULT 8

AAV78047

ID AAY78047 standard; Peptide; 12 AA.

XX AAY78047;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 73; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 12 AA;  
 SQ Query Match 91.3%; Score 63; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00031;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRAMRKVR 12  
 Db 1 CFQWQRAMRKVR 12  
 RESULT 9  
 AAY78095  
 ID AAY78095 standard; Peptide; 12 AA.  
 AC AAY78095;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:95.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS

OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 22; Page 38; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 12 AA;  
 SQ Query Match 91.3%; Score 63; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00031;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRAMRKVR 12  
 Db 1 CFQWQRAMRKVR 12  
 RESULT 10  
 AAY78037  
 ID AAY78037 standard; Peptide; 13 AA.  
 AC AAY78037;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:37.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 PF



```

XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 12; Page 70; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 13 AA;
Query Match 91.3%; Score 63; DB 21; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQRMKVR 12
DB 2 CFQWQRMKVR 13
| | | | |
| | | | |

RESULT 11
AAY78048
ID AAY78048 standard; Peptide; 13 AA.
XX
XX AAY78048;
XX
XX 25-APR-2000 (first entry)
XX
XX Human lactoferrin derived peptide SEQ ID NO:48.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 98WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX

```

```

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 15; Page 74; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumors. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 13 AA;
Query Match 91.3%; Score 63; DB 21; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQRMKVR 12
DB 2 CFQWQRMKVR 13
| | | | |
| | | | |

RESULT 12
AAY78049
ID AAY78049 standard; Peptide; 13 AA.
XX
XX AAY78049;
XX
XX 25-APR-2000 (first entry)
XX
XX Human lactoferrin derived peptide SEQ ID NO:49.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 98WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX

```

PS Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

SQ Query Match 91.3%; Score 63; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.00033;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVR 12

Db ||||| |||||

2 CFQWQRMNRKVR 13

RESULT 13

AAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:36.

XX Human; lactoferrin; modification; infection; inflammation; tumour;

KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 14 AA;

SQ Query Match 91.3%; Score 63; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00036;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVR 12

Db ||||| |||||

3 CFQWQRMNRKVR 14

RESULT 14

AAY78050

ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:50.

XX Human; lactoferrin; modification; infection; inflammation; tumour;

KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 14 AA;

Query Match 91.3%; Score 63; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00036;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12

DB 3 CFQWQRNMRKVR 14

RESULT 15

AAV78051

ID AAV78051 standard; Peptide; 14 AA.

XX AC AAV78051;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:51.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections, -  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 75; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 14 AA;

Query Match 91.3%; Score 63; DB 21; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.00036;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12

DB 3 CFQWQRNMRKVR 14

Search completed: February 21, 2003, 07:37:12

Job time : 28.35 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-74  
Perfect score: 69  
Sequence: 1 CFQQRAMKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	91.3	18	1	US-08-204-487-3
2	63	91.3	18	2	US-08-485-948-8
3	63	91.3	18	2	US-08-528-380-8
4	63	91.3	18	2	US-08-475-055-8
5	63	91.3	20	1	US-07-755-161A-3
6	63	91.3	20	1	US-07-891-174-3
7	63	91.3	20	1	US-08-204-487-1
8	63	91.3	20	1	US-08-256-771-24
9	63	91.3	20	1	US-08-256-771-25
10	63	91.3	20	1	US-08-381-984-24
11	63	91.3	20	1	US-08-381-984-25
12	63	91.3	22	4	US-09-508-734-4
13	63	91.3	24	4	US-09-508-734-6
14	63	91.3	25	1	US-07-755-161A-10
15	63	91.3	25	1	US-07-891-174-10
16	63	91.3	25	1	US-08-204-487-7
17	63	91.3	29	4	US-09-508-734-8
18	63	91.3	36	1	US-07-755-161A-8
19	63	91.3	36	1	US-07-891-174-8
20	63	91.3	36	1	US-08-256-771-30
21	63	91.3	36	1	US-08-381-984-29
22	63	91.3	47	2	US-08-464-182A-6
23	63	91.3	47	2	US-08-406-271-6
24	63	91.3	50	2	US-08-693-274A-7
25	63	91.3	52	4	US-09-017-043A-3
26	63	91.3	53	2	US-08-464-182A-5
27	63	91.3	53	2	US-08-406-271-5

28	63	91.3	54	2	US-08-464-182A-2
29	63	91.3	54	2	US-08-406-271-2
30	63	91.3	694	3	US-08-724-586-2
31	63	91.3	694	4	US-09-421-632-2
32	63	91.3	694	4	US-09-932-190-2
33	63	91.3	705	2	US-08-655-640-2
34	63	91.3	708	2	US-08-655-640-4
35	63	91.3	711	1	US-08-154-019-4
36	63	91.3	711	1	US-08-461-333-4
37	63	91.3	711	3	US-08-464-167-4
38	63	91.3	711	3	US-09-158-313-4
39	63	91.3	711	4	US-08-476-798-4
40	60	87.0	711	1	US-08-145-681-2
41	60	87.0	711	1	US-08-250-308-2
42	60	87.0	711	1	US-08-453-703-2
43	60	87.0	711	2	US-08-456-106-2
44	60	87.0	711	3	US-08-456-108-2
45	60	87.0	711	4	US-09-265-577-2

#### ALIGNMENTS

RESULT 1  
US-08-204-487-3  
; Sequence 3, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESS: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..18  
; OTHER INFORMATION: /note= "HUMAN LACTOPERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 91.3%; Score 63; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00012;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12  
|||||  
DB 1 CFQWQRMRKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/485,948  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LP-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 91.3%; Score 63; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00012;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12  
|||||  
DB 1 CFQWQRMRKVR 12

OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 91.3%; Score 63; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00012;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12  
|||||  
DB 1 CFQWQRMRKVR 12

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/485,948  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LP-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 91.3%; Score 63; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00012;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12  
|||||  
DB 1 CFQWQRMRKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI YONG MING  
; APPLICANT: VLASSARA, HELEN  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LP-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 91.3%; Score 63; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00012;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12  
|||||  
DB 1 CFQWQRMRKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-CI, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match          91.3%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12
Db 1 CFQWQRMRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURES:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match          91.3%; Score 63; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12  
| | | | | | | | | |  
Db 2 CFQWQRAMRKVR 13

RESULT 6  
US-07-891-174-3  
; Sequence 3, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Wenderoth, Lind & Ponack  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURES:  
; NAME/KEY: modified site

LOCATION: 2  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 19"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 19  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 2"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-3

Query Match 91.3%; Score 63; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12  
| | | | | | | | | |  
Db 2 CFQWQRAMRKVR 13

RESULT 7  
US-08-204-487-1  
; Sequence 1, Application US/08204487  
; Patent No. 5563425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: PJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1-20  
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE  
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"  
US-08-204-487-1

Query Match 91.3%; Score 63; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
Db 2 CFQWQRMKVR 13

RESULT 8  
US-08-256-771-24  
; Sequence 24, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are linked by  
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 91.3%; Score 63; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
Db 2 CFQWQRMKVR 13

RESULT 9  
US-08-256-771-25  
; Sequence 25, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

TELEX:  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are protected to  
OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25  
Query Match 91.3%; Score 63; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
Db 2 CFQWQRMKVR 13

RESULT 10  
US-08-381-984-24



; Sequence 24, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,984  
; FILING DATE: April 11, 1995  
; CLASSIFICATION: 252  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "cysteine residues at positions 2  
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
; US-08-381-984-24

Query Match 91.3%; Score 63; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12  
DB 2 CFQWQRMRKVR 13

RESULT 11  
US-08-381-984-25  
; Sequence 25, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,984  
; FILING DATE: April 11, 1995  
; CLASSIFICATION: 252  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "cysteine residues at positions 2  
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"  
; US-08-381-984-25

Query Match 91.3%; Score 63; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRKVR 12  
DB 2 CFQWQRMRKVR 13

RESULT 12  
US-09-508-734-4  
; Sequence 4, Application US/09508734  
; Patent No. 6423509  
; GENERAL INFORMATION:  
; APPLICANT: Samyang Genex Corporation  
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
; TITLE OF INVENTION: useful microorganism thereof  
; FILE REFERENCE: PA/SYG/00139  
; CURRENT APPLICATION NUMBER: US/09/508,734  
; CURRENT FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: PCT/KR99/00373  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: KR1998-29351  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 4

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;
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
Query Match          91.3%; Score 63; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 0.00015;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKVR 12
Db 2 CFQWQRAMRKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 643509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SVG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6
Query Match          91.3%; Score 63; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKVR 12
Db 3 CFQWQRAMRKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
Query Match          91.3%; Score 63; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00017;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKVR 12
Db 4 CFQWQRAMRKVR 15
```

RESULT 15  
US-07-891-174-10  
Sequence 10, Application US/07891174  
Patent No. 5317084  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptides and an  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/891,174  
FILING DATE: 29-MAY-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/755,161  
FILING DATE: 05-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 4  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 21"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 21

IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 4"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-10  
Query Match 91.3%; Score 63; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 0.00017;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CFQWRMRKVR 12  
Db 4 CFQWRMRKVR 15  
Search completed: February 21, 2003, 07:50:34  
Job time : 9.7 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35,508 Million cell updates/sec

Title: US-09-743-107B-74  
Perfect score: 69  
Sequence: 1 CFQWRMRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	91.3	15	9	US-09-798-869-2
2	63	91.3	25	9	US-09-798-869-20
3	63	91.3	694	9	US-10-023-098-2
4	55	79.7	15	9	US-09-798-869-6
5	53	76.8	15	9	US-09-798-869-3
6	53	76.8	25	9	US-09-798-869-23
7	45	65.2	15	9	US-09-798-869-7
8	44	63.8	15	9	US-09-798-869-4
9	44	63.8	25	9	US-09-798-869-22
10	41	59.4	15	9	US-09-798-869-8
11	41	59.4	15	9	US-09-798-869-29
12	41	59.4	15	9	US-09-798-869-30
13	37	53.6	21	10	US-09-864-761-47985
14	37	53.6	489	9	US-09-888-320-2
15	36	52.2	209	10	US-09-904-536-8
16	36	52.2	209	10	US-09-904-536-9
17	36	52.2	209	10	US-09-904-536-11
18	36	52.2	209	10	US-09-904-536-12
19	36	52.2	209	10	US-09-904-536-13

20	36	52.2	209	10	US-09-904-536-14
21	36	52.2	209	10	US-09-904-536-15
22	36	52.2	209	10	US-09-904-536-16
23	36	52.2	209	10	US-09-904-536-17
24	36	52.2	209	10	US-09-904-536-18
25	36	52.2	212	10	US-09-904-536-10
26	36	52.2	235	9	US-10-095-449-6
27	36	52.2	235	10	US-09-448-378-1
28	36	52.2	235	10	US-09-983-806-6
29	36	52.2	235	10	US-09-904-536-1
30	35	50.7	86	9	US-09-738-628-5715
31	35	50.7	1192	9	US-10-170-103-2
32	34	49.3	95	10	US-09-764-864-1031
33	34	49.3	846	9	US-10-051-409-4
34	34	49.3	1617	9	US-10-090-453A-2
35	33	47.8	15	9	US-09-798-869-5
36	33	47.8	46	10	US-09-864-761-48879
37	33	47.8	138	9	US-10-013-373-14
38	33	47.8	411	10	US-09-764-864-899
39	33	47.8	411	10	US-09-764-864-1346
40	33	47.8	978	9	US-09-938-901-8
41	32.5	47.1	124	10	US-09-864-761-44327
42	32	46.4	13	9	US-09-798-869-26
43	32	46.4	14	9	US-09-798-869-25
44	32	46.4	15	9	US-09-798-869-1
45	32	46.4	15	9	US-09-798-869-10

## ALIGNMENTS

RESULT 1					
US-09-798-869-2					
; Sequence 2, Application US/09798869					
; Publication No. US20030022821A1					
; GENERAL INFORMATION:					
; APPLICANT: JOHN SIGURD SVENDSEN					
; APPLICANT: (YSTEIN REKDAL					
; APPLICANT: BALDUR SVEINBJ (RNSSON					
; APPLICANT: LARS VORLAND					
; TITLE OF INVENTION: BIOACTIVE PEPTIDES					
; FILE REFERENCE: A34049-PCT-USA-A					
; CURRENT APPLICATION NUMBER: US/09/798,869					
; CURRENT FILING DATE: 2001-02-27					
; PRIOR APPLICATION NUMBER: PCT/GB99/02851					
; PRIOR FILING DATE: 1999-08-31					
; PRIOR APPLICATION NUMBER: GB9818938.4					
; PRIOR FILING DATE: 1998-08-28					
; NUMBER OF SEQ ID NOS: 30					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 2					
; LENGTH: 15					
; TYPE: PRT					
; ORGANISM: HOMO SAPIENS					
US-09-798-869-2					
Query Match					
Best Local Similarity 91.3%; Score 63; DB 9; Length 15;					
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy 1 CFQWRMRKVR 12					
Db 3 CFQWRMRKVR 14					
RESULT 2					
US-09-798-869-20					
; Sequence 20, Application US/09798869					
; Publication No. US20030022821A1					
; GENERAL INFORMATION:					
; APPLICANT: JOHN SIGURD SVENDSEN					
; APPLICANT: (YSTEIN REKDAL					
; APPLICANT: BALDUR SVEINBJ (RNSSON					

```
/ APPLICANT: LARS VORLAND
/ TITLE OF INVENTION: BIOACTIVE PEPTIDES
/ FILE REFERENCE: A34049-PCT-USA-A
/ CURRENT APPLICATION NUMBER: US/09/798,869
/ CURRENT FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: PCT/GB99/02851
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: GB9818938.4
/ PRIOR FILING DATE: 1998-08-28
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
/ US-09-798-869-20

Query Match      91.3%; Score 63; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12
   |||||
DB 3 CFQWQRAMRKVR 14

RESULT 3
US-10-023-096-2
/ Sequence 2, Application US/10023096
/ Patent No. US20020160941A1
/ GENERAL INFORMATION:
/ APPLICANT: Kruzel, Marian L.
/ APPLICANT: Kurecki, Tomasz
/ APPLICANT: Gollnick, Paul D.
/ APPLICANT: Doyle, Darrell J.
/ TITLE OF INVENTION: Cloning, Expression, and Uses of Human
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Jacobson, Price, Holman & Stern
/ STREET: 400 Seventh St. N.W.
/ CITY: Washington D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,096
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/724,586
/ FILING DATE: 30-SEPT-1996
/ APPLICATION NUMBER: US 08/238,445
/ FILING DATE: 05-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10505/P58185C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 638-6666
/ TELEFAX: (202) 393-5350
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 694 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-10-023-096-2
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Query Match      91.3%; Score 63; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12
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DB 22 CFQWQRAMRKVR 33

RESULT 4
US-09-798-869-6
/ Sequence 6, Application US/09798869
/ Publication No. US20030022821A1
/ GENERAL INFORMATION:
/ APPLICANT: JOHN SIGURD SVENDSEN
/ APPLICANT: (YSTEIN REKDAL
/ APPLICANT: BALDUR SVEINBJ (RNSSON
/ APPLICANT: LARS VORLAND
/ TITLE OF INVENTION: BIOACTIVE PEPTIDES
/ FILE REFERENCE: A34049-PCT-USA-A
/ CURRENT APPLICATION NUMBER: US/09/798,869
/ CURRENT FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: PCT/GB99/02851
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: GB9818938.4
/ PRIOR FILING DATE: 1998-08-28
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
/ OTHER INFORMATION: sequence)
/ US-09-798-869-6

Query Match      79.7%; Score 55; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRAMRKVR 12
   |||||
DB 3 CFQWQRAMRKVR 14

RESULT 5
US-09-798-869-3
/ Sequence 3, Application US/09798869
/ Publication No. US20030022821A1
/ GENERAL INFORMATION:
/ APPLICANT: JOHN SIGURD SVENDSEN
/ APPLICANT: (YSTEIN REKDAL
/ APPLICANT: BALDUR SVEINBJ (RNSSON
/ APPLICANT: LARS VORLAND
/ TITLE OF INVENTION: BIOACTIVE PEPTIDES
/ FILE REFERENCE: A34049-PCT-USA-A
/ CURRENT APPLICATION NUMBER: US/09/798,869
/ CURRENT FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: PCT/GB99/02851
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: GB9818938.4
/ PRIOR FILING DATE: 1998-08-28
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: CAPRINE
/ US-09-798-869-3

Query Match      76.8%; Score 53; DB 9; Length 15;
Best Local Similarity 72.7%; Pred. No. 0.0037;
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Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKV 11  
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Db 3 CYQWQRMRL 13

RESULT 6  
US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 76.8%; Score 53; DB 9; Length 25;  
Best Local Similarity 72.7%; Pred. No. 0.0062;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKV 11  
|:|||||:  
Db 3 CYQWQRMRL 13

RESULT 7  
US-09-798-869-7  
; Sequence 7, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-7

Query Match 65.2%; Score 45; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.084;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKV 11  
|:|||||:  
Db 3 CYQWQRMRL 13

RESULT 8  
US-09-798-869-4  
; Sequence 4, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-4

Query Match 63.8%; Score 44; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.12;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKV 11  
|:|||||:  
Db 3 CLRWQNMRL 13

RESULT 9  
US-09-798-869-22  
; Sequence 22, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-22

Query Match 63.8%; Score 44; DB 9; Length 25;  
Best Local Similarity 63.6%; Pred. No. 0.21;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRAMRKV 11  
|:|||||:  
Db 3 CLRWQNMRL 13

RESULT 10  
US-09-798-869-8  
; Sequence 8, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine  
; OTHER INFORMATION: sequence)  
US-09-798-869-8

Query Match 59.4%; Score 41; DB 9; Length 15;  
Best Local Similarity 63.6%; Pred. No. 0.4;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11  
|:|:|:|:|  
DB 3 CLRQWQWEMK 13

RESULT 11  
US-09-798-869-29  
; Sequence 29, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-29

Query Match 59.4%; Score 41; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.4;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11  
|:|:|:|:|  
DB 3 CFRQWQWEMK 13

RESULT 12  
US-09-798-869-30

; Sequence 30, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-30

Query Match 59.4%; Score 41; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.4;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11  
|:|:|:|:|  
DB 3 CFRQWQWEMK 13

RESULT 13  
US-09-864-761-47985  
; Sequence 47985, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn. Sharron G.  
; APPLICANT: Rankel, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661

;  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 47985  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL096701.14  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6  
; OTHER INFORMATION: EST\_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06  
US-09-864-761-47985

Query Match 53.6%; Score 37; DB 10; Length 21;  
Best Local Similarity 83.3%; Pred. No. 2.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CFQWQR 6  
| | | | |  
Db 16 CFQWRR 21

RESULT 14  
US-09-888-320-2  
; Sequence 2, Application US/09888320  
; Publication No. US20030013090A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry III, Clifton E.  
; APPLICANT: DeBarber, Andrea E.  
; APPLICANT: Mdululi, Khisimuzi  
; APPLICANT: Bekker, Linda-Gail  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis  
; FILE REFERENCE: 015280-413100US  
; CURRENT APPLICATION NUMBER: US/09/888,320  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/214,187  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: wild-type EtAa monooxygenase (RV3854c, EthA)  
US-09-888-320-2

Query Match 53.6%; Score 37; DB 9; Length 489;  
Best Local Similarity 54.5%; Pred. No. 63;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CFQWQRKV 11  
| | | | |  
Db 253 CQWPRRMRKM 263

RESULT 15  
US-09-904-536-8  
; Sequence 8, Application US/09904536  
; Patent No. US20020111475A1  
; GENERAL INFORMATION:

;  
; APPLICANT: Graddis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/904,536  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-536-8

Query Match 52.2%; Score 36; DB 10; Length 209;  
Best Local Similarity 50.0%; Pred. No. 40;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CFQWQRMRK 10  
| | | | |  
Db 178 CLHWQTRRR 187

Search completed: February 21, 2003, 08:08:04  
Job time : 10.55 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-74

Perfect score: 69

Sequence: 1 CFQWQRAMKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	63	91.3	711	1 TFHUL	lactotransferrin p
2	53	76.8	708	2 JC323	lactoferrin - goat
3	50	72.5	33	2 S52107	lactoferrin - sheep
4	44	63.8	707	1 A28438	lactoferrin precursor
5	43	62.3	4568	2 T08030	dynein beta heavy
6	42	60.9	1135	2 T14803	phytochrome C - so
7	41	59.4	275	2 T22597	hypothetical prote
8	41	59.4	932	2 T28820	hypothetical prote
9	40	58.0	1391	2 T20642	hypothetical prote
10	40	58.0	1397	2 H97998	protein F09C3.1 [i
11	39	56.5	206	2 E87451	pyridoxamine 5'-ph
12	39	56.5	206	2 AB3670	probable pyridoxam
13	39	56.5	208	2 AG3441	hypothetical prote
14	39	56.5	1746	2 D83181	kinase-related pro
15	39	56.5	2594	2 A35774	32K protein - vacc
16	38	55.1	275	2 A36415	hypothetical prote
17	38	55.1	377	2 T28558	35K myristylprotei
18	38	55.1	377	2 T37403	17L protein - var
19	38	55.1	377	2 F72165	hypothetical prote
20	38	55.1	378	2 T29518	hypothetical prote
21	38	55.1	433	2 T34605	ADP/ATP carrier pr
22	38	55.1	500	2 T71633	probable cytochrom
23	38	55.1	515	2 T00510	cytochrome P450 ho
24	38	55.1	543	2 AG0513	polymyxin B resist
25	37	53.6	85	2 AG0794	hypothetical prote
26	37	53.6	121	2 AH1417	hypothetical prote
27	37	53.6	202	2 C71306	33.3K hypothetical
28	37	53.6	289	2 G86403	probable dUDP-4-de
29	37	53.6	294	2 T00104	

#### RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

A/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence, revision 21-Nov-1997 #text, change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74: R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GE/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R/Rev, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5289, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52559; NID:G263311; PIDN:AAB24877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

hypothetical prote  
probable monooxyge  
probable carboxydr  
phytochrome - Scot  
kinase-related pro  
F1511.22 [imported  
hypothetical prote  
hypothetical prote  
probable glutathio  
hypothetical prote  
flt3 ligand - huma  
signal peptidase I  
interleukin-2 rece  
interleukin-2 rece  
gene 20 protein -  
hypothetical prote

#### ALIGNMENTS

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70, 989-993, 1987  
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A;Reference number: S07160; PMID:88001031; PMID:3477300  
 A;Accession: S07160  
 A;Molecule type: mRNA  
 A;Residues: 436-487, 'A', 489-711 <RAD>  
 A;Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855  
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51, 3037-3043, 1991  
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A;Reference number: A61169; PMID:91235214; PMID:1674448  
 A;Accession: A61169  
 A>Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 3-701, 'SWKPVN' <PAN>  
 A;Experimental source: normal breast tissue  
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;  
 Eur. J. Biochem. 145, 659-666, 1984  
 A>Title: Human lactotransferrin: amino acid sequence and structural comparisons with other  
 A;Reference number: A31000; PMID:85076667; PMID:6510420  
 A;Accession: A31000  
 A;Molecule type: protein  
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4  
 A;Note: this is the final paper in a series  
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.  
 Eur. J. Biochem. 241, 303-308, 1996  
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity  
 A;Reference number: S74119; PMID:97054624; PMID:8898921  
 A;Accession: S74119  
 A;Molecule type: protein  
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A;Experimental source: neutrophil granulocytes  
 C;Genetics:  
 A;Gene: GDB:150210  
 A;Cross-references: GDB:119368; OMIM:150210  
 A;Map position: 3q21-3q23  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein; iron binding; milk  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-71/Product: lactotransferrin #status experimental <MAT>  
 F;21-356/Domain: transferrin repeat homology <TRH1>  
 F;360-699/Domain: transferrin repeat homology <TRH2>  
 F;29-65, 39-55, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status  
 F;157-498/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;358-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 91.3%; Score 63; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.0023;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQARMKRV 12  
 DB 39 CFQWQARMKRV 50  
 |||||  
 |||||

RESULT 2  
 JC2323  
 lactoferrin - goat  
 C;Species: Capra aegagrus hircus (domestic goat)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C;Accession: JC2323  
 R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.  
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994  
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus  
 A;Reference number: JC2323; PMID:94380047; PMID:8093048  
 A;Accession: JC2323  
 A;Molecule type: mRNA  
 A;Residues: 1-708 <LEP>  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein  
 F;359-696/Domain: transferrin repeat homology <TRH2>  
 F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.8%; Score 53; DB 2; Length 708;  
 Best Local Similarity 72.7%; Pred. No. 0.14;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQARMKRV 11  
 DB 38 CYQWQARMKRL 48  
 |||||  
 |||||

## RESULT 3

S52107  
 lactoferrin - sheep (fragment)  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 14-Jul-1995 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997  
 C;Accession: S52107  
 R;Olan, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.  
 Biochim. Biophys. Acta 1243, 25-32, 1995  
 A>Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet  
 A;Reference number: S52107; PMID:95127729; PMID:7827104  
 A;Accession: S52107  
 A>Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-33 <OJA>  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication

Query Match 72.5%; Score 50; DB 2; Length 33;  
 Best Local Similarity 63.6%; Pred. No. 0.024;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQARMKRV 11  
 DB 19 CYQWQARMKRL 29  
 |||||  
 |||||

## RESULT 4

A28438  
 lactoferrin precursor - mouse  
 N;Alternate names: lactotransferrin  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A28438; A41205  
 R;Pentecost, B.T.; Teng, C.T.  
 J. Biol. Chem. 262, 10134-10139, 1987  
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret  
 A;Reference number: A92596; PMID:87280033; PMID:3611056  
 A;Accession: A28438  
 A;Molecule type: mRNA  
 A;Residues: 3-707 <PEN>  
 C;Cross-references: EMBL:J03298  
 R;Liu, Y.; Teng, C.T.  
 J. Biol. Chem. 266, 21880-21885, 1991  
 A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.  
 A;Reference number: A41205; PMID:92042099; PMID:1939212  
 A;Accession: A41205  
 A;Molecule type: DNA  
 A;Residues: 1-15 <LIU>  
 A;Cross-references: GB:M74778  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-707/Product: lactotransferrin #status predicted <MAT>  
 F;358-695/Domain: transferrin repeat homology <TRH2>  
 F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.8%; Score 44; DB 1; Length 707;  
 Best Local Similarity 63.8%; Pred. No. 5.7;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQARMKRV 11  
 DB 37 CLRQWARMKRV 47  
 |||||  
 |||||

Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: D83181  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1746 <STO>  
A;Cross-references: GB:AE004791; GB:AE004091; NID:g9949882; PIDN:AAG07115.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3728

Query Match 56.5%; Score 39; DB 2; Length 1746;  
Best Local Similarity 60.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FQWQAMRKV 11  
|:|||||:  
Db 205 FEWQATREM 214

## RESULT 15

A35774  
Kinase-related protein sevenless - fruit fly (*Drosophila virilis*)  
C;Species: *Drosophila virilis*  
C;Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_charge 24-Apr-1998  
C;Accession: A35774  
R;Michael, W.M.; Bowtell, D.D.L.; Rubin, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5351-5353, 1990  
A;Title: Comparison of the sevenless genes of *Drosophila virilis* and *Drosophila melanoga*  
A;Reference number: A35774; MUID:90319110; PMID:2115169  
A;Accession: A35774  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-2594 <MIC>  
A;Cross-references: GB:M34543  
C;Genetics:  
A;Gene: FlyBase:Dvir/sev  
A;Cross-references: FlyBase:FBgn0013140  
C;Superfamily: sevenless; fibronectin type III repeat homology; LDL receptor YWTD-contai  
C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein  
E;9-26/Region: glutamine-rich  
E;465-555/Domain: fibronectin type III repeat homology <FN3>  
F;2222-2499/Domain: protein kinase homology <KIN>  
F;2230-2238/Region: protein kinase ATP-binding motif

Query Match 56.5%; Score 39; DB 2; Length 2594;  
Best Local Similarity 45.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQAMRKV 11  
|:|||||:  
Db 305 CAQWYALKKEI 315

Search completed: February 21, 2003, 07:47:45  
Job time : 10.65 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107b-74  
Perfect score: 69  
Sequence: 1 CFQWRAMRVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	63	91.3	711	1 TRFL_HUMAN
2	53	76.8	708	1 TRFL_CAMDR
3	53	76.8	708	1 TRFL_CAPHI
4	44	63.8	707	1 TRFL_MOUSE
5	43	62.3	4568	1 DYHB_CHLRE
6	42	60.9	1135	1 PHYC_SORBI
7	40	58.0	1137	1 PHYC_ORYSA
8	39	56.5	292	1 NLA_DROME
9	39	56.5	2594	1 7LES_DROVI
10	38	55.1	146	1 RPOB_LIBAF
11	38	55.1	275	1 VA16_VACCV
12	38	55.1	378	1 VA16_VACCC
13	38	55.1	500	1 TLCE_RICPR
14	38	55.1	695	1 TRFL_HORSE
15	37	53.6	85	1 PMRD_SALTY
16	37	53.6	1131	1 PHY_PINSV
17	37	53.6	2554	1 7LES_DROME
18	36	52.2	214	1 YFCF_ECOLI
19	36	52.2	235	1 FL3L_HUMAN
20	36	52.2	275	1 IL2A_BOVIN
21	36	52.2	275	1 IL2A_SHEEP
22	36	52.2	303	1 UL24_HSVPA
23	36	52.2	538	1 RO60_HUMAN
24	36	52.2	538	1 RO60_MOUSE
25	36	52.2	538	1 RO60_XENIA
26	36	52.2	1111	1 PHYB_ARATH
27	36	52.2	1156	1 PHYB_SOYEN
28	36	52.2	1164	1 PHYB_ARATH
29	36	52.2	1172	1 PHYB_ARATH
30	36	52.2	1179	1 ATX1_ARATH
31	35	50.7	211	1 LOLS_VIBCH
32	35	50.7	270	1 PDXH_MYXXA
33	35	50.7	306	1 BUB2_YEAST

## RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788;	Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;		
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUN-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RL	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RT	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RL	"Molecular cloning and sequence analysis of human lactoferrin.";			
RN	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RL	"Human neutrophil lactoferrin coding and 5' flanking region DNA sequences.";			
RN	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RL	"cDNA cloning and sequence analysis of human lactoferrin.";			
RN	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Straussberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

34	35	50.7	317	1	MOCA_RHIME	P49307 rhizobium m
35	35	50.7	363	1	CTNS_DROME	O9YCR7 drosophila
36	35	50.7	435	1	DCOR_PANRE	P43725 panagrellus
37	35	50.7	502	1	C911_ARATH	Q9EG65 arabidopsis
38	35	50.7	558	1	NCAP_LYCV	P09992 lymphocytic
39	35	50.7	558	1	NCAP_LYCV	P07400 lymphocytic
40	35	50.7	601	1	WD66_PHYPO	P90587 physarum po
41	35	50.7	805	1	L100_ADE02	P24932 human adeno
42	35	50.7	807	1	L100_ADE05	P24933 human adeno
43	35	50.7	1121	1	PHY2_CERPU	Q39557 ceratodon p
44	35	50.7	1132	1	PHY1_PHYPA	P36505 physcomitre
45	35	50.7	1355	1	ATC3_YEAST	P39524 saccharomyc

## ALIGNMENTS

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Ogden J.E.;  
RL "Nucleotide sequence of human lactoferrin cDNA.";  
RN Nucleic Acids Res. 18:4013-4013(1990).  
[9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
RA Metz-Boutigue M.-H., Jolles J., Jolles P.;  
RL "Human lactotransferrin: amino acid sequence and structural  
RT comparisons with other transferrins.";  
RL Eur. J. Biochem. 145:659-666(1994).  
[10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
RA Jolles P.;  
RL "The present state of the human lactotransferrin sequence. Study and  
RT alignment of the cyanogen bromide fragments and characterization of  
RT N- and C-terminal domains.";  
RL Biochim. Biophys. Acta 670:243-254(1981).  
[11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
RA Jolles P.;  
RL "An 88 amino acid long C-terminal sequence of human  
RT lactotransferrin.";  
RL FEBS Lett. 142:107-110(1982).  
[12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Radó T.A., Wei X., Benz E.J. Jr.;  
RL "Isolation of lactoferrin cDNA from a human myeloid library and  
RT expression of mRNA during normal and leukemic myelopoiesis.";  
RL Blood 70:989-993(1987).  
[13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie M.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang X., Porcel B.M.,  
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RA Sagripanti J.L.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
[14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2585506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RL "Structure of human lactoferrin: crystallographic structure analysis  
RT and refinement at 2.8-A resolution.";  
RL J. Mol. Biol. 209:711-734(1989).  
[15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RL "Structure of human diferric lactoferrin refined at 2.2-A  
RT resolution.";  
RL Acta Crystallogr. D 51:629-646(1995).  
[16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
RA Baker E.N.;  
RL "Mutagenesis of the histidine ligand in human lactoferrin: iron  
RT binding properties and crystal structure of the histidine-  
RT 253->methionine mutant.";  
RL Biochemistry 36:341-346(1997).  
[17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RL "Structure of recombinant human lactoferrin expressed in Aspergillus  
RT awamori.";  
RL Acta Crystallogr. D 55:403-407(1999).  
[18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RL "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
RT and analysis of ligand-induced conformational change.";  
RL Acta Crystallogr. D 54:1319-1335(1998).  
[19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RL "Isolation and characterization of opioïd antagonist peptides derived  
RT from human lactoferrin.";  
RL Agric. Biol. Chem. 54:1803-1810(1990).  
[20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Kluntworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,  
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejmancik J.F., Teng C.T.;  
RL "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RL Mol. Vision 4:31-32(1998).  
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
CC OF AN ANION, USUALLY BICARBONATE.  
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST  
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
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DR EMBL; X53961; CAA37914.1; -;  
DR EMBL; U07643; AAB60324.1; -;  
DR EMBL; M93150; AAA36159.1; -;  
DR EMBL; M83202; AAA59511.1; -;  
DR EMBL; M83205; AAA58656.1; -;  
DR EMBL; M18642; AAA86665.1; -;  
DR EMBL; AF332168; AAG48753.1; -;  
DR EMBL; EC015822; AAH15822.1; -;  
DR EMBL; BC015823; AAH15823.1; -;  
DR EMBL; M73700; AAA59479.1; -;  
DR EMBL; X52941; CAA37116.1; -;  
DR EMBL; U95626; AAB57795.1; -;  
DR PIR; S1128; TFFUL;  
DR PDB; 1LCF; 31-AUG-94.  
DR PDB; 1LCT; 31-OCT-93.  
DR PDB; 1LFG; 31-JUL-94.  
DR PDB; 1LFH; 31-OCT-93.  
DR PDB; 1LFI; 31-OCT-93.  
DR PDB; 1LGB; 31-AUG-94.  
DR PDB; 1LGC; 31-AUG-94.  
DR PDB; 1BKA; 08-NOV-96.  
DR PDB; 1DSN; 08-MAR-96.  
DR PDB; 1HSE; 12-MAR-97.  
DR PDB; 1VFD; 21-APR-97.

Query Match 91.3%; Score 63; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00073;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
 |||||  
 DB 39 CFQWQRMKVR 50

RESULT 2  
 ID TRFL CAMDR STANDARD; PRT; 708 AA.  
 AC Q9TUMG; Q9MZS5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN Lf.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 OF AN ANION. USUALLY BICARBONATE (BY SIMILARITY).  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; AJ131674; CAB53387.1; -;  
 DR EMBL; AF165879; AAF82241.1; -;  
 DR HSSP; 077811; 1B1X.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER\_2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 Signal.  
 FT SIGNAL 1 19 BY SIMILARITY.  
 FT CHAIN 20 708 LACTOTRANSFERRIN.  
 FT REPEAT 20 363 1.  
 FT REPEAT 364 708 2.  
 FT REPEAT 28 64 BY SIMILARITY.  
 FT DISULFID 38 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 080C175A0B69D430 CRC64;

Query Match 76.8%; Score 53; DB 1; Length 708;  
 Best Local Similarity 75.0%; Pred. No. 0.046;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
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 DB 38 CAQWQRMKVR 49

RESULT 3  
 ID TRFL CAPHI STANDARD; PRT; 708 AA.  
 AC Q29477; Q29479;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=94380047; PubMed=8093048;  
 RA le Provost F., Noca M., Guerin G., Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the  
 relevant locus to bovine U12 synteny group.";  
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 OF AN ANION. USUALLY BICARBONATE.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.

```

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC -----
CC EMBL; U53857; AAA97958.1; --
CC EMBL; X78902; CAA55517.1; --
CC DR HSP; 077698; 1CE2.
CC DR InterPro; IPR001156; Transferrin.
CC DR Pfam; PF00405; transferrin; 2.
CC DR PRINTS; PR00422; TRANSFERRIN.
CC DR SMART; SM00094; TR_FER; 2.
CC DR PROSITE; PS00205; TRANSFERRIN_1; 2.
CC DR PROSITE; PS00206; TRANSFERRIN_2; 2.
CC DR PROSITE; PS00207; TRANSFERRIN_3; 2.
CC KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
CC Signal.
CC FT SIGNAL 1 19 BY SIMILARITY.
CC FT CHAIN 20 708 LACTOTRANSFERRIN.
CC FT REPEAT 20 363 1.
CC FT REPEAT 364 708 2.
CC FT DISULFID 28 64 BY SIMILARITY.
CC FT DISULFID 38 55 BY SIMILARITY.
CC FT DISULFID 134 217 BY SIMILARITY.
CC FT DISULFID 176 192 BY SIMILARITY.
CC FT DISULFID 189 200 BY SIMILARITY.
CC FT DISULFID 250 264 BY SIMILARITY.
CC FT DISULFID 367 399 BY SIMILARITY.
CC FT DISULFID 377 390 BY SIMILARITY.
CC FT DISULFID 424 703 BY SIMILARITY.
CC FT DISULFID 444 666 BY SIMILARITY.
CC FT DISULFID 476 551 BY SIMILARITY.
CC FT DISULFID 500 694 BY SIMILARITY.
CC FT DISULFID 510 524 BY SIMILARITY.
CC FT DISULFID 521 534 BY SIMILARITY.
CC FT DISULFID 592 606 BY SIMILARITY.
CC FT DISULFID 644 649 BY SIMILARITY.
CC FT METAL 79 79 IRON 1 (BY SIMILARITY).
CC FT METAL 111 111 IRON 1 (BY SIMILARITY).
CC FT METAL 211 211 IRON 1 (BY SIMILARITY).
CC FT METAL 272 272 IRON 1 (BY SIMILARITY).
CC FT METAL 414 414 IRON 2 (BY SIMILARITY).
CC FT METAL 452 452 IRON 2 (BY SIMILARITY).
CC FT METAL 545 545 IRON 2 (BY SIMILARITY).
CC FT METAL 614 614 IRON 2 (BY SIMILARITY).
CC FT BINDING 140 140 ANION (BY SIMILARITY).
CC FT BINDING 482 482 ANION (BY SIMILARITY).
CC FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 495 495 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 564 564 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CONFLICT 56 56 I -> V (IN REF. 2).
CC FT CONFLICT 88 88 L -> R (IN REF. 2).
CC FT CONFLICT 124 124 Q -> K (IN REF. 2).
CC FT CONFLICT 154 154 F -> P (IN REF. 2).
CC FT CONFLICT 304 304 S -> R (IN REF. 2).
CC FT CONFLICT 414 414 D -> G (IN REF. 2).
CC FT SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;
CC -----
CC Query Match 76.8%; Score 53; DB 1; Length 708;
CC Best Local Similarity 72.7%; Pred. No. 0.046;
CC Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 CFQWQRMARKV 11
CC |:|||||:
CC Db 38 CYQWQRMARKL 48

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RESULT 4
TRFL_MOUSE STANDARD; PRT; 707 AA.
ID TRFL_MOUSE AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (lactoferrin).
GN Ltf.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA MEDLINE=87280033; PubMed=3611056;
RX Pentecost B.T.; Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
RT uterine secretions.";
EL J. Biol. Chem. 262:10134-10139 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishita K.;
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RN [4]
RP Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RX SEQUENCE OF 1-14 FROM N.A.
RA MEDLINE=92042099; PubMed=19392112;
RT Liu Y.; Teng C.T.;
RL "Characterization of estrogen-responsive mouse lactoferrin promoter.";
CC J. Biol. Chem. 266:21880-21885 (1991).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03298; AAA40525.1; --
CC EMBL; D88510; BAA13633.1; --
CC EMBL; BC006904; AAH06904.1; --
CC EMBL; M74778; AAA39427.1; --
CC PIR; A28438; A28436.
CC HSSP; P02788; 1CB6.
CC MGD; MGI:96837; Ltf.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 1.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
CC KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
CC Signal.
CC FT SIGNAL 1 19 BY SIMILARITY.
CC FT CHAIN 20 707 LACTOTRANSFERRIN.
CC FT REPEAT 20 357 1.

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FT REPEAT 358 707
FT DISULFID 27 63
FT DISULFID 37 54
FT DISULFID 133 216
FT DISULFID 178 191
FT DISULFID 188 199
FT DISULFID 249 263
FT DISULFID 366 398
FT DISULFID 376 389
FT DISULFID 423 702
FT DISULFID 443 665
FT DISULFID 479 550
FT DISULFID 499 693
FT DISULFID 509 523
FT DISULFID 520 533
FT DISULFID 591 605
FT DISULFID 643 648
FT METAL 78 78
FT METAL 110 110
FT METAL 210 210
FT METAL 271 271
FT METAL 413 413
FT METAL 451 451
FT METAL 544 544
FT METAL 613 613
FT METAL 139 139
FT BINDING 481 481
FT CARBOHYD 118 118
FT CARBOHYD 494 494
FT CONFLICT 1 2
FT CONFLICT 25 25
FT CONFLICT 82 82
FT CONFLICT 359 359
FT CONFLICT 382 382
FT CONFLICT 449 449
FT CONFLICT 629 629
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340AC19A8 CRC64;

Query Match 63.8%; Score 44; DB 1; Length 707;
Best Local Similarity 63.6%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWGRMRKV 11
Db 37 CLRQWNRKV 47

RESULT 5
ID_DYHB_CHLRE STANDARD; PRT; 4568 AA.
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21gr;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes";
RL J. Cell Sci. 107:635-644(1994).
CC -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

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CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC -----
DR EMBL; U02963; AAA19956.1; -.
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 62.3%; Score 43; DB 1; Length 4568;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWGRMRKV 12
Db 1852 CFQWSQLRYIQ 1863

RESULT 6
ID_PHYC_SORBI STANDARD; PRT; 1135 AA.
AC P93528;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97198556; PubMed=9046599;
RA Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
RA Morgan P.W., Millet J.E.;
RT "The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";
RL Plant Physiol. 113:611-619(1997).
CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCOVERSION OF PR IN PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RUBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY

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CC SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC
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CC
CC EMBL: U56731; AAB41399.1;
CC InterPro: IPR003594; ATPbind_ATPase.
CC InterPro: IPR003018; GAF.
CC InterPro: IPR004359; HIS_KIN_sig.
CC InterPro: IPR003661; His_kinA.
CC InterPro: IPR001610; PAC.
CC InterPro: IPR000014; PAS domain.
CC InterPro: IPR001294; Phytochrome.
CC Pfam: PF00360; Phytochrome; 1.
CC Pfam: PF00512; signal; 1.
CC Pfam: PF00989; PAS; 2.
CC Pfam: PF01590; GAF; 1.
CC Pfam: PF02518; HATPase_c; 1.
CC PRINTS: PR01033; PHYTOCHROME.
CC SMART: SM00065; GAF; 1.
CC SMART: SM00387; HATPase_c; 1.
CC SMART: SM00388; HSKA; 1.
CC SMART: SM00086; PAC; 1.
CC SMART: SM00091; PAS; 2.
CC TIGRFS: TIGR00229; sensory_box; 2.
CC PROSITE: PS50109; HIS_KIN; 1.
CC PROSITE: PS00245; PHYTOCHROME_1; FALSE_NEG.
CC PROSITE: PS0046; PHYTOCHROME_2; 1.
CC Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
KW Repeat; Multigene family.
FT DOMAIN 618 688 PAS 1.
FT DOMAIN 748 822 PAS 2.
FT DOMAIN 902 1122 HISTIDINE KINASE.
FT BINDING 321 321 CHROMOPHORE (BY SIMILARITY).
SQ SEQUENCE 1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;

Query Match 60.9%; Score 42; DB 1; Length 1135;
Best Local Similarity 45.5%; Pred. No. 7.2;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQWQAMRKV 11
Db 775 CLEWKAQKX 785
| : : : :
| : : : :

RESULT 7
PHYC_ORYSA STANDARD; PRT; 1137 AA.
AC Q9ZWI9; P93429;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Cryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=cv. Nipponbare;
RA Tahir M., Kanegae H., Takano M.;
RT "Phytochrome C (PHYC) gene in rice: isolation and characterization of
RT a complete coding sequence.";
RL (In) Plant Gene Register PGR98-210.
RN [2]
RP SEQUENCE OF 275-378 FROM N.A.
RX MEDLINE=97019052; PubMed=8865668;
RA Mathews S., Sharrock R.A.;
RT "The phytochrome gene family in grasses (Poaceae): a phylogeny and
RT evidence that grasses have a subset of the loci found in dicot
RT angiosperms";
RL Mol. Biol. Evol. 13:1141-1150(1996).
CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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CC
CC EMBL: AB018442; BAB74448.1;
CC EMBL: U61207; AAB41996.1;
CC InterPro: IPR003594; ATPbind_ATPase.
CC InterPro: IPR003018; GAF.
CC InterPro: IPR004359; HIS_KIN_sig.
CC InterPro: IPR003661; His_kinA.
CC InterPro: IPR001610; PAC.
CC InterPro: IPR000014; PAS domain.
CC InterPro: IPR001294; Phytochrome.
CC Pfam: PF00360; phytochrome; 1.
CC Pfam: PF00512; signal; 1.
CC Pfam: PF00989; PAS; 2.
CC Pfam: PF01590; GAF; 1.
CC Pfam: PF02518; HATPase_c; 1.
CC PRINTS: PR01033; PHYTOCHROME.
CC SMART: SM00065; GAF; 1.
CC SMART: SM00387; HATPase_c; 1.
CC SMART: SM00388; HSKA; 1.
CC SMART: SM00086; PAC; 1.
CC SMART: SM00091; PAS; 2.
CC TIGRFS: TIGR00229; sensory_box; 2.
CC PROSITE: PS50109; HIS_KIN; 1.
CC PROSITE: PS00245; PHYTOCHROME_1; 1.
CC PROSITE: PS0046; PHYTOCHROME_2; 1.
KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
KW Repeat; Multigene family.
FT DOMAIN 620 690 PAS 1.
FT DOMAIN 750 824 PAS 2.
FT DOMAIN 904 1124 HISTIDINE KINASE.
FT BINDING 322 322 CHROMOPHORE (BY SIMILARITY).
FT CONFLICT 279 279 F -> S (IN REF. 2).
FT CONFLICT 292 292 C -> S (IN REF. 2).
SQ SEQUENCE 1137 AA; 125982 MW; F2A520181CFE7B32 CRC64;

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DR InterPro; IPR000033; Ldl receptor_rep.
DR InterPro; IPR002811; RTKinase1.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk pkinase; 1.
DR SMART; SM00060; FN3; 5.
DR SMART; SM00135; LV; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR Transferrase; Tyrosine-protein kinase; Receptor; Vision; Transmembrane;
KW Glycoprotein; ATP-binding; Phosphorylation; Repeat.
PT DOMAIN 1 2139
PT DOMAIN 2 2140
PT TRANSMEM 2140 2163
FT DOMAIN 2164 2594
FT DOMAIN 2164 2594
FT DOMAIN 26 26
FT DOMAIN 356 459
FT DOMAIN 454 555
FT DOMAIN 835 935
FT DOMAIN 1328 1421
FT DOMAIN 1706 1816
FT DOMAIN 1817 1916
FT DOMAIN 1917 2007
FT DOMAIN 2057 2063
FT DOMAIN 2224 2495
FT NP_BIND 2230 2238
FT BINDING 2257 2257
FT MOD_RES 2391 2391
FT CARBOHYD 77 77
FT CARBOHYD 401 401
FT CARBOHYD 508 508
FT CARBOHYD 532 532
FT CARBOHYD 641 641
FT CARBOHYD 667 667
FT CARBOHYD 778 778
FT CARBOHYD 797 797
FT CARBOHYD 874 874
FT CARBOHYD 980 980
FT CARBOHYD 1257 1257
FT CARBOHYD 1344 1344
FT CARBOHYD 1382 1382
FT CARBOHYD 1577 1577
FT CARBOHYD 1587 1587
FT CARBOHYD 1665 1665
FT CARBOHYD 1752 1752
FT CARBOHYD 1776 1776
FT CARBOHYD 1824 1824
FT CARBOHYD 1908 1908
FT CARBOHYD 1966 1966
FT CARBOHYD 2088 2088
FT CARBOHYD 2088 2088
SQ SEQUENCE 2594 AA; 289130 MW; 77D8A356CBAD0BBD CRC64;

Query Match 56.5%; Score 39; DB 1; Length 2594;
Best Local Similarity 45.5%; Pred. No. 58;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRARMKV 11
DB 305 CAQWYRAKKEI 315

RESULT 10
RPOB_LIBAF
ID RPOB_LIBAF STANDARD; PRT; 146 AA.
AC P41187;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit) (Fragment).

GN RPOB.
OS Liberibacter africanus (Liberibacter africanum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Candidatus Liberibacter.
OX NCBI_TaxID=34020;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nelpelut;
RA Planet P., Jagueix S., Bove J.M., Garnier M.;
RT Detection and characterization of the African Citrus Greening
RT Liberibacter by amplification, cloning and sequencing of the rplKJL-
RT rpoBC operon.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC
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CC
CC EMBL; U09675; AAA19557.1; -
CC InterPro; IPR001572; RNA_pol_B.
CC Pfam; PF00562; RNA_pol_B; 1.
CC PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
CC Transferrase; Transcription; DNA-directed RNA polymerase.
CC NON_TER 146 146
CC SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWRARMK 10
DB 10 CVQWSRGARK 19

RESULT 11
ID VAL6_VACCV STANDARD; PRT; 275 AA.
AC P16710;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein A16 (Fragment).
DE A16L.
OS Vaccinia virus (strain WR).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90317884; PubMed=2370683;
RA Pacha R.F., Meis R.J., Condit R.C.;
RT "Structure and expression of the vaccinia virus gene which prevents
RT virus-induced breakdown of RNA.";
RL J. Virol. 64:3853-3863(1990).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.
CC
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DR EMBL; M32064; AAA48348.2; -.  
DR PIR; A36415; A36415.  
DR InterPro; IPR004251; DUF230.  
DR Pfam; PF03003; DUF230; 1.  
FT NON TER 275 275  
SQ SEQUENCE 275 AA; 31811 MW; E2461AB1DB7B93A3 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 275;  
Best Local Similarity 60.0%; Pred.No. 8.8;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRAVRK 10  
DB 185 CLEWLRARXK 194

## RESULT 12

ID VAL6 VACCC STANDARD; PRT; 378 AA.  
AC P20923;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Protein A16.  
GN A16L.  
OS Vaccinia virus (strain Copenhagen).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10249;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91021027; PubMed=2219722;  
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
RA Paoletti E.;  
RT "The complete DNA sequence of vaccinia virus.";  
RL Virology 179:247-266(1990).  
RN [2]  
RP COMPLETE GENOME.  
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
RA Paoletti E.;  
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";  
RL Virology 179:517-563(1990).  
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.

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DR EMBL; M35027; AAA48138.1; -.  
DR PIR; I42518; I42518.  
DR InterPro; IPR004251; DUF230.  
DR Pfam; PF03003; DUF230; 1.  
SQ SEQUENCE 378 AA; 43561 MW; 05ED614AA1D11A19 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 378;  
Best Local Similarity 60.0%; Pred.No. 12;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRAVRK 10  
DB 185 CLEWLRARXK 194

## RESULT 13

TLCE RICPR STANDARD; PRT; 500 AA.  
ID AC 005962;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE ADP, ATP carrier protein 5 (ADP/ATP translocase 5).  
GN TLCE OR TLCS OR RP739.  
OS Rickettsia prowazekii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=782;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Madrid E;  
RX MEDLINE=99039499; PubMed=9823893;  
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,  
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,  
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
RT "The genome sequence of Rickettsia prowazekii and the origin of  
RT mitochondria.";  
RL Nature 396:133-140(1998).  
RN [2]  
RP SEQUENCE OF 325-500 FROM N.A.  
RC STRAIN=Madrid E;  
RX MEDLINE=97419517; PubMed=9274032;  
RA Andersson J.O., Andersson S.G.E.;  
RT "Genomic rearrangements during evolution of the obligate  
RT intracellular parasite Rickettsia prowazekii as inferred from an  
RT analysis of 52015 bp nucleotide sequence.";  
RL Microbiology 143:2783-2795(1997).  
CC -1- FUNCTION: PROVIDES THE RICKETTSIAL CELL WITH HOST ATP IN  
CC EXCHANGE FOR RICKETTSIAL ADP. THIS IS AN OBLIGATE EXCHANGE SYSTEM.  
CC THIS ENERGY ACQUIRING ACTIVITY IS AN IMPORTANT COMPONENT OF  
CC RICKETTSIAL PARASITISM (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE ADP/ATP TRANSLOCASE TLC FAMILY.

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DR EMBL; AJ235273; CAA15167.1; -.  
DR EMBL; Y11778; CAA72457.1; -.  
DR InterPro; IPR004667; ADP\_ATP\_car.  
DR Pfam; PF03219; TLC; 1.  
DR TIGRfam; TIGR00769; AAA; 1.  
KW Transmembrane; Transport; ATP-binding; Multigene family;  
FT TRANSMEM 26 46 POTENTIAL.  
FT TRANSMEM 62 82 POTENTIAL.  
FT TRANSMEM 94 114 POTENTIAL.  
FT TRANSMEM 149 169 POTENTIAL.  
FT TRANSMEM 184 204 POTENTIAL.  
FT TRANSMEM 224 244 POTENTIAL.  
FT TRANSMEM 287 307 POTENTIAL.  
FT TRANSMEM 328 348 POTENTIAL.  
FT TRANSMEM 357 377 POTENTIAL.  
FT TRANSMEM 381 401 POTENTIAL.  
FT TRANSMEM 469 489 POTENTIAL.  
SQ SEQUENCE 500 AA; 57073 MW; FE3DB48D08CF5F72 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 500;  
Best Local Similarity 54.5%; Pred.No. 16;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRAVRK 11  
DB 482 CFAMTYAVRK 492

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DR EMBL; U02281; AAA21322.1; --  
DR EMBL; AE008603; AAL21205.1; --  
DR StyGene; SG10304; pmrD.  
KW Antibiotic resistance; Complete proteome.  
SQ SEQUENCE 85 AA; 9749 MW; 1E1922419EA50CCA CRC64;

Query Match 53.6%; Score 37; DB 1; Length 85;  
Best Local Similarity 60.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 CFQWQRAWRK 10  
| : ||| |  
Db 74 CDEWQLTRK 83

Search completed: February 21, 2003, 07:27:48  
Job time : 5.6 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107B-74

Perfect score: 69

Sequence: 1 CFQWQRMKRV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTEMBL 21.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_mhc.\*  
9: sp\_organelle.\*  
10: sp\_phase.\*  
11: sp\_plant.\*  
12: sp\_rodent.\*  
13: sp\_virus.\*  
14: sp\_vertebrate.\*  
15: sp\_unclassified.\*  
16: sp\_rvirus.\*  
17: sp\_bacteriap.\*  
18: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	84.1	711	4 Q8TCD2	Q8tcd2 homo sapien
2	54	78.3	38	4 Q9UCY5	Q9ucy5 homo sapien
3	50	72.5	33	6 Q9TR80	Q9tr80 ovis aries
4	42	60.9	1121	10 Q9SWS6	Q9sws6 lycopersico
5	41	59.4	105	10 Q9XFD5	Q9xfds oryza sativ
6	41	59.4	148	10 Q9XHP1	Q9xhpl sesamum ind
7	41	59.4	275	5 Q93780	Q93780 caenorhabdi
8	41	59.4	932	5 Q19153	Q19153 caenorhabdi
9	40	58.0	279	16 Q8XSE2	Q8xse2 ralstonia s
10	40	58.0	830	10 Q945T7	Q945t7 hordeum vul
11	40	58.0	1137	10 Q9M7A9	Q9m7a9 oryza sativ
12	40	58.0	1139	10 Q9VMN1	Q9vmn1 triticum ae
13	40	58.0	1391	5 O17772	O17772 caenorhabdi
14	39	56.5	205	16 Q986A0	Q986a0 rhizobium l
15	39	56.5	206	16 Q8UHC2	Q8unc2 agrobacteri
16	39	56.5	206	16 Q92RH8	Q92rh8 rhizobium m

17	39	56.5	208	16 Q8YFK3	Q8yfk3 brucella me
18	39	56.5	274	4 Q96M21	Q96m21 homo sapien
19	39	56.5	306	4 Q8TAX2	Q8tax2 homo sapien
20	39	56.5	466	4 Q9NUS2	Q9nus2 homo sapien
21	39	56.5	1746	16 Q9HXR4	Q9hxr4 pseudomonas
22	38	55.1	57	4 Q96I36	Q96i36 homo sapien
23	38	55.1	91	15 Q77855	Q77855 human immun
24	38	55.1	91	15 Q77856	Q77856 human immun
25	38	55.1	377	12 Q89164	Q89164 variola vir
26	38	55.1	377	12 Q85389	Q85389 variola maj
27	38	55.1	377	12 Q93122	Q93122 vaccinia vi
28	38	55.1	377	12 Q8V2N9	Q8v2n9 camelpox vi
29	38	55.1	377	12 Q8QMT7	Q8qmt7 cowpox viru
30	38	55.1	396	17 Q8ZUT0	Q8zut0 pyrobaculum
31	38	55.1	433	5 Q44473	Q44473 caenorhabdi
32	38	55.1	509	10 Q9LHA1	Q9lha1 arabidopsis
33	38	55.1	515	10 Q22185	Q22185 arabidopsis
34	38	55.1	543	10 Q22188	Q22188 arabidopsis
35	38	55.1	1444	5 Q9GY67	Q9gy67 leishmania
36	37	53.6	85	16 Q8Z536	Q8z536 salmonella
37	37	53.6	109	15 Q9YQC1	Q9yqc1 human immun
38	37	53.6	109	15 Q9YQC0	Q9yqc0 human immun
39	37	53.6	109	15 Q9YQB9	Q9yqb9 human immun
40	37	53.6	109	15 Q9YQB8	Q9yqb8 human immun
41	37	53.6	109	15 Q9YJ17	Q9yj17 human immun
42	37	53.6	109	15 Q9YJ32	Q9yj32 human immun
43	37	53.6	115	15 Q9Q9L0	Q9q9l0 human immun
44	37	53.6	119	15 Q8Q454	Q8q454 human immun
45	37	53.6	121	16 Q8U6K3	Q8u6k3 agrobacteri

## ALIGNMENTS

### RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.  
AC Q8TCD2; 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strauberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022347; AAH22347.1; -.  
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 84.1%; Score 58; DB 4; Length 711;  
Best Local Similarity 90.9%; Pred. No. 0.038; Mismatches 0; Gaps 0;  
Matches 10; Conservative 0; Indels 1;

QY 1 CFQWQRMKRV 11  
Db 39 CFQWQRMKRV 49

### RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.  
ID Q9UCY5  
AC Q9UCY5; 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE Lactoferrin homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96081613; PubMed=8551695;  
 RX Sato I.;  
 RT "Characterization of the 84-kDa protein with ABH activity in human seminal plasma";  
 RL Jpn. J. Legal Med. 49:281-293(1995).  
 DR HSP; P02788; IRLKA.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 1.  
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDD5B CRC64;  
 Query Match 78.3%; Score 54; DB 4; Length 38;  
 Best Local Similarity 90.9%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;  
 QY 2 FQWQRMKVR 12  
 Db 21 FQWQRMKVR 31  
 RESULT 3  
 Q9TR80 PRELIMINARY; PRT; 33 AA.  
 AC Q9TR80;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Lactoferrin (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95127729; PubMed=7827104;  
 RA Qian Z.X., Jolles P., Migliore-Samouri D., Fiat A.M.;  
 RL Biochim. Biophys. Acta 1243:25-32(1995).  
 DR HSP; O77698; ICE2.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 1.  
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;  
 Query Match 72.5%; Score 50; DB 6; Length 33;  
 Best Local Similarity 63.6%; Pred. No. 0.045; Mismatches 3; Indels 0; Gaps 0;  
 Matches 7; Conservative 3;  
 QY 1 CFQWQRMKVR 11  
 Db 19 CYQWQRMKVR 29  
 RESULT 4  
 Q9SW56 PRELIMINARY; PRT; 1121 AA.  
 AC Q9SW56;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Phytochrome B2.  
 GN PHYB2.  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99413290; PubMed=10485280;  
 RA Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,

PA Kendrick R.E., Hanhart C.J., Koornneef M., Pratt L.H.,  
 RA Cordonnier-Bratt M.M.;  
 RT "Characterization of the gene encoding the apoprotein of phytochrome B2 in tomato, and identification of molecular lesions in two mutant alleles";  
 RL Mol. Gen. Genet. 261:901-907(1999).  
 DR EMBL; AF122901; AAD50631.1; -;  
 DR InterPro; IPR002198; ADH short.  
 DR InterPro; IPR003594; ATPbind\_ATPase.  
 DR InterPro; IPR003018; GAF.  
 DR InterPro; IPR003661; His\_KinA.  
 DR InterPro; IPR004359; His\_Kin\_sig.  
 DR InterPro; IPR001610; PAC.  
 DR InterPro; IPR000014; PAS domain.  
 DR InterPro; IPR001294; Phytochrome.  
 DR Pfam; PF01590; GAF; 1.  
 DR Pfam; PF02518; HATPase\_c; 1.  
 DR Pfam; PF00989; PAS; 2.  
 DR Pfam; PF00360; phytochrome; 1.  
 DR Pfam; PF00512; signal; 1.  
 DR PRINTS; PR01033; PHYTOCHROME.  
 DR SMART; SM00065; GAF; 1.  
 DR SMART; SM00387; HATPase\_c; 1.  
 DR SMART; SM00388; HSKA; 1.  
 DR SMART; SM00086; PAC; 1.  
 DR SMART; SM00091; PAS; 2.  
 DR TIGRFAMs; TIGR00229; sensory\_box; 2.  
 DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN\_1.  
 DR PROSITE; PS00245; PHYTOCHROME\_1; 1.  
 DR PROSITE; PS00046; PHYTOCHROME\_2; 1.  
 SQ SEQUENCE 1121 AA; 125308 MW; ED9EDA704BB37F27 CRC64;  
 Query Match 60.9%; Score 42; DB 10; Length 1121;  
 Best Local Similarity 54.5%; Pred. No. 44; Mismatches 6; Conservative 2; Indels 0; Gaps 0;  
 Matches 6; Conservative 2;  
 QY 1 CFQWQRMKVR 11  
 Db 777 CFQWQRMKVR 787  
 RESULT 5  
 Q9XFD5 PRELIMINARY; PRT; 105 AA.  
 AC Q9XFD5;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Cytochrome P450 (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PANICLE;  
 RA Liu J., Yang J.;  
 RT "Suppression subtractive hybridization (SSH) identified candidate genes that are differentially expressed at rice young panicle";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AF140486; AAD29699.1; -;  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 FT NON TER 1  
 SQ SEQUENCE 105 AA; 11912 MW; B0EEFCD487E19F9 CRC64;  
 Query Match 59.4%; Score 41; DB 10; Length 105;  
 Best Local Similarity 60.0%; Pred. No. 5.9;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRAMRK 10  
 |||||:|:|  
 Db 61 CFQWRLGKK 70

## RESULT 6

ID Q9XHP1 PRELIMINARY; PRT; 148 AA.  
 AC Q9XHP1  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE 2S albumin.  
 OS Sesamum indicum (Oriental sesame) (Gingelly).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.  
 OX NCBI\_TaxID=4182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TAINAN 1;  
 RX MEDLINE=20074970; PubMed=10606554;  
 RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;  
 RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed  
 storage proteins in sesame.";  
 RL J. Agric. Food Chem. 47:4932-4938(1999).  
 DR EMBL: AF091841; AAD42943.1; -;  
 DR InterPro; IPR003612; RAI;  
 DR InterPro; IPR000617; RAI.  
 DR InterPro; IPR001768; try/amy1 inhbr.  
 DR Pfam; PF00234; tryf\_alpha\_amy1; 1.  
 DR PRINTS; PR00496; NAFIN.  
 DR SMART; SMC0499; AAI; 1.  
 SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 59.4%; Score 41; DB 10; Length 148;  
 Best Local Similarity 66.7%; Pred. No. 8.4;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRAMR 9  
 |||||:|:|  
 Db 54 CMQWRMR 62

## RESULT 7

ID Q93780 PRELIMINARY; PRT; 275 AA.  
 AC Q93780  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE F53H4.4 protein.  
 DE F53H4.4.  
 GN F53H4.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dobson R.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 investigating biology.";  
 RL Science 282:2012-2018(1998).  
 DR EMBL; Z81089; CAB03137.1; -;  
 SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 59.4%; Score 41; DB 5; Length 275;  
 Best Local Similarity 63.6%; Pred. No. 16;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWRAMRKVR 12  
 |||||:|:|  
 Db 262 FQWKSMRKTR 272

## RESULT 8

ID Q19153 PRELIMINARY; PRT; 932 AA.  
 AC Q19153  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical 105.1 kDa protein.  
 GN F07C3.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Favello A., Gattung S.;  
 RT "The sequence of C. elegans cosmid F07C3.";  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U50308; AAG24025.1; -;  
 DR InterPro; IPR000731; HMGR/patch\_5TM.  
 DR PROSITE; PS50156; SSD; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match 59.4%; Score 41; DB 5; Length 932;  
 Best Local Similarity 63.6%; Pred. No. 55;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWRAMRKVR 12  
 |||||:|:|  
 Db 579 FQWRSMRLVK 589

## RESULT 9

ID Q8XSE2 PRELIMINARY; PRT; 279 AA.  
 AC Q8XSE2;  
 DT 01-WAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative ICC protein homolog.  
 GN ICC OR RSP0534 OR RS00414.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
 OC Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RC STRAIN=CM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangerot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigvier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR EMBL; AL646079; CAD17685.1; -.
DR InterPro; IPR004843; M-peptidase.
DR Pfam; PF00149; Metallophos; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 58.0%; Score 40; DB 16; Length 279;
Best Local Similarity 41.7%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFOWQAMRKVR 12
Db 244 CFOWGRTAK 255

RESULT 10
Q945T7 PRELIMINARY; PRT; 830 AA.
AC Q945T7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phytochrome C (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong Y., Costa J.M., Deitzer G.F.;
RT "Hordeum vulgare phytochrome C (PHYC) mRNA, 3' end.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF406643; AAK97634.1; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001294; Phytochrome.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR TIGRfam; TIGR00229; sensory_box; 2.
DR PROSITE; PS00245; PHYTOCHROME_1; UNKNOWN_1.
DR PROSITE; PS00446; PHYTOCHROME_2; 1.
FT NON_TER 1
SQ SEQUENCE 830 AA; 92060 MW; 61D29FC7B6564C5A CRC64;

Query Match 58.0%; Score 40; DB 10; Length 830;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOWQAMRKVR 11
Db 460 CLEWNEAMQKI 470

RESULT 11
Q9M7A9 PRELIMINARY; PRT; 1137 AA.
ID Q9M7A9

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AC Q9M7A9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Shrublandae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. IR36;
RX MEDLINE=20544086; PubMed=11094977;
RA Basu D., Dehesh K., Schneider-Poetsch H.J., Harrington S.E.,
RA McCouch S.R., Quail P.H.;
RT "rice PHYC gene: structure, expression, map position and evolution.";
RL Plant Mol. Biol. 44:27-42 (2000).
DR EMBL; AF141942; AAF66603.1; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR004359; His_KIN_sig.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001294; Phytochrome.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR PRINTS; PR01033; PHYTOCHROME.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HisKA; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRfam; TIGR00229; sensory_box; 2.
DR PROSITE; PS00245; PHYTOCHROME_1; 1.
DR PROSITE; PS00446; PHYTOCHROME_2; 1.
SQ SEQUENCE 1137 AA; 125937 MW; 782B0B75B904370A CRC64;

Query Match 58.0%; Score 40; DB 10; Length 1137;
Best Local Similarity 45.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOWQAMRKVR 11
Db 777 CLEWNEAMQKI 787

RESULT 12
Q8VWN1 PRELIMINARY; PRT; 1139 AA.
AC Q8VWN1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ETIOLATED SHOOT;
RA Kulshreshtha R., Khurana J.P.;
RT "Nucleotide sequence and characterization of a gene encoding
RT phytochrome C from wheat (Triticum aestivum).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

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RA Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nestor E.W.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58",  
 RL Science 294:2317-2323(2001).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 RA Roumieu K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu P.,  
 RA Wollam C., Allinger M., Doughty D., Scott C., Iappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58",  
 RL Science 294:2323-2328(2001).  
 DR EMBL; AF009043; AAL41776.1; -;  
 DR EMBL; AF008009; AAK8569.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;

Query Match 56.5%; Score 39; DB 16; Length 206;  
 Best Local Similarity 50.0%; Pred. No. 27;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CPQWQRAMRKVR 12  
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 Db 88 CPHWKSLLRQVR 99

Search completed: February 21, 2003, 07:44:27  
 Job time : 21.8 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)

56.502 Million cell updates/sec

Title: US-09-743-107B-75

Perfect score: 70

Sequence: 1 CFQWQRNARKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78075 Human lactoferrin
2	65	92.9	12	21	AAV78038 Human lactoferrin
3	65	92.9	12	21	AAV78046 Human lactoferrin
4	65	92.9	12	21	AAV78047 Human lactoferrin
5	65	92.9	12	21	AAV78082 Human lactoferrin
6	65	92.9	13	21	AAV78037 Human lactoferrin
7	65	92.9	13	21	AAV78037 Human lactoferrin
8	65	92.9	13	21	AAV78048 Human lactoferrin
9	65	92.9	13	21	AAV78049 Human lactoferrin
10	65	92.9	14	21	AAV78036 Human lactoferrin
			14	21	AAV78050 Human lactoferrin

11	65	92.9	14	21	AAV78051 Human lactoferrin
12	65	92.9	15	17	AAV78055 Peptide for anti-u
13	65	92.9	15	21	AAV78035 Human lactoferrin
14	65	92.9	15	21	AAV78062 Human lactoferrin
15	65	92.9	15	21	AAV78083 Human lactoferrin
16	65	92.9	16	21	AAV78031 Human lactoferrin
17	65	92.9	16	21	AAV78064 Human lactoferrin
18	65	92.9	16	21	AAV78065 Human lactoferrin
19	65	92.9	17	21	AAV78034 Human lactoferrin
20	65	92.9	17	21	AAV78066 Human lactoferrin
21	65	92.9	17	21	AAV78067 Human lactoferrin
22	65	92.9	18	15	AAV78067 Human lactoferrin
23	65	92.9	18	17	AAV78033 Advanced glycosyla
24	65	92.9	18	21	AAV78033 Human lactoferrin
25	65	92.9	19	21	AAV78067 Amino acid sequenc
26	65	92.9	19	21	AAV78032 Human lactoferrin
27	65	92.9	20	13	AAV78032 Anti microbial pep
28	65	92.9	20	14	AAV78032 Lactoferrin-relate
29	65	92.9	20	15	AAV78032 Lactoferrin-derive
30	65	92.9	20	15	AAV78032 Lactoferrin-derive
31	65	92.9	20	15	AAV78032 Lactoferrin-derive
32	65	92.9	20	15	AAV78032 Lactoferrin-derive
33	65	92.9	20	16	AAV78032 Bovine lactoferrin
34	65	92.9	20	16	AAV78032 Bovine lactoferrin
35	65	92.9	20	16	AAV78032 Anti-parasitic lac
36	65	92.9	20	16	AAV78032 Anti-parasitic lac
37	65	92.9	20	17	AAV78032 Peptide for anti-u
38	65	92.9	20	17	AAV78032 Lactoferrin-derive
39	65	92.9	20	17	AAV78032 Lactoferrin-derive
40	65	92.9	20	17	AAV78032 Lactoferrin-derive
41	65	92.9	20	17	AAV78032 Lactoferrin-derive
42	65	92.9	20	17	AAV78032 Lactoferrin-derive
43	65	92.9	20	18	AAV78032 Lactoferrin-derive
44	65	92.9	20	18	AAV78032 Anti-parasitic pep
45	65	92.9	20	19	AAV78032 Thrombus formation

#### ALIGNMENTS

#### RESULT 1

AAV78075  
ID AAV78075 standard; Peptide; 12 AA.  
XX AAV78075;  
AC AAV78075;  
XX  
XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:75.  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.  
XX Homo sapiens.  
XX OS Synthetic.  
XX  
XX WO200001730-A1.  
XX  
XX 13-JAN-2000.  
XX  
XX 06-JUL-1999; 99WO-SE01230.  
XX  
XX 06-JUL-1998; 98SE-0002441.  
XX 17-JUL-1998; 98SE-0002562.  
XX 29-DEC-1998; 98SE-0004614.  
XX  
XX (ASCI-) A+ SCI INVEST AB.  
XX  
XX Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI, 2000-147388/13.  
XX

XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX Sequence 12 AA;  
SQ

Query Match 100.0%; Score 70; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
| | | | | | | | | | | |  
Db 1 CFQWQNRNARKVR 12

RESULT 2  
AAY78038  
ID AAY78038 standard; Peptide; 12 AA.  
XX  
AC AAY78038;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:38.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
DR WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 12; Page 70; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX Sequence 12 AA;  
SQ

Query Match 92.9%; Score 65; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
| | | | | | | | | | | |  
Db 1 CFQWQNRNARKVR 12

RESULT 3  
AAY78046  
ID AAY78046 standard; Peptide; 12 AA.  
XX  
AC AAY78046;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human lactoferrin derived peptide SEQ ID NO:46.  
XX  
KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 06-JUL-1999; 99WO-SE01230.  
XX  
PR 06-JUL-1998; 98SE-0002441.  
XX  
PR 17-JUL-1998; 98SE-0002562.  
XX  
PR 29-DEC-1998; 98SE-0004614.  
XX  
PA (ASCI-) A+ SCI INVEST AB.  
XX  
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX  
DR WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 15; Page 35; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00022;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
 DB 1 CFQWQNRNARKVR 12

## RESULT 4

AAV78047  
 ID AAV78047 standard; Peptide; 12 AA.

XX AC AAV78047;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:47.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;  
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 73; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00022;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
 DB 1 CFQWQNRNARKVR 12

## RESULT 5

AAV78082  
 ID AAV78082 standard; Peptide; 12 AA.

XX AC AAV78082;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:82.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;  
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 22; Page 36; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.00022;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 CFQWQNRNARKVR 12  
 |||||  
 DB 1 CFQWQNRNARKVR 12

## RESULT 6

AAV78037  
 ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;  
 AC AAY78037;

XX 25-APR-2000 (first entry)  
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.  
 DE Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.  
 PN WO200001730-A1.

XX 13-JAN-2000.  
 PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.  
 PR 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.  
 PR 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.  
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.  
 PA (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.  
 DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.  
 PS Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;  
 SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 0.00024; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
 |||||  
 DB 2 CFQWQNRNARKVR 13

## RESULT 7

AAV78048

ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;  
 AC AAY78048;

XX 25-APR-2000 (first entry)  
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.  
 DE Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.  
 PN WO200001730-A1.

XX 13-JAN-2000.  
 PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.  
 PR 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.  
 PR 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.  
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.  
 PA (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.  
 DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.  
 PS Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;  
 SQ Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 0.00024; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
 |||||  
 DB 2 CFQWQNRNARKVR 13

## RESULT 8

AAV78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;  
 AC AAY78049;

XX 25-APR-2000 (first entry)  
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.  
 DE Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PT  
 XX Claim 18; Page 74; 102pp; English.  
 PS  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 0.00024;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNARKVR 12  
 Db |||||  
 2 CFQWQRNARKVR 13  
 RESULT 9  
 AAY78036  
 ID AAY78036 standard; Peptide; 14 AA.  
 XX  
 AC AAY78036;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:36.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PT  
 XX Claim 12; Page 69; 102pp; English.  
 PS  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 0.00026;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNARKVR 12  
 Db |||||  
 3 CFQWQRNARKVR 14  
 RESULT 10  
 AAY78050  
 ID AAY78050 standard; Peptide; 14 AA.  
 XX  
 AC AAY78050;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:50.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 XX PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 0.00026;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKVR 12  
 DB |||||  
 3 CFQWQNRKVR 14  
 RESULT 11  
 AAY78051  
 ID AAY78051 standard; Peptide; 14 AA.  
 XX AAY78051;  
 AC 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:51.  
 XX Human, lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 PD 06-JUL-1998; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 0.00026;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKVR 12  
 DB |||||  
 3 CFQWQNRKVR 14  
 RESULT 12  
 AAR98554  
 ID AAR98554 standard; Peptide; 15 AA.  
 XX AAR98554;  
 AC 12-NOV-1996 (first entry)  
 DT Peptide for anti-ulcer agent.  
 XX anti-ulcer agent; low toxicity; stable; heat-resistant.  
 OS Synthetic.  
 XX JP08143468-A.  
 PN 04-JUN-1996.  
 PD 17-NOV-1994; 94JP-0283869.  
 XX 17-NOV-1994; 94JP-0283869.  
 PR (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1996-318857/32.  
 DR Anti-ulcer agent contg. peptide - has low toxicity, is  
 PT heat-resistant and water-soluble  
 PS Claim 1; Page 11; 11pp; Japanese.  
 XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low  
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be  
 CC administered orally and be produced in large amounts.  
 XX Sequence 15 AA;

Query Match 92.9%; Score 65; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00028;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
 DB 2 CFQWQNRNARKVR 13

## RESULT 13

AAV78035  
 ID AAY78035 standard; Peptide; 15 AA.

XX AC AAY78035;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:35.  
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;  
 XX KW bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 XX PT inflammations and tumors and for use in infant formula food -  
 XX PS Claim 12; Page 69; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00028;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
 DB 4 CFQWQNRNARKVR 15

## RESULT 14

AAV78062  
 ID AAY78062 standard; Peptide; 15 AA.

XX AC AAY78062;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:62.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;  
 XX KW bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.  
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 XX PT inflammations and tumors and for use in infant formula food -  
 XX PS Claim 15; Page 81; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00028;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
 DB 4 CFQWQNRNARKVR 15

## RESULT 15

AAV78063  
 ID AAY78063 standard; Peptide; 15 AA.

XX AC AAY78063;

XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:63.  
XX  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200001730-A1.  
XX  
XX 13-JAN-2000.  
XX  
XX 06-JUL-1999; 99WO-SE01230.  
XX  
XX 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX  
XX (ASCI-) A+ SCI INVEST AB.  
XX  
XX Hanson LA, Maltzby-Baltzer I, Baltzer L, Dolphin GT;  
PI  
XX WPI; 2000-147388/13.  
XX  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 18; Page 81; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 92.9%; Score 65; DB 21; Length 15;  
Best Local Similarity 91.7%; Pred. No. 0.00028;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQNRNARKVR 12  
DB 4 CFQWQNRNARKVR 15

Search completed: February 21, 2003, 07:37:12  
Job time : 28.35 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-75  
Perfect score: 70  
Sequence: 1 CFQWQNRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-09-508-734-4
13	65	92.9	24	4	US-09-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	36	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-693-274A-7
25	65	92.9	52	4	US-09-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28	65	92.9	54	2	US-08-464-182A-2
29	65	92.9	54	2	US-08-406-271-2
30	65	92.9	694	3	US-08-724-586-2
31	65	92.9	694	4	US-08-421-632-2
32	65	92.9	694	4	US-09-932-190-2
33	65	92.9	705	2	US-08-655-640-2
34	65	92.9	708	2	US-08-655-640-4
35	65	92.9	711	1	US-08-154-019-4
36	65	92.9	711	1	US-08-461-333-4
37	65	92.9	711	3	US-08-464-167-4
38	65	92.9	711	3	US-09-158-313-4
39	65	92.9	711	4	US-08-476-798-4
40	62	88.6	711	1	US-08-145-681-2
41	62	88.6	711	1	US-08-250-308-2
42	62	88.6	711	1	US-08-453-703-2
43	62	88.6	711	2	US-08-456-106-2
44	62	88.6	711	3	US-08-456-108-2
45	62	88.6	711	4	US-09-265-577-2

## ALIGNMENTS

RESULT 1  
US-08-204-487-3  
; Sequence 3, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: MAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FUN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..18  
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 8.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRNARKVR 12  
| | | | | | | | | | | | | | | | | |  
Db 1 CFQWQNRNARKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,948  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 8.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRNARKVR 12  
| | | | | | | | | | | | | | | | | |  
Db 1 CFQWQNRNARKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI, YONG MING  
; APPLICANT: VLASSARA, HELEN  
; APPLICANT: CERAMI, ANTHONY  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 8.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRNARKVR 12  
| | | | | | | | | | | | | | | | | |  
Db 1 CFQWQNRNARKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 8.le-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNRKVR 12
Db 1 CFQWRNRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 9e-05; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12  
| | | | | | | | | |  
Db 2 CFQWQRNARKVR 13

## RESULT 6

US-07-891-174-3  
; Sequence 3, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Displaywrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:

## INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY: modified site

; LOCATION: 2  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 19"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 19  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 2"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12

| | | | | | | | | |

Db 2 CFQWQRNARKVR 13

## RESULT 7

US-08-204-487-1  
; Sequence 1, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEAKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIAKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: RJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE  
DERIVED FROM HUMAN LACTOFERRIN"  
US-08-204-487-1

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
DB 2 CFQWQNRNARKVR 13

## RESULT 8

US-08-256-771-24  
Sequence 24, Application US/08256771  
Patent No. 5656591

GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
PRODUCTS THEREWITH

NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:

IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are linked by  
disulfide bond"

## US-08-256-771-24

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
DB 2 CFQWQNRNARKVR 13

## RESULT 9

US-08-256-771-25  
Sequence 25, Application US/08256771  
Patent No. 5656591

GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
PRODUCTS THEREWITH  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,771  
FILING DATE: July 22, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:

IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "Cys residues are protected to  
prevent disulfide bond"

## US-08-256-771-25

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12  
DB 2 CFQWQNRNARKVR 13

## RESULT 10

US-08-381-984-24

; Sequence 24, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,984  
; FILING DATE: April 11, 1995  
; CLASSIFICATION: 252  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:

## INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "cysteine residues at positions 2  
; OTHER INFORMATION: and 19 are bonded by disulfide linkage".  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"

US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12  
Db 2 CFQWQRNARKVR 13

## RESULT 11

US-08-381-984-25  
; Sequence 25, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,984  
; FILING DATE: April 11, 1995  
; CLASSIFICATION: 252  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:

## INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"

US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNARKVR 12  
Db 2 CFQWQRNARKVR 13

## RESULT 12

US-09-508-734-4  
; Sequence 4, Application US/09508734  
; Patent No. 6423509  
; GENERAL INFORMATION:  
; APPLICANT: Samyang Genex Corporation  
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
; FILE REFERENCE: PA/SYG/00139  
; CURRENT APPLICATION NUMBER: US/09/508,734  
; CURRENT FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: PCT/KR99/00373  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: KR1998-29351  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 4





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107B-75  
Perfect score: 70  
Sequence: 1 CFQWQNRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08 NEW PUB. pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT NEW PUB. pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06 NEW PUB. pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06 PUBCOMB. pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07 NEW PUB. pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07 PUBCOMB. pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS PUBCOMB. pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08 PUBCOMB. pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09 NEW PUB. pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09 PUBCOMB. pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10 NEW PUB. pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10 PUBCOMB. pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60 NEW PUB. pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB. pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	40	57.1	15	9	US-09-798-869-7
8	39	55.7	15	9	US-09-798-869-4
9	39	55.7	25	9	US-09-798-869-22
10	39	55.7	747	9	US-10-066-500-58
11	39	55.7	747	9	US-10-002-796-58
12	39	55.7	747	9	US-10-066-273-58
13	39	55.7	747	9	US-10-066-494-58
14	38	54.3	255	9	US-09-738-626-5071
15	38	54.3	338	9	US-09-978-295A-119
16	38	54.3	338	9	US-09-978-697-119
17	38	54.3	338	9	US-09-978-192A-119
18	38	54.3	338	9	US-09-999-832A-119
19	38	54.3	338	9	US-09-978-189-119

US-09-798-869-2

38	54.3	553	9	US-09-796-753-14	Sequence 14, Appl	
38	54.3	553	10	US-09-981-649A-6	Sequence 6, Appl	
38	54.3	553	10	US-09-981-649A-24	Sequence 24, Appl	
38	54.3	554	10	US-09-981-649A-30	Sequence 30, Appl	
38	54.3	554	10	US-09-981-649A-32	Sequence 32, Appl	
38	54.3	559	10	US-09-981-649A-28	Sequence 28, Appl	
37	52.9	21	10	US-09-864-761-47985	Sequence 47985, A	
36	51.4	15	9	US-09-798-869-8	Sequence 8, Appl	
36	51.4	15	9	US-09-798-869-29	Sequence 29, Appl	
36	51.4	15	9	US-09-798-869-30	Sequence 30, Appl	
36	51.4	33	10	US-09-864-761-40025	Sequence 40025, A	
36	51.4	199	9	US-09-764-868-963	Sequence 963, App	
36	51.4	209	10	US-09-904-536-8	Sequence 8, Appl	
36	51.4	209	10	US-09-904-536-9	Sequence 9, Appl	
36	51.4	209	10	US-09-904-536-11	Sequence 11, Appl	
36	51.4	209	10	US-09-904-536-12	Sequence 12, Appl	
36	51.4	209	10	US-09-904-536-13	Sequence 13, Appl	
36	51.4	209	10	US-09-904-536-14	Sequence 14, Appl	
36	51.4	209	10	US-09-904-536-15	Sequence 15, Appl	
36	51.4	209	10	US-09-904-536-16	Sequence 16, Appl	
40	36	51.4	209	10	US-09-904-536-17	Sequence 17, Appl
41	36	51.4	209	10	US-09-904-536-18	Sequence 18, Appl
42	36	51.4	212	10	US-09-904-536-10	Sequence 10, Appl
43	36	51.4	235	9	US-10-095-449-6	Sequence 6, Appl
44	36	51.4	235	10	US-09-448-378-1	Sequence 1, Appl
45	36	51.4	235	10	US-09-983-806-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1

US-09-798-869-2

; Sequence 2, Application US/09798869

; Publication No. US20030022821A1

; GENERAL INFORMATION:

; APPLICANT: JOHN SIGURD SVENDSEN

; APPLICANT: (YSTEIN REKDAL

; APPLICANT: BALDUR SVEINBJ (RNSN

; APPLICANT: LARS VORLAND

; TITLE OF INVENTION: BIOACTIVE PEPTIDES

; FILE REFERENCE: A34049-PCT-USA-A

; CURRENT APPLICATION NUMBER: US/09/798.869

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: PCT/GB99/02851

; PRIOR FILING DATE: 1999-08-31

; PRIOR APPLICATION NUMBER: GB9818938.4

; PRIOR FILING DATE: 1998-08-28

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 15

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;  
Best Local Similarity 91.7%; Pred. No. 6.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12  
Db 3 CFQWQNRKVR 14

RESULT 2

US-09-798-869-20

; Sequence 20, Application US/09798869

; Publication No. US20030022821A1

; GENERAL INFORMATION:

; APPLICANT: JOHN SIGURD SVENDSEN

; APPLICANT: (YSTEIN REKDAL

; APPLICANT: BALDUR SVEINBJ (RNSN

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match          92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||||
Db 3 CFQWQNRNARKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2
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Query Match          92.9%; Score 65; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||||
Db 22 CFQWQNRNARKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON)
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match          81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||||
Db 3 CFQWQNRNARKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON)
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match          68.6%; Score 48; DB 9; Length 15;
Best Local Similarity 63.8%; Pred. No. 0.043;
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Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11  
|:|||||  
Db 3 CYQWQNRKRL 13

RESULT 6  
US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 69.6%; Score 48; DB 9; Length 25;  
Best Local Similarity 63.6%; Pred. No. 0.07;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11  
|:|||||  
Db 3 CYQWQNRKRL 13

RESULT 7  
US-09-798-869-7  
; Sequence 7, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.89;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11  
|:|||||  
Db 3 CYQWQNRKRL 13

RESULT 8  
US-09-798-869-4  
; Sequence 4, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11  
|:|||||  
Db 3 CLRWQNRKRV 13

RESULT 9  
US-09-798-869-22  
; Sequence 22, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;  
Best Local Similarity 54.5%; Pred. No. 2.1;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11  
|:|||||  
Db 3 CLRWQNRKRV 13



RESULT 10  
US-10-066-500-58  
Sequence 58, Application US/10066500  
Patent No. US2002017165A1  
GENERAL INFORMATION:  
APPLICANT: Avi J. Ashkenazi  
APPLICANT: Kevin P. Baker  
APPLICANT: David A. Botstein  
APPLICANT: Luc Desnoyers  
APPLICANT: Dan L. Eaton  
APPLICANT: Napoleone Ferrara  
APPLICANT: Sherman Fong  
APPLICANT: Wei-Qiang Gao  
APPLICANT: Hanspeter Gerber  
APPLICANT: Mary E. Gerritsen  
APPLICANT: Audrey Goddard  
APPLICANT: Paul J. Godowski  
APPLICANT: Austin L. Gurney  
APPLICANT: Ivar J. Kijavlin  
APPLICANT: Jennie P. Mather  
APPLICANT: Mary A. Napier  
APPLICANT: James Pan  
APPLICANT: Nicholas P. Paoni  
APPLICANT: Margaret Ann Roy  
APPLICANT: Timothy A. Stewart  
APPLICANT: Daniel Tumas  
APPLICANT: Colin K. Watanabe  
APPLICANT: P. Mickey Williams  
APPLICANT: William I. Wood  
APPLICANT: Zemin Zang  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3130R1C7  
CURRENT APPLICATION NUMBER: US/10/066,500  
CURRENT FILING DATE: 2002-02-01  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062285  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
PRIOR FILING DATE: 1997-10-31  
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PRIOR FILING DATE: 2000-09-18  
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PRIOR FILING DATE: 2000-09-18  
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PRIOR APPLICATION NUMBER: PCT/US99/21090  
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PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 55.7%; Score 39; DB 9; Length 747;

Best Local Similarity 45.5%; Pred. No. 57;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFOWQNRKRV 11

Db 311 CWRQWNSREI 321

RESULT 11

US-10-002-796-58

; Sequence 58, Application US/10002796

; Publication No. US20030032057A1

; GENERAL INFORMATION:

; APPLICANT: Avi J. Ashkenazi

; APPLICANT: Kevin P. Baker

APPLICANT: David A. Botstein  
APPLICANT: Luc Desnoyers  
APPLICANT: Dan L. Eaton  
APPLICANT: Napoleone Ferrara  
APPLICANT: Sherman Fong  
APPLICANT: Wei-Qiang Gao  
APPLICANT: Hanspeter Gerber  
APPLICANT: Mary E. Gerritsen  
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APPLICANT: Daniel Tumas  
APPLICANT: Colin K. Watanabe  
APPLICANT: P. Mickey Williams  
APPLICANT: William I. Wood  
APPLICANT: Zemin Zang  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3130RIC1  
CURRENT APPLICATION NUMBER: US/10/002,796  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059115  
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PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 55.7%; Score 39; DB 9; Length 747;

Best Local Similarity 45.5%; Pred. No. 57;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQNRKV 11

Db 311 CVRWQINSRI 321

# RESULT 12

US-10-066-273-58  
Sequence 58, Application US/10066273  
Publication No. US20030032062A1  
GENERAL INFORMATION:  
APPLICANT: Avi J. Ashkenazi  
APPLICANT: Kevin P. Baker  
APPLICANT: David A. Botstein  
APPLICANT: Luc Desnoyers  
APPLICANT: Dan L. Eaton  
APPLICANT: Napoleon Ferrara  
APPLICANT: Sherman Fong  
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APPLICANT: Margaret Ann Roy  
APPLICANT: Timothy A. Stewart  
APPLICANT: Daniel Tumas  
APPLICANT: Colin K. Watanabe  
APPLICANT: P. Mickey Williams  
APPLICANT: William I. Wood  
APPLICANT: Zemin Zang  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: F31301C2  
CURRENT APPLICATION NUMBER: US/10/066,273  
CURRENT FILING DATE: 2002-02-01  
PRIOR APPLICATION NUMBER: 10/002,796  
PRIOR FILING DATE: 2001-11-15  
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PRIOR FILING DATE: 1999-04-15  
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Query Match 55.7%; Score 39; DB 9; Length 747;

Best Local Similarity 45.5%; Pred. No. 57;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKRV 11

Db 311 CVRWQNSRRI 321

RESULT 13

US-10-066-494-58  
Sequence 58, Application US/10066494

Publication No. US20030032063A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi  
APPLICANT: Kevin P. Baker  
APPLICANT: David A. Botstein  
APPLICANT: Luc Desnoyers  
APPLICANT: Dan L. Eaton  
APPLICANT: Napoleone Ferrara  
APPLICANT: Sherman Fong  
APPLICANT: Wei-Qiang Gao  
APPLICANT: Hanspeter Gerber  
APPLICANT: Mary E. Gerritsen  
APPLICANT: Audrey Goddard  
APPLICANT: Paul J. Godowski  
APPLICANT: Austin L. Gurney  
APPLICANT: Ivar J. Kljavin  
APPLICANT: Jennie P. Mather  
APPLICANT: Mary A. Napier

APPLICANT: James Pan  
APPLICANT: Nicholas F. Paoni  
APPLICANT: Margaret Ann Roy  
APPLICANT: Timothy A. Stewart  
APPLICANT: Daniel Tumas  
APPLICANT: Colin K. Watanabe  
APPLICANT: P. Mickey Williams  
APPLICANT: William I. Wood  
APPLICANT: Zemin Zang  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3130RIC9  
CURRENT APPLICATION NUMBER: US/10/066,494  
CURRENT FILING DATE: 2002-02-01  
PRIOR APPLICATION NUMBER: 10/002,796  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059115  
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PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
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;; PRIOR APPLICATION NUMBER: PCT/US99/20111  
;; PRIOR FILING DATE: 1999-09-01  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 55.7%; Score 39; DB 9; Length 747;  
Best Local Similarity 45.5%; Pred No. 57;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQMORARKV 11

Db 311 CVRWQINSRI 321

#### RESULT 14

US-09-738-626-5071  
; Sequence 5071, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 5071

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/ LENGTH: 255
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-5071

Query Match          54.3%; Score 38; DB 9; Length 255;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QWQARNK 10
    |||||:
Db 110 QWQDARR 117

RESULT 15
US-09-978-295A-119
/ Sequence 119, Application US/09978295A
/ Patent No. US2002015606A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC11
/ CURRENT APPLICATION NUMBER: US/09/978,295A
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
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Query Match 54.3%; Score 38; DB 9; Length 338;  
Best Local Similarity 45.5%; Pred. No. 39;

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Qy 1 CFOWORNARKY 11  
Db 50 CYGWRNRNSKGV 60  
|:|:|:|:|

Search completed: February 21, 2003, 08:08:05  
Job time : 11.55 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-75  
Perfect score: 70  
Sequence: 1 CFQWQRNARKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 73:.\*  
1: Pirl:.\*  
2: Pirl:.\*  
3: Pirl:.\*  
4: Pirl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 JC2323	lactoferrin - goat
3	46	65.7	932	2 T28820	hypothetical prote
4	45	64.3	33	2 S52107	lactoferrin - shee
5	43	61.4	1432	2 B85431	trichohyalin like
6	42	60.0	289	2 G86403	33.3K hypothetical
7	42	60.0	511	2 AB0858	hypothetical prote
8	41	58.6	228	2 AD2346	hypothetical prote
9	41	58.6	4568	2 T08030	dyein beta heavy
10	40	57.1	255	2 T87515	signal peptidase I
11	40	57.1	681	2 T19429	hypothetical prote
12	39	55.7	518	2 B84514	probable cytochrom
13	39	55.7	570	2 T46261	hypothetical prote
14	39	55.7	707	1 A28438	lactoferrin precu
15	38	54.3	121	2 AH3147	hypothetical prote
16	38	54.3	283	2 D72378	sugar ABC transpo
17	38	54.3	340	2 T51386	probable protein w
18	38	54.3	365	2 T37477	MHC class I histoc
19	38	54.3	515	2 T00510	probable cytochrom
20	38	54.3	536	2 T24218	hypothetical prote
21	38	54.3	543	2 T00513	cytochrome P450 ho
22	38	54.3	558	2 T17324	hypothetical prote
23	38	54.3	749	2 A45687	outer capsid prote
24	38	54.3	6642	2 T29757	protein UNC-89 - C
25	37	52.9	89	2 G97365	hypothetical prote
26	37	52.9	194	2 AF1269	hypothetical GTP b
27	37	52.9	194	2 AH1631	hypothetical GTP b
28	37	52.9	206	2 H97451	pyridoxamine 5'-ph
29	37	52.9	206	2 AB2670	pyridoxamine 5'-ph

#### ALIGNMENTS

##### RESULT 1

###### TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence\_revision 21-Nov-1997 #text\_change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74;

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AA60324.1; PID:G467237

R/Rev. M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferi

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: SB:S52659; NID:G263311; PIDN:AA624877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA371116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <STI>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

probable pyridoxam  
probable peroxisom  
hypothetical prote  
type IV prelin p  
pre-pilin leader p  
hypothetical prote  
pectate lyase (EC  
glutamine syntheta  
pectate lyase (EC  
pectate lyase (EC  
pectase lyase 2 pr  
hypothetical prote  
NADH2 dehydrogenas  
protein kinase (EC  
hypothetical prote  
cytochrome P450 -

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70, 983-993, 1987  
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A;Reference number: S07160; MUID:88001031; PMID:3477300  
 A;Accession: S07160  
 A;Molecule type: mRNA  
 A;Residues: 436-487, 'A', 489-711 <RAD>  
 A;Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855  
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51, 3037-3043, 1991  
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A;Reference number: A61169; MUID:91235214; PMID:167448  
 A;Accession: A61169  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 3-701, 'SWKPVN' <PAN>  
 A;Experimental source: normal breast tissue  
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;  
 Eur. J. Biochem. 145, 659-666, 1984  
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other  
 A;Reference number: A31000; MUID:85076667; PMID:6510420  
 A;Accession: A31000  
 A;Molecule type: protein  
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4  
 A;Note: this is the final paper in a series  
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.  
 Eur. J. Biochem. 241, 303-308, 1996  
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affinity  
 A;Reference number: S74119; MUID:97054624; PMID:8898921  
 A;Accession: S74119  
 A;Molecule type: protein  
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A;Experimental source: neutrophil granulocytes  
 C;Genetics:  
 A;Gene: GDB:LTF  
 A;Cross-references: GDB:119368; OMIM:150210  
 A;Map position: 3q21-3q23  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein; iron binding; milk  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-711/Product: lactotransferrin #status experimental <MAT>  
 F;21-356/Domain: transferrin repeat homology <TRH1>  
 F;360-699/Domain: transferrin repeat homology <TRH2>  
 F;29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e  
 F;157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat  
 Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.0015; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNRNARKV 12  
 Db 39 CFQWQNRNARKV 50  
 RESULT 2  
 JC2323  
 lactoferrin - goat  
 C;Species: Capra aegagrus hircus (domestic goat)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C;Accession: JC2323  
 R;Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.  
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994  
 A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus  
 A;Reference number: JC2323; MUID:94380047; PMID:8093048  
 A;Accession: JC2323  
 A;Molecule type: mRNA  
 A;Residues: 1-708 cLEP>  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein  
 F;359-696/Domain: transferrin repeat homology <TRH2>  
 F;252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.6%; Score 48; DB 2; Length 708;  
 Best Local Similarity 63.8%; Pred. No. 1.5; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKV 11  
 Db 38 CFQWQNRNARKV 48

RESULT 3  
 T28820  
 hypothetical protein F07C3.1 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C;Accession: T28820  
 R;Favella, A.; Gattung, S.  
 submitted to the EMBL Data Library, March 1996  
 A;Description: The sequence of C. elegans cosmid F07C3.  
 A;Reference number: Z20528  
 A;Accession: T28820  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-932 <FAV>  
 A;Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1  
 A;Experimental source: strain Bristol N2; clone F07C3  
 C;Genetics:  
 A;Gene: CESP:F07C3.1  
 A;Map position: 5  
 A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 59;  
 Query Match 65.7%; Score 46; DB 2; Length 932;  
 Best Local Similarity 72.7%; Pred. No. 4.3; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNRNARKV 12  
 Db 579 FQWQNRNARKV 589

RESULT 4  
 S52107  
 lactoferrin - sheep (fragment)  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 14-Jul-1995 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997  
 C;Accession: S52107  
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samouri, D.; Fiat, A.M.  
 Biochim. Biophys. Acta 1243, 25-32, 1995  
 A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet  
 A;Reference number: S52107; MUID:95127729; PMID:7827104  
 A;Accession: S52107  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-33 <QIA>  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication

Query Match 64.3%; Score 45; DB 2; Length 33;  
 Best Local Similarity 54.5%; Pred. No. 0.27; Indels 0; Gaps 0;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKV 11  
 Db 19 CFQWQNRNARKV 29

RESULT 5  
 B85431  
 trichohyalin like protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
 C;Accession: B85431  
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.  
A;Reference number: AB05001; MUID:20083488; PMID:10617198  
A;Accession: B85431  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1432 <STO>  
A;Cross-references: GB:NC\_001268; NID:G270600; PIDN:CA880318.1; GSPDB:GN00140  
C;Genetics:  
A;Gene: AT4g36520  
A;Map position: 4

Query Match 61.4%; Score 43; DB 2; Length 1432;

Best Local Similarity 54.3%; Pred. No. 22; Indels 0; Gaps 0;  
Matches 6; Conservative 4; Mismatches 1;

QY 2 FQWQNRKVR 12

Db 583 YDWEQNARKLR 593

RESULT 6

G86403

33.3K hypothetical protein F28L5.13 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Nov-2001

C;Accession: G86403

R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lores, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G86403

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-289 <STO>

A;Cross-references: GB:AE005172; NID:G1098925; PIDN:AAG26065.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match 60.0%; Score 42; DB 2; Length 289;

Best Local Similarity 58.3%; Pred. No. 7.1;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12

Db 8 CFTWEYARHVR 19

RESULT 7

AB0858

hypothetical protein STY3070 [imported] - *Salmonella enterica* subsp. *enterica* serovar Ty

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001

C;Accession: AB0858

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A;Reference number: AB0502; PMID:11677608

A;Accession: AB0858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-511 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:G16504016; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY3070

Query Match 60.0%; Score 42; DB 2; Length 511;  
Best Local Similarity 58.3%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12

Db 350 CFQWQNRKVR 361

RESULT 8

AD2346

hypothetical protein alr4323 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp.

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C;Accession: AD2346

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing *Cyanobacterium* Anal

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AD2346

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-298 <KUR>

A;Cross-references: GB:BA000019; PIDN:BA876022.1; PID:G17133459; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr4323

Query Match 59.6%; Score 41; DB 2; Length 298;

Best Local Similarity 77.8%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRK 10

Db 163 FQWQNRK 171

RESULT 9

T08030

dynein beta heavy chain - *Chlamydomonas reinhardtii*

C;Species: *Chlamydomonas reinhardtii*

C;Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 02-Feb-2001

C;Accession: T08030

R;Mitchell, D.R.; Brown, K.S.

J. Cell Sci. 107, 635-644, 1994

A;Title: Sequence analysis of the *Chlamydomonas* alpha and beta dynein heavy chain genes.

A;Reference number: Z16302; MUID:94274778; PMID:8006077

A;Accession: T08030

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-4568 <MIT>

A;Cross-references: EMBL:U02963; NID:G409965; PIDN:AAA19956.1; PID:G514215

A;Experimental source: strain 21gr

C;Genetics:

A;Gene: ODA4

A;Map position: IX

A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 1

3334/3; 3686/3; 3882/3; 4240/3

C;Superfamily: dynein heavy chain, ciliary

C;Keywords: nucleotide binding, P-loop

F;1919-1926/Region: nucleotide-binding motif A (P-loop)

F;2202-2209/Region: nucleotide-binding motif A (P-loop)

F;2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 59.6%; Score 41; DB 2; Length 4568;

Best Local Similarity 50.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12  
|||||  
Db 1852 CFQWQSLRYIQ 1863

## RESULT 10

signal peptidase I [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C:Accession: E87515  
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A>Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; PMID:21173698; PMID:11259647  
A:Accession: E87515  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <STO>  
A:Cross-references: GB:AE005673; NID:gl3423643; PIDN:AAK24121.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC2150  
C:Superfamily: signal peptidase I

Query Match 57.1%; Score 40; DB 2; Length 255;  
Best Local Similarity 63.6%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12  
|||||  
Db 245 FQWDFARPFR 255

## RESULT 11

hypothetical protein C24H11.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T19429  
R.Lloyd, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19123  
A:Accession: T19429  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-681 <WIL>  
A:Cross-references: EMBL:Z81475; PIDN:CAB03914.1; GSPDB:GN00021; CESP:C24H11.8  
A:Experimental source: clone C24H11  
C:Genetics:  
A:Gene: CESP:C24H11.8  
A:Map position: 3  
A:Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2; 56

Query Match 57.1%; Score 40; DB 2; Length 681;  
Best Local Similarity 60.0%; Pred. No. 36;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRKVR 12  
|||||  
Db 192 RWQKRRVR 201

## RESULT 12

probable cytochrome P450 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana [mouse-ear cross]  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 23-Mar-2001  
C:Accession: B84514  
R.Liu, X.; Kaul, S.; Rounleay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.  
Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: B84514  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-518 <STO>  
A:Cross-references: GB:AE002093; NID:g4587680; PIDN:AAD25850.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g14100

A:Map position: 2  
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C:Keywords: heme; iron; metalloprotein  
F:453/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 39; DB 2; Length 518;  
Best Local Similarity 54.5%; Pred. No. 42;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 11  
|||||  
Db 473 CFQWRTNGDKV 483

## RESULT 13

T46261  
hypothetical protein DKFPZ761E1824.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T46261  
R.Biocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z23032  
A:Accession: T46261  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-570 <AAA>

A:Cross-references: EMBL:AL137432  
A:Experimental source: adult amygdala; clone DKFPZ761E1824  
C:Genetics:  
A>Note: DKFPZ761E1824.1

Query Match 55.7%; Score 39; DB 2; Length 570;  
Best Local Similarity 45.5%; Pred. No. 46;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 11  
|||||  
Db 134 CVRWQINSRRI 144

## RESULT 14

A28438  
lactoferrin precursor - mouse  
N:Alternate names: lactotransferrin  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
R:Accession: A28438; A41205  
R:Pentecost, B.T.; Teng, C.T.  
J. Biol. Chem. 262, 10134-10139, 1987  
A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret  
A:Reference number: A92596; PMID:87280033; PMID:3611056  
A:Accession: A28438  
A:Molecule type: mRNA  
A:Residues: 3-707 <PEN>

A:Cross-references: EMBL:J03298

R.Liu, Y.; Teng, C.T.

J. Biol. Chem. 266, 21880-21885, 1991

A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A:Reference number: A41205; PMID:92042099; PMID:1939212

A:Accession: A41205

A:Molecule type: DNA

A;Residues: 1-15 <LIU>  
A;Cross-references: GB:M74778  
C;Superfamily: transferrin; transferrin repeat homology  
C;Keywords: duplication; Glycoprotein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-707/Product: lactotransferrin #status predicted <MAT>  
F;358-695/Domain: transferrin repeat homology <TRH2>  
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 707;  
Best Local Similarity 54.5%; Pred. No. 56;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRKV 11  
| | | | |  
Db 37 CLRWQNRKV 47

RESULT 15  
AH3147  
hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
C;Accession: AH3147  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; PMID:11743193  
A;Accession: AH3147  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-121 <KUR>  
A;Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187  
C;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: Atu4804  
A;Map position: linear chromosome

Query Match 54.3%; Score 38; DB 2; Length 121;  
Best Local Similarity 54.5%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRKV 11  
| | | | |  
Db 14 CLAWQNRKV 24

Search completed: February 21, 2003, 07:47:47  
Job time : 11.65 secs

GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107b-75  
Perfect score: 70  
Sequence: 1 CFQWQNRKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1	TREL_HUMAN
2	48	68.6	708	1	TREL_CAMDR
3	48	68.6	708	1	TREL_CAPHI
4	43	61.4	146	1	RPOB_LIBAF
5	41	58.6	458	1	DYHB_CHLRE
6	40	57.1	695	1	TREL_HORSE
7	39	55.7	707	1	TREL_MOUSE
8	38	54.3	365	1	1A34_HUMAN
9	38	54.3	749	1	VP4_ROTGA
10	38	54.3	783	1	YNR2_CAEEL
11	37	52.9	238	1	PELX_ERWCA
12	37	52.9	238	1	YBN9_SCHPO
13	37	52.9	287	1	LEP4_XANCP
14	37	52.9	292	1	NLA_DROME
15	37	52.9	374	1	PEL2_ERWCA
16	37	52.9	455	1	YKVL_CAEEL
17	37	52.9	480	1	YQ31_CAEEL
18	37	52.9	493	1	NURM_NEUCR
19	37	52.9	510	1	YAGF_SCHPO
20	36	51.4	85	1	PMRD_SALTY
21	36	51.4	211	1	LOLB_VIBCH
22	36	51.4	214	1	VIF_SIVS4
23	36	51.4	235	1	FL3L_HUMAN
24	36	51.4	241	1	AGL9_PETHY
25	36	51.4	374	1	PEL3_ERWCA
26	36	51.4	375	1	PELB_ERWCH
27	35	50.0	62	1	RL28_THETN
28	35	50.0	208	1	FGFA_HUMAN
29	35	50.0	209	1	FGFA_MOUSE
30	35	50.0	215	1	FGFA_RAT
31	35	50.0	275	1	IL2A_BOVIN
32	35	50.0	275	1	IL2A_SHEEP
33	35	50.0	288	1	LEP4_PSEPU

## RESULT 1

ID	TREL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9HI23; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
FX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Conneely O.M.;			
RT	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Redo T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RN	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

34	35	50.0	306	1	BUB2 YEAST
35	35	50.0	355	1	MURG_NEIMA
36	35	50.0	355	1	MURG_NEIMB
37	35	50.0	487	1	HEP_DROME
38	35	50.0	502	1	C91I_ARATH
39	35	50.0	665	1	YLL4_CAEEL
40	35	50.0	2671	1	IP3T_HUMAN
41	34	48.6	160	1	RNH_SYNY3
42	34	48.6	289	1	PA1_SALTY
43	34	48.6	401	1	O88A_DROME
44	34	48.6	467	1	DCEC_LISIN
45	34	48.6	467	1	DCEC_LISMO

## ALIGNMENTS

P26448	saccharomyc
Q9J877	neisseria m
Q9K0V2	neisseria m
Q23977	drosofila
Q9F65	arabidopsis
Q11100	caenorhabdi
Q14573	homo sapien
Q55801	synecocyst
P37442	salmonella
Q9VFN2	drosofila
Q928K4	listeria in
Q8Y4K4	listeria mo

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE-Mammary Gland;  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Ogden J.E.;  
RT "Nucleotide sequence of human lactoferrin cDNA.";  
RL Nucleic Acids Res. 18:4013-4013(1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
RA Legrand D., Spik G., Montreuil J., Jolles P.;  
RT "Human lactotransferrin: amino acid sequence and structural  
RT comparisons with other transferrins.";  
RL Eur. J. Biochem. 145:659-666(1984).  
RN [10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
RA Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
RT alignment of the cyanogen bromide fragments and characterization of  
RT N- and C-terminal domains.";  
RL Biochim. Biophys. Acta 670:243-254(1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
RA Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
RT lactotransferrin";  
RL FEBS Lett. 142:107-110(1982).  
RN [12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
RT expression of mRNA during normal and leukemic myelopoiesis.";  
RL Blood 70:989-993(1987).  
RN [13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RA Sagripanti J.L.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2585506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
RT and refinement at 2.8-A resolution.";  
RL J. Mol. Biol. 209:711-734(1989).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
RT resolution.";  
RL Acta Crystallogr. D 51:629-646(1995).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
RA Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
RT binding properties and crystal structure of the histidine-  
RT 253-->methionine mutant.";  
RL Biochemistry 36:341-346(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in Aspergillus  
RT awamori.";  
RL Acta Crystallogr. D 55:403-407(1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
RT and analysis of ligand-induced conformational change.";  
RL Acta Crystallogr. D 54:1319-1335(1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioid antagonist peptides derived  
RT from human lactoferrin.";  
RL Agric. Biol. Chem. 54:1803-1810(1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,  
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejtmancik J.F., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RL Mol. Vision 4:31-32(1998).  
RN [21]  
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
RP CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
RP OF AN ANION, USUALLY BICARBONATE.  
CC [22]  
RP FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST  
CC ACTIVITY. LACTOFERRONIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERRONIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC [23]  
RP SUBUNIT: MONOMER.  
CC [24]  
RP SUBCELLULAR LOCATION: Secreted.  
CC [25]  
RP DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC [26]  
RP SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC [27]  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC [28]  
EMBL; X53961; CA37914.1; -  
EMBL; U07643; AAB60324.1; -  
EMBL; M3150; AAA36159.1; -  
EMBL; M83202; AAA59511.1; -  
EMBL; M83205; AAA58656.1; -  
EMBL; M18642; AAA86665.1; -  
EMBL; AF332168; AAG48753.1; -  
EMBL; BC015822; AAH15822.1; -  
EMBL; BC015823; AAH15823.1; -  
EMBL; M73700; AAA59479.1; -  
EMBL; X52941; CA37116.1; -  
EMBL; U95626; AAB57795.1; -  
PIR; S11228; TFFUL.  
DR PDB; 1LCF; 31-AUG-94.  
DR PDB; 1LCT; 31-OCT-93.  
DR PDB; 1LEG; 31-JUL-94.  
DR PDB; 1LFG; 31-OCT-93.  
DR PDB; 1LFT; 31-OCT-93.  
DR PDB; 1LGB; 31-AUG-94.  
DR PDB; 1LGC; 31-AUG-94.  
DR PDB; 1BKA; 08-NOV-96.  
DR PDB; 1DSN; 08-MAR-96.  
DR PDB; 1HSE; 12-MAR-97.  
DR PDB; 1VFD; 21-APR-97.

Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00035;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12  
 |||||  
 Db 39 CFQWQNRKVR 50

## RESULT 2

TRFL\_CAMDR STANDARD; PRT; 708 AA.

AC Q9TUM0; Q9MZS5; Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R., Ackermann M., Farah Z., Puhani Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION. USUALLY BICARBONATE (BY SIMILARITY).  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 CC -----

DR EMBL; AJ131674; CAB53387.1; -  
 DR EMBL; AF165879; AAF82241.1; -  
 DR HSP; O77811; 1313.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.  
 KW Transport; iron transport; Glycoprotein; Metal-binding; Repeat;  
 Signal.

FT SIGNAL 1 19 BY SIMILARITY.  
 FT CHAIN 20 708 LACTOTRANSFERRIN.  
 FT REPEAT 20 363 1.  
 FT REPEAT 364 708 2.  
 FT REPEAT 64 64 BY SIMILARITY.  
 FT DISULFID 28 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 708;  
 Best Local Similarity 66.7%; Pred. No. 0.4;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12  
 |||||  
 Db 38 CAQWQRRMKVR 49

## RESULT 3

TRFL\_CAPHI STANDARD; PRT; 708 AA.

AC Q29477; Q29479; Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.

OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=94380047; PubMed=8093048;  
 RA Le Provost F., Nocart M., Guerin G., Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 synteny group."  
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION. USUALLY BICARBONATE.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.



CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; U53857; AAA97958.1; -;  
 CC EMBL; X78902; CAA55517.1; -;  
 CC HSP; 077698; ICE2.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SM00094; TR FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN\_1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN\_2; 2.  
 CC PROSITE; PS00207; TRANSFERRIN\_3; 2.  
 CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 CC Signal.  
 CC  
 CC FT SIGNAL 1 19 BY SIMILARITY.  
 CC FT CHAIN 20 708 LACTOTRANSFERRIN.  
 CC FT REPEAT 20 363 1.  
 CC FT REPEAT 364 708 2.  
 CC FT DISULFID 28 64 BY SIMILARITY.  
 CC FT DISULFID 38 55 BY SIMILARITY.  
 CC FT DISULFID 134 217 BY SIMILARITY.  
 CC FT DISULFID 176 192 BY SIMILARITY.  
 CC FT DISULFID 189 200 BY SIMILARITY.  
 CC FT DISULFID 250 264 BY SIMILARITY.  
 CC FT DISULFID 367 399 BY SIMILARITY.  
 CC FT DISULFID 377 393 BY SIMILARITY.  
 CC FT DISULFID 424 703 BY SIMILARITY.  
 CC FT DISULFID 444 686 BY SIMILARITY.  
 CC FT DISULFID 476 551 BY SIMILARITY.  
 CC FT DISULFID 500 694 BY SIMILARITY.  
 CC FT DISULFID 510 534 BY SIMILARITY.  
 CC FT DISULFID 521 534 BY SIMILARITY.  
 CC FT DISULFID 592 606 BY SIMILARITY.  
 CC FT DISULFID 644 649 BY SIMILARITY.  
 CC FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 CC FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 CC FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 CC FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 CC FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 CC FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 CC FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 CC FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 CC FT BINDING 140 140 ANION (BY SIMILARITY).  
 CC FT BINDING 482 482 ANION (BY SIMILARITY).  
 CC FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC FT CARBOHYD 495 495 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC FT CARBOHYD 564 564 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC FT CONFLICT 56 56 I -> V (IN REF. 2).  
 CC FT CONFLICT 88 88 L -> R (IN REF. 2).  
 CC FT CONFLICT 124 124 Q -> K (IN REF. 2).  
 CC FT CONFLICT 154 154 F -> P (IN REF. 2).  
 CC FT CONFLICT 304 304 S -> R (IN REF. 2).  
 CC FT CONFLICT 414 414 D -> G (IN REF. 2).  
 CC SQ SEQUENCE 708 AA; 77358 MW; F2DA3C83539960D CRC64;  
 CC  
 CC Query Match 68.6%; Score 48; DB 1; Length 708;  
 CC Best Local Similarity 63.6%; Pred. No. 0.4;  
 CC Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 CC  
 CC QY 1 CFQWQNRKRV 11  
 CC |:|:|:|:|:  
 CC Db 38 CQWQRRMRKL 48

RESULT 4  
 RPOB LIBAF STANDARD; PRT; 146 AA.  
 ID AC P41187;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-OCT-2001 (Rel. 40, Last annotation update)  
 DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase  
 DE beta chain) (RNA polymerase beta subunit) (Fragment).  
 GN RPOB.  
 OS Liberibacter africanus (Liberibacter africanus).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Candidatus Liberibacter.  
 OX NCBI\_TaxID=34020;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nelspruit;  
 RA Planet P., Jagoueix S., Bove J.M., Garnier M.;  
 RT "Detection and characterization of the African Citrus Greening  
 RT Liberibacter by amplification, cloning and sequencing of the rplKJL-  
 RT rpoBC operon.";  
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
 CC SUBSTRATES.  
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC (RNA)(N).  
 CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE  
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1  
 CC BETA' CHAIN.  
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U09675; AAA19557.1; -;  
 CC InterPro; IPR001572; RNA\_pol\_B.  
 CC Pfam; PF00562; RNA\_pol\_B; 1.  
 CC PROSITE; PS01166; RNA\_POL\_BETA; PARTIAL.  
 CC Transferase; Transcription; DNA-directed RNA polymerase.  
 CC FT NON TER 146 146  
 CC SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;  
 CC  
 CC Query Match 61.4%; Score 43; DB 1; Length 146;  
 CC Best Local Similarity 70.0%; Pred. No. 0.64;  
 CC Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 CC  
 CC QY 1 CFQWQNRKRV 10  
 CC |:|:|:|:|:  
 CC Db 10 CVQWNRGARK 19  
 CC  
 CC RESULT 5  
 CC DYHB CHLRE STANDARD; PRT; 4568 AA.  
 ID AC Q39565;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Dynein beta chain, flagellar outer arm.  
 GN ODA4 OR ODA-4 OR SUP1.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=21gr;
RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R.; Brown K.S.;
RT "sequence analysis of the Chlamydomonas alpha and beta dynein heavy
RL chain genes";
RJ J. Cell Sci. 107:635-644(1994).
CC -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC
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CC
CC EMBL; U02963; AAA19956.1; -.
DR InterPro; IPR004273; Dynein_heavy;
DR Pfam; PF03028; Dynein_heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 COILED COIL (POTENTIAL).
FT DOMAIN 2831 2848 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 58.6%; Score 41; DB 1; Length 4568;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRVARKVR 12
Db 1852 CFQWQNRVARKVR 1863

RESULT 6
ID TRFL HORSE STANDARD; PRT; 695 AA.
AC 077811.
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) (Fragment).
GN LTP.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RT "cDNA sequence of mare lactoferrin";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC TISSUE=Milk;

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RX MEDLINE=99296631; PubMed=10366507;
RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
RL resolution.";
RJ J. Mol. Biol. 289:303-317(1999).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
CC EMBL; AJ010930; CAA09407.1; -.
DR PDB; 1B1X; 02-DEC-98.
DR PDB; 1B7U; 02-FEB-99.
DR PDB; 1B7Z; 02-FEB-99.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; 3D-structure.
FT SIGNAL 1 6
FT NON_TER 1 1
FT CHAIN 7 695 LACTOTRANSFERRIN.
FT REPEAT 7 350 1.
FT REPEAT 351 695 2.
FT DISULFID 15 51
FT DISULFID 25 42
FT DISULFID 121 204
FT DISULFID 163 179
FT DISULFID 166 189
FT DISULFID 176 187
FT DISULFID 237 251
FT DISULFID 354 386
FT DISULFID 364 377
FT DISULFID 411 690
FT DISULFID 431 653
FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 66 66 IRON 1 (BY SIMILARITY).
FT METAL 98 98 IRON 1 (BY SIMILARITY).
FT METAL 198 198 IRON 1 (BY SIMILARITY).
FT METAL 259 259 IRON 1 (BY SIMILARITY).
FT METAL 401 401 IRON 2 (BY SIMILARITY).
FT METAL 439 439 IRON 2 (BY SIMILARITY).
FT METAL 532 532 IRON 2 (BY SIMILARITY).
FT METAL 601 601 IRON 2 (BY SIMILARITY).
FT BINDING 127 127 ANION (BY SIMILARITY).
FT BINDING 143 143 ANION (BY SIMILARITY).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 57.1%; Score 40; DB 1; Length 695;
Best Local Similarity 58.3%; Pred. No. 11;

```

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQNRKRV 12  
| : ||| : |||  
Db 25 CAXFQNRKRV 36

## RESULT 7

TRFL MOUSE STANDARD; PRT; 707 AA.  
AC P08071; P70690; Q61799; Q922P2;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Lactotransferrin precursor (Lactoferrin).  
GN LTF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RX MEDLINE=87280033; PubMed=3611056;  
RA Pentecost B.T.; Teng C.T.;  
RT "Lactotransferrin is the major estrogen inducible protein of mouse uterine secretions.";  
RL J. Biol. Chem. 262:10134-10139 (1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Morishita K.;  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-14 FROM N.A.  
RX MEDLINE=92042099; PubMed=1939212;  
RA Liu Y.; Teng C.T.;  
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";  
RL J. Biol. Chem. 266:21880-21885 (1991).

CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC  
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CC  
CC EMBL; J03298; AAA40525.1; -  
CC DR EMBL; D88510; BAAL3633.1; -  
CC DR EMBL; BC006904; AAA06904.1; -  
CC DR EMBL; M74778; AAA39427.1; -  
CC DR PIR; A28438; A28438.  
CC DR HSP; P02788; 1CB8.  
CC DR MGD; MG196837; Lcf.  
CC DR InterPro; IPR001156; Transferrin.  
CC DR Pfam; PF00405; transferrin; 2.  
CC DR PRINTS; PR00422; TRANSFERRIN.  
CC DR SMART; SM00094; TR\_FER; 2.  
CC DR PROSITE; PS00205; TRANSFERRIN\_1; 1.  
CC DR PROSITE; PS00206; TRANSFERRIN\_2; 2.  
CC DR PROSITE; PS00207; TRANSFERRIN\_3; 2.

KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
Signal.  
FT CHAIN 20 707 BY SIMILARITY.  
FT REPEAT 358 707 LACTOTRANSFERRIN.  
FT REPEAT 357 707 1.  
FT REPEAT 358 707 2.  
FT DISULFID 27 63 BY SIMILARITY.  
FT DISULFID 37 54 BY SIMILARITY.  
FT DISULFID 133 216 BY SIMILARITY.  
FT DISULFID 175 191 BY SIMILARITY.  
FT DISULFID 188 199 BY SIMILARITY.  
FT DISULFID 249 263 BY SIMILARITY.  
FT DISULFID 366 398 BY SIMILARITY.  
FT DISULFID 376 389 BY SIMILARITY.  
FT DISULFID 423 702 BY SIMILARITY.  
FT DISULFID 443 665 BY SIMILARITY.  
FT DISULFID 475 550 BY SIMILARITY.  
FT DISULFID 499 693 BY SIMILARITY.  
FT DISULFID 509 523 BY SIMILARITY.  
FT DISULFID 520 533 BY SIMILARITY.  
FT DISULFID 591 605 BY SIMILARITY.  
FT DISULFID 643 648 BY SIMILARITY.  
FT METAL 78 78 IRON 1 (BY SIMILARITY).  
FT METAL 110 110 IRON 1 (BY SIMILARITY).  
FT METAL 210 210 IRON 1 (BY SIMILARITY).  
FT METAL 271 271 IRON 1 (BY SIMILARITY).  
FT METAL 413 413 IRON 2 (BY SIMILARITY).  
FT METAL 451 451 IRON 2 (BY SIMILARITY).  
FT METAL 544 544 IRON 2 (BY SIMILARITY).  
FT METAL 613 613 IRON 2 (BY SIMILARITY).  
FT BINDING 139 139 ANION (POTENTIAL).  
FT BINDING 481 481 ANION (POTENTIAL).  
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).  
FT CONFLICT 25 25 R -> Q (IN REF. 2).  
FT CONFLICT 82 82 M -> L (IN REF. 2).  
FT CONFLICT 359 359 S -> T (IN REF. 2).  
FT CONFLICT 382 382 A -> D (IN REF. 1).  
FT CONFLICT 449 449 E -> G (IN REF. 2).  
FT CONFLICT 629 629 L -> V (IN REF. 1).  
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340AC19A8 CRC64;

Query Match 55.7%; Score 39; DB 1; Length 707;

Best Local Similarity 54.5%; Pred. No. 17; Mismatches 4; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNRKRV 11  
| : ||| : |||  
Db 37 CLRQWNRKRV 47

## RESULT 8

1A34 HUMAN STANDARD; PRT; 365 AA.  
ID 1A34 HUMAN  
AC P30453; P30454;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE HLA class I histocompatibility antigen, A\*34(A-10) alpha chain precursor.  
DE HLA-A OR HLA-A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (A\*3401/A\*3402).  
RX MEDLINE=93056508; PubMed=1431115;  
RA Madrigal J.A.; Belich M.P.; Hildebrand W.H.; Benjamin R.J.;  
RA Little A.-M.; Zemmour J.; Ennis P.D.; Ward F.E.; Petzl-Erler M.L.;  
RA Martell R.W.; du Toit E.D.; Parham P.;  
RT "Distinctive HLA-A,B antigens of black populations formed by

interallelic conversion.";  
 J. Immunol. 149:3411-3415(1992).  
 (2)  
 SEQUENCE FROM N.A. (A\*3401/A\*3402).  
 MEDLINE=9235211; PubMed=9475492.  
 Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,  
 Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,  
 du Toit E.D., Farham P.;  
 "Structural diversity in the HLA-A10 family of alleles: correlations  
 with serology.";  
 Tissue Antigens 41:72-80(1993).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).  
 CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A\*3401  
 (AW-34.1) AND A\*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF  
 A\*3401.  
 CC -----  
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 CC -----  
 DR EMBL; X61704; CAA43873.1; -;  
 DR EMBL; X61705; CAA43874.1; -;  
 DR PIR; S16767; S16767.  
 DR PIR; S16771; S16771.  
 DR HSP; O19673; IHSB.  
 DR MM; 142800; -;  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig\_1.  
 DR Pfam; PF00129; MHC\_I\_1.  
 DR ProDom; PD000050; MHC\_I\_1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.  
 FT SIGNAL 1 24  
 FT CHAIN 25 365  
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 AW-34 (A-10) ALPHA CHAIN.  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 308  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 365  
 FT DOMAIN 110 110  
 FT CARBOHYD 125 188  
 FT DISULFID 227 283  
 FT VARIANT 3 3  
 FT VARIANT 90 90  
 FT VARIANT 121 121  
 FT VARIANT 129 129  
 FT VARIANT 138 138  
 FT VARIANT 180 180  
 FT VARIANT 312 312  
 FT VARIANT 365 365  
 FT SEQUENCE 365 AA; 41055 MW; 063BF63E56E01F6 CRC64;  
 Query Match 54.3%; Score 38; DB 1; Length 365;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WORNARKVR 12  
 DB 84 WDRNTRKVK 92  
 RESULT 9  
 VP4\_ROTGA  
 ID VP4\_ROTGA STANDARD; PRT; 749 AA.  
 AC Q04316;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).  
 GN S4.  
 OS Rotavirus (group B / strain ADRV) (Adult diarrhoea rotavirus).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 OX NCBI\_TaxID=12705;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93233240; PubMed=8386274;  
 RA Mackow E.R., Werner-Eckert R., Ray M.E., Tao H., Chen G.-M.;  
 "Identification and baculovirus expression of the VP4 protein of the  
 human group B rotavirus ADRV.";  
 J. Virol. 67:2730-2738(1993).  
 CC -1- SUBCELLULAR LOCATION: Outer capsid.  
 CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M91434; AAA47338.1; -;  
 DR InterPro; IPR000416; Cap\_VP4.  
 DR Pfam; PF00426; VP4; 1.  
 DR Coat protein; Glycoprotein.  
 FT CARBOHYD 29 29  
 FT CARBOHYD 53 53  
 FT CARBOHYD 109 109  
 FT CARBOHYD 133 133  
 FT CARBOHYD 407 407  
 FT CARBOHYD 527 527  
 FT CARBOHYD 568 568  
 FT CARBOHYD 620 620  
 FT CARBOHYD 681 681  
 FT CARBOHYD 698 698  
 FT SEQUENCE 749 AA; 84362 MW; D1223527DEAE0F21 CRC84;  
 Query Match 54.3%; Score 38; DB 1; Length 749;  
 Best Local Similarity 50.0%; Pred. No. 27;  
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 CFQWQRMARKVR 12  
 DB 195 CFTWDMNCANVR 206  
 RESULT 10  
 YNR2\_CAEL  
 ID YNR2\_CAEL STANDARD; PRT; 783 AA.  
 AC Q21988;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein R3G10.2 in chromosome III.  
 GN R3G10.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.

```

OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RD Gardner A.E.;
RE Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
RL [2]
RM REVISIONS.
RN Durbin R.;
RA Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RL [1]
RF COFACTOR: FAD (POTENTIAL).
RC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z35602; CAA84671.2;
DR WormPep; R13G10.2; CR25088.
DR InterPro; IPR002937; Amino_oxidase.
DR Pfam; PF01593; Amino_oxidase; 1.
KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
FT NP_BIND 311 366 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 12
DB 540 CIDWGRDRKVK 551

RESULT 11
ID PELX ERWCA STANDARD; PRT; 238 AA.
AC P16530;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Putative pectate lyase X precursor (EC 4.2.2.2).
GN PEL X.
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ER;
RA Ito K., Kobayashi R., Nikaide N., Izaki K.;
RT "DNA structure of pectate lyase I gene cloned from Erwinia
RT carotovora.";
RL Agric. Biol. Chem. 52:479-487(1988).
CC -1- FUNCTION: INVOLVED IN MACERATION AND SOFT-ROTTING OF PLANT TISSUE.
CC -1- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
CC their non-reducing ends.
CC -1- INDUCTION: BY PECTIN.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00218; BAA00156.1;
DR HSP; P11073; IAIK.
DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
KW Lyase; Multigene family; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 238 PUTATIVE PECTATE LYASE X.
SQ SEQUENCE 238 AA; 26094 MW; 46800EBA1CF41B64 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 238;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 12
DB 93 CGQWSKDARGVQ 104

RESULT 12
ID YEM9 SCHPO STANDARD; PRT; 238 AA.
AC Q1033;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C582.09 in chromosome II.
GN SPC582.09.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs W., Fritzc C., Holzer E., Mostl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Leinhardt R., Reinhardt R., Fohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Ruvellta J.B., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -----
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CC -----
DR EMBL; AL096788; CAB46672.1;
KW Hypothetical protein.
```

DR InterPro: IPR000045; Peptidase\_C20.  
DR Pfam: PF01478; Peptidase\_C20; 1.  
DR PRINTS: PR00864; PREPILNPTASE.  
DR KW Multifunctional enzyme; Hydrolase; Protease; Transferase;  
KW Methyltransferase; Transmembrane; Inner membrane.  
FT FT TRANSFEM 10 30 POTENTIAL.  
FT TRANSFEM 101 121 POTENTIAL.  
FT TRANSFEM 125 145 POTENTIAL.  
FT TRANSFEM 177 197 POTENTIAL.  
FT TRANSFEM 226 246 POTENTIAL.  
FT TRANSFEM 253 273 POTENTIAL.  
SQ SEQUENCE 287 AA; 31843 MW; A58DDIA514F9ECC2 CRC64;

Query Match 52.9%; Score 37; DB 1; Length 287;  
Best Local Similarity 50.0%; Pred. NO. 15;  
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps

QY 2 FQWNRARKV 11  
:||:|:|:  
Db 39 QWNRDAREI 48

RESULT 14

NLA DROME  
ID NLA DROME STANDARD; PRT; 292 AA.  
AC Q9XZL8; Q9V391;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Nebula protein.  
GN NLA OR CG6072.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC McCormick A.V., Goldberg M.L.;  
RT "Gene required for elongation of meiosis I spindle in Drosophila females."  
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkelley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamis I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapperton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*";  
RL Science 287:2185-2195(2000).  
CC -1- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.  
CC -1- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.  
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CC -----  
DR EMBL; AF147700; AAD33987.1; -;  
DR EMBL; AF003712; AAF55285.1; -;  
DR FlyBase; FBN0026629; nla.  
SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;  
Query Match 52.9%; Score 37; DB 1; Length 292;  
Best Local Similarity 54.5%; Pred. No. 16;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 FQWQNRKVR 12  
DB 150 FQWLSFRLR 160  
RESULT 15  
ID PEL2\_ERWCA STANDARD; PRT; 374 AA.  
AC P11431; Q06112; Q47469;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Pectate lyase II precursor (EC 4.2.2.2) (PEL II) (PEB).  
GN PEL2 OR PELB.  
OS Erwinia carotovora.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Pectobacterium.  
OX NCBI\_TaxID=554;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ER / IAM1088;  
RX MEDLINE=93113068; PubMed=1369060;  
RA Yoshida A., Matsuo Y., Kamio Y., Izaki K.;  
RT "Molecular cloning and sequencing of the extracellular pectate lyase  
RT II gene from *Erwinia carotovora* Er";  
RL Biosci. Biotechnol. Biochem. 56:1596-1600(1992).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN=SP. atroseptica EC;  
RX MEDLINE=87308030; PubMed=3040692;  
RA Lei S.-P., Lin H.-C., Wang S.-S., Callaway J., Wilcox G.;  
RT "Characterization of the *Erwinia carotovora* pelB gene and its product  
RT pectate lyase";  
RL J. Bacteriol. 169:4379-4383(1987).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SP. atroseptica C18;  
RX MEDLINE=95291436; PubMed=7773390;  
RA Bartling S., Wegener C., Olsen O.;  
RT "Synergism between *Erwinia* pectate lyase isoenzymes that depolymerize  
RT both pectate and pectin";  
RL Microbiology 141:873-881(1995).

CC -1- FUNCTION: INVOLVED IN MACERATION AND SOFT-ROTTING OF PLANT TISSUE.  
CC -1- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give  
CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at  
CC their non-reducing ends.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1. PLADES  
CC SUBFAMILY.  
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CC -----  
DR EMBL; S51475; AAC60422.1; -;  
DR EMBL; M17364; AAA24848.1; -;  
DR EMBL; X81847; CAA57440.1; -;  
DR HSSP; P11073; IAIR.  
DR InterPro; IPR002022; Amb allergen.  
DR Pfam; PF00544; pec lyase; 1.  
DR Lyase; Multigene family; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 374 PECTATE LYASE II.  
FT DISULFID 93 176 BY SIMILARITY.  
FT DISULFID 350 373 BY SIMILARITY.  
FT ACT SITE 239 239 POTENTIAL.  
FT VARIANT 35 35 E -> D (IN STRAIN EC).  
FT VARIANT 47 48 MK -> LQ (IN STRAIN EC).  
FT VARIANT 58 58 Q -> K (IN STRAIN EC).  
FT VARIANT 78 78 S -> N (IN STRAIN EC).  
FT VARIANT 136 136 V -> L (IN STRAIN C18).  
FT VARIANT 139 139 M -> I (IN STRAIN C18).  
FT VARIANT 144 144 D -> H (IN STRAIN C18).  
FT VARIANT 150 150 M -> I (IN STRAIN C18).  
FT VARIANT 156 156 I -> V (IN STRAIN EC).  
FT VARIANT 168 168 E -> K (IN STRAIN EC).  
FT VARIANT 172 173 KN -> QS (IN STRAIN EC).  
FT VARIANT 234 234 R -> S (IN STRAIN C18).  
FT VARIANT 252 252 N -> T (IN STRAIN EC).  
FT VARIANT 280 280 N -> I (IN STRAIN EC).  
FT VARIANT 306 311 SPSDEA -> KPADF5 (IN STRAINS C18 AND EC).  
FT VARIANT 314 314 K -> N (IN STRAIN EC).  
FT VARIANT 319 319 K -> R (IN STRAIN EC).  
FT VARIANT 322 322 S -> T (IN STRAIN EC).  
FT VARIANT 325 325 I -> V (IN STRAIN EC).  
FT VARIANT 329 329 N -> D (IN STRAINS C18 AND EC).  
FT VARIANT 338 339 SI -> AV (IN STRAIN C18).  
SQ SEQUENCE 374 AA; 40380 MW; FA83FD00ACD29ED5 CRC64;  
Query Match 52.9%; Score 37; DB 1; Length 374;  
Best Local Similarity 50.0%; Pred. No. 20;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CFQWQNRKVR 12  
DB 93 CQWKSQDARGVQ 104

Search completed: February 21, 2003, 07:27:49  
Job time : 5.6 secs

GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107b-75  
Perfect score: 70  
Sequence: 1 CFQWQNRKRV 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp archaea.\*
- 2: sp bacteria.\*
- 3: sp fungi.\*
- 4: sp human.\*
- 5: sp invertebrate.\*
- 6: sp mammal.\*
- 7: sp mhc.\*
- 8: sp organelle.\*
- 9: sp phase.\*
- 10: sp plant.\*
- 11: sp rodent.\*
- 12: sp virus.\*
- 13: sp vertebrate.\*
- 14: sp unclassified.\*
- 15: sp rvirus.\*
- 16: sp bacteriaph.\*
- 17: sp archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	85.7	711	4 Q8TCD2	Q8tcd2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9ucy5 homo sapien
3	46	65.7	932	5 Q19153	Q19153 caenorhabdi
4	45	64.3	33	6 Q9TR80	Q9tr80 ovine aries
5	43	61.4	1432	10 Q23230	Q23230 arabidopsis
6	43	61.4	2186	5 Q9N906	Q9n906 trypanosoma
7	42	60.0	105	10 Q9KFD5	Q9kfd5 oryza sativ
8	42	60.0	289	10 Q9C6N2	Q9c6n2 arabidopsis
9	42	60.0	511	16 Q8Z462	Q8z462 salmonella
10	41	58.6	279	16 Q8XSE2	Q8xse2 raietonia s
11	41	58.6	298	16 Q9YP77	Q9yp77 anabaena sp
12	40	57.1	255	16 Q9A6E4	Q9a6e4 caulobacter
13	40	57.1	372	10 Q81653	Q81653 hemerocalli
14	40	57.1	397	9 Q38229	Q38229 lactococcus
15	40	57.1	514	5 Q9VI18	Q9vi18 drosophila
16	40	57.1	543	5 Q9XZ30	Q9xz30 drosophila

```

17 40 57.1 681 5 Q9XVD1
18 40 57.1 1376 3 Q8X1P2
19 39 55.7 253 12 Q68541
20 39 55.7 349 5 Q9VII2
21 39 55.7 355 5 Q9S051
22 39 55.7 513 10 Q9LJY8
23 39 55.7 518 10 Q98I49
24 39 55.7 570 4 Q9NTA7
25 39 55.7 570 4 Q96DM9
26 39 55.7 620 4 Q8WX60
27 38 54.3 121 16 Q8U6K3
28 38 54.3 137 10 Q9FYI2
29 38 54.3 148 11 Q9CFX3
30 38 54.3 274 4 Q96M21
31 38 54.3 283 16 Q9WYQ1
32 38 54.3 314 5 Q9WIG8
33 38 54.3 339 10 Q8RWE0
34 38 54.3 340 10 Q9LFS1
35 38 54.3 514 10 Q98F27
36 38 54.3 515 10 Q22185
37 38 54.3 543 10 Q22188
38 38 54.3 553 4 Q9NZL7
39 38 54.3 554 4 Q9NV67
40 38 54.3 558 4 Q9URK6
41 38 54.3 1778 5 Q9NE65
42 38 54.3 5636 4 Q96RW7
43 38 54.3 6632 5 Q17362
44 38 54.3 6632 5 Q01761
45 37 52.9 89 16 Q8U5P6

```

## ALIGNMENTS

## RESULT 1

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Q8TCD2 PRELIMINARY; PRT; 711 AA.
ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2; 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DR 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
EL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH22347.1; -.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EB097C45FAF CRC64;

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Query Match 85.7%; Score 60; DB 4; Length 711;  
Best Local Similarity 90.9%; Pred. No. 0.0087;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 CFQWQNRKRV 11
Db 39 CFQWQNRKRV 49

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## RESULT 2

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Q9UCY5 PRELIMINARY; PRT; 38 AA.
ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
AC Q9UCY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DR 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96081613; PubMed=8551695;  
RA Sato I.;  
RT "Characterization of the 84-kDa protein with ABH activity in human  
RL seminal plasma.";  
RL Jpn. J. Legal Med. 49:281-293(1995).  
DR HSP; P02788; IBCA.  
DR InterPro; IPR001156; Transferrin.  
DR Pfam; PF00405; transferrin; 1.  
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5BDDDB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;  
Best Local Similarity 90.9%; Pred. No. 0.002;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FQWQNRKVR 12  
Db 21 FQWQNRKVR 31

RESULT 3

Q19153  
ID Q19153 PRELIMINARY; PRT; 932 AA.  
AC Q19153;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical 105.1 kDa protein.  
GN F07C3.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]\_TaxID=6239;  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Favella A., Gattung S.;  
RT "The sequence of C. elegans cosmid F07C3";  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Waterston R.;  
RT "Direct Submission.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U50308; AAG24025.1; -;  
DR InterPro; IPR000731; HMGCR/patch\_5TM.  
DR PROSITE; P850156; SSD; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match 65.7%; Score 46; DB 5; Length 932;  
Best Local Similarity 72.7%; Pred. No. 4.8;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 FQWQNRKVR 12  
Db 579 FQWQNRKVR 589

RESULT 4

Q9TR80

ID Q9TR80 PRELIMINARY; PRT; 33 AA.  
AC Q9TR80;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Lactoferrin (Fragment).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95127729; PubMed=7827104;  
RA Qian Z.Y., Jolles P., Migliore-Samouir D., Fiat A.M.;  
RL Biochim. Biophys. Acta 1243:25-32(1995).  
DR HSP; O77698; ICE2.  
DR InterPro; IPR001156; Transferrin.  
DR Pfam; PF00405; transferrin; 1.  
SQ SEQUENCE 33 AA; 3914 MW; D1904CAB15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;  
Best Local Similarity 54.5%; Pred. No. 0.19;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 CFQWQNRKVR 11  
Db 19 CYQWQNRKVR 29

RESULT 5

O23230  
ID O23230 PRELIMINARY; PRT; 1432 AA.  
AC O23230;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Trichovalin like protein.  
GN C7A10.840 OR AT4G36520.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Terry N., Vos P., Heijnen L., Mewes H.W., Schueller C.,  
RA Chalwatzis N.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z99708; CAB16841.1; -;  
DR EMBL; AL161589; CAB80318.1; -;  
SQ SEQUENCE 1432 AA; 163973 MW; 96C65FECB9BF0538 CRC64;

Query Match 61.4%; Score 43; DB 10; Length 1432;  
Best Local Similarity 54.5%; Pred. No. 28;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 FQWQNRKVR 12  
Db 583 YDMEQNRKVR 593

RESULT 6

Q9N906  
ID Q9N906 PRELIMINARY; PRT; 2186 AA.  
AC Q9N906;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Conserved hypothetical protein CHRI.67.  
GN CHRI.67.  
OS Trypanosoma brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OC NCBI\_TaxID=5691;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TREU927;  
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,  
RA Leonard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,  
RA Gerrard C., Rajandream M.A., Barrell B.G.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL359782; CAS95377.1; -;  
DR InterPro; IPR002035; VNF\_A.  
DR SMART; SM00327; VNF; 1.  
DR PROSITE; PS0234; VNF; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 2186 AA; 245737 MW; 78BB75505012005A CRC64;  
Query Match 61.4%; Score 43; DB 5; Length 2186;  
Best Local Similarity 50.0%; Pred. No. 44;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQARNK 10  
Db 588 CYEWERNASR 597  
RESULT 7  
Q9XFD5 PRELIMINARY; PRT; 105 AA.  
AC Q9XFD5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Cytochrome P450 (Fragment).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OC NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PANICLE;  
RA Liu J., Yang J.;  
RT "Suppression subtractive hybridization (SSH) identified candidate  
RT genes that are differentially expressed at rice young panicle.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
DR EMBL: AF140486; AAD29699.1; -;  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00057; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
KW Heme; Monooxygenase; Oxidoreductase.  
FT NON TER 1  
SQ SEQUENCE 105 AA; 11912 MW; B0EEFCDD487E19F9 CRC64;  
Query Match 60.0%; Score 42; DB 10; Length 105;  
Best Local Similarity 60.0%; Pred. No. 2.4;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CFQWQARNK 10  
Db 61 CFQWRLGKK 70  
RESULT 8  
Q9C6N2 PRELIMINARY; PRT; 289 AA.  
ID Q9C6N2  
AC Q9C6N2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Hypothetical 33.3 kDa protein.  
GN F28L5.13.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OC NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV COLUMBIA;  
RX MEDLINE=21016719; PubMed=11130712;  
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,  
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
RA Dunn P., Btgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
RA Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
RA Miltschker J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
RA Utterback T., Van Aken S., Vaysberg M., Vysocka V.S., Walker M.,  
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
RT thaliana";  
RL Nature 408:816-820(2000).  
DR EMBL; AC079280; AAG50577.1; -;  
SQ SEQUENCE 289 AA; 33338 MW; 753AA27BED0F840C CRC64;  
Query Match 60.0%; Score 42; DB 10; Length 289;  
Best Local Similarity 58.3%; Pred. No. 7.4;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CFQWQARNKVR 12  
Db 8 CFTWBYARHVR 19  
RESULT 9  
Q8Z462 PRELIMINARY; PRT; 511 AA.  
ID Q8Z462  
AC Q8Z462;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein STY3070.  
GN STY3070.  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OC NCBI\_TaxID=601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrell B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
RT enterica serovar Typhi CT18";  
RL Nature 413:848-852(2001).  
DR EMBL; AL627276; CAD06049.1; -;

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KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DDDD124E.0D178B CRC64;

Query Match 60.0%; Score 42; DB 16; Length 511;
Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||
   |||
Db 350 CFQWQNRNARKVR 361

RESULT 10
Q8XSE2 PRELIMINARY; PRT; 279 AA.
AC Q8XSE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ICC protein homolog.
GN ICC OR RSP0534 OR RS00414.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000.
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave P., Gouzy J., Mangerot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choigne N., Claudel-Renard C., Cunnac S., Demange N.,
RA Caspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RT Nature 415:497-502(2002).
DR EMBL; AL646079; CAD17685.1; -.
DR InterPro; IPR004843; M-peptidase.
DR Pfam; PF00149; Metallophos. 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 279 AA; 31541 MW; AB338818004B2EDA CRC64;

Query Match 58.6%; Score 41; DB 16; Length 279;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRNARKVR 12
   |||
   |||
Db 244 CFQWQNRNARKVR 255

RESULT 11
Q8YP77 PRELIMINARY; PRT; 298 AA.
AC Q8YP77;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr4323.
GN ALR4323.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003596; BAB76022.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;

Query Match 58.6%; Score 41; DB 16; Length 298;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRNARK 10
   |||
   |||
Db 163 FQWQNRNARK 171

RESULT 12
Q9A6E4 PRELIMINARY; PRT; 255 AA.
AC Q9A6E4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Signal peptidase I.
GN CC2150.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005887; AA24121.1; -.
DR HSP; P00803; IB12.
DR TIGR; CC2150; -.
DR InterPro; IPR000508; SigPase.
DR InterPro; IPR000223; SigPase_S26A.
DR Pfam; PF00461; Peptidase_S26; 1.
DR PRINTS; PR00727; LEADERPTASE.
DR PROSITE; PS00501; SPASE_I_1; UNKNOWN_1.
DR PROSITE; PS00760; SPASE_I_2; 1.
DR PROSITE; PS00761; SPASE_I_3; 1.
KW Complete proteome.
SQ SEQUENCE 255 AA; 28041 MW; 0D1D2A11781A9DEE CRC64;

Query Match 57.1%; Score 40; DB 16; Length 255;
Best Local Similarity 63.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FQWQNRNARKVR 12
   |||
   |||
Db 245 FQWQNRNARKVR 255

RESULT 13
Q81653 PRELIMINARY; PRT; 372 AA.
AC Q81653;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Senescence-associated protein 3 (Fragment).

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GN SA3.  
 OS Hemerocallis hybrid cultivar.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;  
 OC Hemerocallidaceae; Hemerocallis.  
 ON NCBI\_TaxID=80862;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;  
 RX MEDLINE=99339248; PubMed=10412903;  
 RA Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker E.L.;  
 RT "Identification of senescence-associated genes from daylily petals."  
 EL Plant Mol. Biol. 40:237-248(1999).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AF082028; AAC34853.1; -  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN\_1.  
 DR Heme; Monooxygenase; Oxidoreductase.  
 FT NON\_TER  
 SQ SEQUENCE 372 AA; 41909 MW; 55FB3EAF96995952 CRC64;  
 Query Match 57.1%; Score 40; DB 10; Length 372;  
 Best Local Similarity 50.0%; Pred. No. 23;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 CFQWQARNK 10  
 ||:|:|:  
 Db 328 CFEMDRNGEE 337  
 ||:|:|:  
 RESULT 14  
 Q38229 PRELIMINARY; PRT; 397 AA.  
 ID Q38229;  
 AC Q38229;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Unidentified ORF36.  
 OS Lactococcus phage bIL67.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC c2-like viruses.  
 ON NCBI\_TaxID=36343;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95111629; PubMed=7812447;  
 RA Schouler C., Ehrlich S.D., Chopin M.C.;  
 RT "Sequence and organization of the lactococcal prolate-headed bIL67  
 RT phage genome."  
 RL Microbiology 140:3061-3069(1994).  
 DR EMBL; L33769; AAA74323.1; -  
 SQ SEQUENCE 397 AA; 45956 MW; 09BCE9281EC0DA6E CRC64;  
 Query Match 57.1%; Score 40; DB 9; Length 397;  
 Best Local Similarity 54.5%; Pred. No. 25;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 FQWQARNKVR 12  
 :|||:|:|:  
 Db 128 YTFQFNARKIK 138  
 ||:|:|:  
 RESULT 15  
 Q9V118 PRELIMINARY; PRT; 514 AA.  
 ID Q9V118;  
 AC Q9V118;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE BCDNA.LD21969 protein.  
 GN BCDNA.LD21969 OR CS1024.  
 OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,  
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003675; AAF54126.1; -  
 DR FlyBase; FBgn0027514; BcDNA:LD21969.  
 DR InterPro; IPR000822; Znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2\_1.  
 DR SMART; SM00355; Znf\_C2H2\_4.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
 DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW DNA-binding; Metal-binding; Zinc-finger.  
 SQ SEQUENCE 514 AA; 59192 MW; 43C7DD7D9FEB86B9 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 514;  
 Best Local Similarity 60.0%; Pred. No. 33;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 CFQWQARNK 10  
 ||:|:|:  
 Db 47 CFKQVENAHK 56  
 ||:|:|:

Search completed: February 21, 2003, 07:44:29  
 Job time : 22.8 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107B-76  
Perfect score: 70  
Sequence: 1 CFQQRNMAKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
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11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78076 Human lactoferrin
2	65	92.9	12	21	AAV78038 Human lactoferrin
3	65	92.9	12	21	AAV78046 Human lactoferrin
4	65	92.9	12	21	AAV78047 Human lactoferrin
5	65	92.9	12	21	AAV78083 Human lactoferrin
6	65	92.9	13	21	AAV78037 Human lactoferrin
7	65	92.9	13	21	AAV78048 Human lactoferrin
8	65	92.9	13	21	AAV78049 Human lactoferrin
9	65	92.9	14	21	AAV78036 Human lactoferrin
10	65	92.9	14	21	AAV78050 Human lactoferrin

11	65	92.9	14	21	AAV78051 Human lactoferrin
12	65	92.9	15	17	AAV78054 Peptide for anti-u
13	65	92.9	15	21	AAV78035 Human lactoferrin
14	65	92.9	15	21	AAV78062 Human lactoferrin
15	65	92.9	15	21	AAV78063 Human lactoferrin
16	65	92.9	16	21	AAV78031 Human lactoferrin
17	65	92.9	16	21	AAV78064 Human lactoferrin
18	65	92.9	16	21	AAV78065 Human lactoferrin
19	65	92.9	17	21	AAV78034 Human lactoferrin
20	65	92.9	17	21	AAV78066 Human lactoferrin
21	65	92.9	17	21	AAV78067 Human lactoferrin
22	65	92.9	18	15	AAV78032 Human lactoferrin
23	65	92.9	18	17	AAV78033 Human lactoferrin
24	65	92.9	18	21	AAV78033 Advanced glycosyla
25	65	92.9	19	21	AAV78033 Human lactoferrin
26	65	92.9	19	21	AAV78032 Amino acid sequenc
27	65	92.9	19	21	AAV78032 Human lactoferrin
28	65	92.9	20	13	AAV78032 Anti microbial pep
29	65	92.9	20	14	AAV78032 Lactoferrin-relate
30	65	92.9	20	15	AAV78032 Lactoferrin derive
31	65	92.9	20	15	AAV78032 Lactoferrin derive
32	65	92.9	20	15	AAV78032 Lactoferrin derive
33	65	92.9	20	16	AAV78032 Bovine lactoferrin
34	65	92.9	20	16	AAV78032 Bovine lactoferrin
35	65	92.9	20	16	AAV78032 Anti-parasitic lac
36	65	92.9	20	16	AAV78032 Peptide for anti-u
37	65	92.9	20	17	AAV78032 Lactoferrin-derive
38	65	92.9	20	17	AAV78032 Lactoferrin-derive
39	65	92.9	20	17	AAV78032 Lactoferrin-derive
40	65	92.9	20	17	AAV78032 Lactoferrin-derive
41	65	92.9	20	17	AAV78032 Lactoferrin-derive
42	65	92.9	20	17	AAV78032 Lactoferrin-derive
43	65	92.9	20	18	AAV78032 Lactoferrin deriva
44	65	92.9	20	18	AAV78032 Anti-parasitic pep
45	65	92.9	20	19	AAV78032 Thrombus formation

#### ALIGNMENTS

RESULT 1  
AAV78076  
ID AAV78076 standard; Peptide; 12 AA.  
XX AAV78076;  
AC AAV78076;  
XX AAV78076;  
DT 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:76.

DE Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.

XX Homo sapiens.  
OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Matthey-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infections and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX SQ Sequence 12 AA;  
Query Match 100.0%; Score 70; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12  
| | | | | | | | | | | |  
Db 1 CFQWQRNNAKVR 12

RESULT 2  
AAY78038  
ID AAY78038 standard; Peptide; 12 AA.  
XX AAY78038;  
AC AAY78038;  
DT 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:38.  
DE Human, lactoferrin; modification; infection; inflammation; tumour;  
XX Human, lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200001730-A1.  
PN 13-JAN-2000.  
XX 06-JUL-1999; 99WO-SE01230.  
XX 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infections and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX SQ Sequence 12 AA;  
Query Match 92.9%; Score 65; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 4.5e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12  
| | | | | | | | | | | |  
Db 1 CFQWQRNNAKVR 12

RESULT 3  
AAY78046  
ID AAY78046 standard; Peptide; 12 AA.  
XX AAY78046;  
AC AAY78046;  
XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:46.  
DE Human, lactoferrin; modification; infection; inflammation; tumour;  
XX Human, lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200001730-A1.  
PN 13-JAN-2000.  
XX 06-JUL-1999; 99WO-SE01230.  
XX 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 4.5e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNKVR 12  
 DB 1 CFQWQRNNKVR 12

RESULT 4

AAV78047  
 ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;

DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:47.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;  
 XX KW bactericidal; preservative.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 73; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 4.5e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNKVR 12  
 DB 1 CFQWQRNNKVR 12

RESULT 5

AAV78083  
 ID AAY78083 standard; Peptide; 12 AA.

XX AC AAY78083;

DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:83.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;  
 XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattesby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,  
 XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 22; Page 36; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 4.5e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12  
 |||||  
 Db 1 CFQWQRNNAKVR 12

## RESULT 6

AAV78037  
 ID AAY78037 standard; Peptide; 13 AA.

AC AAY78037;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:37.

DE Human; lactoferrin; modification; infection; inflammation; tumour;

XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

PS Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumors. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 4.9e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12

|||||

Db 2 CFQWQRNNAKVR 13

|||||

RESULT 7

AAV78048

ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:48.

DE Human; lactoferrin; modification; infection; inflammation; tumour;

XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

PS Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumors. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 4.9e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12

|||||

Db 2 CFQWQRNNAKVR 13

|||||

RESULT 8

AAV78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:49.

XX



XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SB01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147398/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 18; Page 74; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 4.9e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMAKVR 12  
 Db 2 CFQWQRNMAKVR 13  
 XX  
 RESULT 9  
 AAY78036  
 ID AAY78036 standard; Peptide; 14 AA.  
 XX  
 AC AAY78036;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:36.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 XX WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SB01230.  
 XX  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147398/13.  
 XX  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 12; Page 69; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMAKVR 12  
 Db 3 CFQWQRNMAKVR 14  
 XX  
 RESULT 10  
 AAY78050  
 ID AAY78050 standard; Peptide; 14 AA.  
 XX  
 AC AAY78050;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:50.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SB01230.  
 PF

XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations, and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CFQWQRMNAKVR 12  
 Db |||||  
 3 CFQWQRMNAKVR 14  
 RESULT 11  
 AAY78051  
 ID AAY78051 standard; Peptide; 14 AA.  
 AC AAY78051;  
 DT 25-APR-2000 (first entry)  
 XX Human lactoferrin derived peptide SEQ ID NO:51.  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 PD 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations, and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CFQWQRMNAKVR 12  
 Db |||||  
 3 CFQWQRMNAKVR 14  
 RESULT 12  
 AAR98554  
 ID AAR98554 standard; Peptide; 15 AA.  
 AC AAR98554;  
 DT 12-NOV-1996 (first entry)  
 XX Peptide for anti-ulcer agent.  
 DE anti-ulcer agent; low toxicity; stable; heat-resistant.  
 KW Synthetic.  
 OS JP08143468-A.  
 PN 04-JUN-1996.  
 PD 17-NOV-1994; 94JP-0283869.  
 XX 17-NOV-1994; 94JP-0283869.  
 PR (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1996-318857/32.  
 DR Anti-ulcer agent contg. peptide - has low toxicity, is  
 PT heat-resistant and water-soluble  
 XX Claim 1; Page 11; 11pp; Japanese.  
 PS AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low  
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be  
 CC administered orally and be produced in large amounts.  
 XX Sequence 15 AA;

PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations, and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CFQWQRMNAKVR 12  
 Db |||||  
 3 CFQWQRMNAKVR 14  
 RESULT 12  
 AAR98554  
 ID AAR98554 standard; Peptide; 15 AA.  
 AC AAR98554;  
 DT 12-NOV-1996 (first entry)  
 XX Peptide for anti-ulcer agent.  
 DE anti-ulcer agent; low toxicity; stable; heat-resistant.  
 KW Synthetic.  
 OS JP08143468-A.  
 PN 04-JUN-1996.  
 PD 17-NOV-1994; 94JP-0283869.  
 XX 17-NOV-1994; 94JP-0283869.  
 PR (MORG ) MORINAGA MILK IND CO LTD.  
 XX WPI; 1996-318857/32.  
 DR Anti-ulcer agent contg. peptide - has low toxicity, is  
 PT heat-resistant and water-soluble  
 XX Claim 1; Page 11; 11pp; Japanese.  
 PS AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low  
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be  
 CC administered orally and be produced in large amounts.  
 XX Sequence 15 AA;

Query Match 92.9%; Score 65; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 5.7e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRMAKVR 12  
 DB 2 CFQWQNRMAKVR 13

RESULT 13  
 AAY78035  
 ID AAY78035 standard; Peptide; 15 AA.  
 XX AC AAY78035;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:35.  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PN WO200001730-A1.  
 XX PD 13-JAN-2000.  
 XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.  
 XX PA (ASCII-) A+ SCI INVEST AB.  
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX PT New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -  
 PS Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 15 AA;  
 SQ

Query Match 92.9%; Score 65; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 5.7e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRMAKVR 12  
 DB 4 CFQWQNRMAKVR 15

RESULT 15  
 AAY78063  
 ID AAY78063 standard; Peptide; 15 AA.  
 XX AC AAY78063;

RESULT 14  
 AAY78062  
 ID AAY78062 standard; Peptide; 15 AA.  
 XX AC AAY78062;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:62.  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PN WO200001730-A1.  
 XX PD 13-JAN-2000.  
 XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.  
 XX PA (ASCII-) A+ SCI INVEST AB.  
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX PT New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -  
 PS Claim 15; Page 81; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 15 AA;  
 SQ

Query Match 92.9%; Score 65; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 5.7e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNRMAKVR 12  
 DB 4 CFQWQNRMAKVR 15

RESULT 15  
 AAY78063  
 ID AAY78063 standard; Peptide; 15 AA.  
 XX AC AAY78063;

XX 25-APR-2000 (first entry)  
DT Human lactoferrin derived peptide SEQ ID NO:63.  
DE  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200001730-A1.  
PN  
XX 13-JAN-2000.  
PD  
XX 06-JUL-1999; 99WO-SE01230.  
PF  
XX 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
PA  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
PI WPI; 2000-147388/13.  
XX  
PT New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
PS Claim 18; Page 81; 102pp; English.  
XX  
CC AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumors. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.  
XX  
SQ Sequence 15 AA;  
  
Query Match 92.9%; Score 65; DB 21; Length 15;  
Best Local Similarity 91.7%; Pred. No. 5.7e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CFQWQRMNAKVR 12  
| | | | | | | | | |  
DB 4 CFQWQRMNAKVR 15  
  
Search completed: February 21, 2003, 07:37:12  
Job time : 28.35 secs



OTHER INFORMATION: (20-37) "  
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMAKVR 12  
|||||  
Db 1 CFQWQRNMAKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,948  
; FILING DATE: 436  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMAKVR 12  
|||||  
Db 1 CFQWQRNMAKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI, YONG MING  
; APPLICANT: VLASSARA, HELEN  
; APPLICANT: CERAMI, ANTHONY  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMAKVR 12  
|||||  
Db 1 CFQWQRNMAKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE  
; NUMBER OF SEQUENCES: 9

;;  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Klauber & Jackson  
;; STREET: 411 Hackensack Avenue  
;; CITY: Hackensack  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07601  
;;  
;; COMPUTER READABLE FORM: disk  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA: US/08/475,055  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/485,948  
;; FILING DATE:  
;; APPLICATION NUMBER: 08/488,217  
;; FILING DATE: JUNE 7, 1995  
;; APPLICATION NUMBER: 08/418,642  
;; FILING DATE: APRIL 7, 1995  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 947-1-008A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201 343-1684  
;; TELEFAX: 201 343-1684  
;; TELEX: 133521  
;;  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; DESCRIPTION: LF-CL, 8-25  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;;  
US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKVR 12  
| | | | | | | | | | | | | | | |  
Db 1 CFQWQRMNAKVR 12

RESULT 5  
US-07-755-161A-3  
; Sequence 3, Application US/07755161A  
; Patent No. 5304633  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible

;;  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: DisplayWrite  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/755,161A  
;; FILING DATE: 19910905  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX: 202-371-8856  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE:  
;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:  
;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE:  
;; CELL LINE:  
;; ORGANELLE:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:  
;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURE:  
;; NAME/KEY: modified site  
;; LOCATION: 2  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION: /note= "thiol group of  
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
;; OTHER INFORMATION: thiol group of Cys residue at location 19"  
;; FEATURE:  
;; NAME/KEY: modified site  
;; LOCATION: 19  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION: /note= "thiol group of  
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
;; OTHER INFORMATION: thiol group of Cys residue at location 2"  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNMAKVR 12  
Db 2 CFQWQRNMAKVR 13

## RESULT 6

US-07-891-174-3  
Sequence 3, Application US/07891174  
Patent No. 5317084  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptides and an  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/891,174  
FILING DATE: 29-MAY-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/755,161

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY: modified site

LOCATION: 2  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 19"  
FEATURE:  
NAME/KEY: modified site  
LOCATION: 19  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 2"  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-3

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNMAKVR 12

Db 2 CFQWQRNMAKVR 13

## RESULT 7

US-08-204-487-1  
Sequence 1, Application US/08204487  
Patent No. 5565425  
GENERAL INFORMATION:  
APPLICANT: YAMAMOTO, NAOKI  
APPLICANT: NAKASHIMA, HIDEKI  
APPLICANT: MOSUCHI, WATARU  
APPLICANT: TANAKA, SHIGEKI  
APPLICANT: DOSAKO, SHUN'ICHI  
APPLICANT: KAWASAKI, YOSHIHIRO  
APPLICANT: UCHIDA, TOSHIKI  
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
TITLE OF INVENTION: INHIBITORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
ADDRESSEE: THIBEAULT  
STREET: 53 STATE STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,487  
FILING DATE: 02-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, PAULA A.  
REGISTRATION NUMBER: 32,503  
REFERENCE/DOCKET NUMBER: FUN-019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000



```

; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..20
; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
; US-08-204-487-1

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Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels

Qy	1	CFWQRNMAKVR	12
Db	2	CFWQRNMKVR	13

RESULT 8  
US-08-256-771-34  
; Sequence 24, Application US/08256771  
; Patent No. 5656391  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH

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? IDEX:
? INFORMATION FOR SEQ ID NO:   24 :
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY:
? LOCATION:
? IDENTIFICATION METHOD:
? OTHER INFORMATION: /note= "Cys residues are linked by
? OTHER INFORMATION: disulfide bond"
?
```

```
US-08-256-771-24
```

	Query Match	92.9%;	Score 65;	DB 1;	Length 20;
	Best Local Similarity	91.7%;	Pred. No. 2.3e-05;		
	Matches 11; Conservative	0;	Mismatches	1;	Indels
QY	1 CFQWQRNMAKVR	12			
Dd	2 CFQWRNMKVR	13			

RESULT 9  
US-08-256-771-25  
; Sequence 25. Application US/08256771  
; Patent No. 565591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH

```

? ? INFORMATION FOR SEQ ID NO: 25:
? ? SEQUENCE CHARACTERISTICS:
? ? LENGTH: 20 amino acids
? ? TYPE: amino acid
? ? STRANDEDNESS: single
? ? TOPOLOGY: linear
? ? MOLECULE TYPE: peptide
? ? FEATURE:
? ? NAME/KEY:
? ? LOCATION:
? ? IDENTIFICATION METHOD:
? ? OTHER INFORMATION: /note= "Cys residues are protected to
? ? OTHER INFORMATION: prevent disulfide bond"
US-08-0256-771-25

```

```

Query Match          92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches -1; Indels 0; Gaps 0;

QY      1 CFQWRNNKVR 12
        |||||
Db       2 CFQWRNNKVR 13

```

RESULT 10  
US-08-381-984-24

; Sequence 24, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; FILING DATE: April 11, 1995  
; APPLICATION NUMBER: 252  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "cysteine residues at positions 2  
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
; US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNNAKVR 12  
Db 2 CFQWRNNAKVR 13

RESULT 11  
US-08-381-984-25  
; Sequence 25, Application US/08381984  
; Patent No. 5804555  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIOXIDANT  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; FILING DATE: April 11, 1995  
; APPLICATION NUMBER: 252  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "the specified peptide as well as  
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "cysteine residues at positions 2  
; OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"  
; US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNNAKVR 12  
Db 2 CFQWRNNAKVR 13

RESULT 12  
US-09-508-734-4  
; Sequence 4, Application US/09508734  
; Patent No. 6423509  
; GENERAL INFORMATION:  
; APPLICANT: Samyang Genex Corporation  
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
; TITLE OF INVENTION: useful microorganism thereof  
; FILE REFERENCE: PA/SYG/00139  
; CURRENT APPLICATION NUMBER: US/09/508,734  
; CURRENT FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: PCT/KR99/00373  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: KR1998-29351  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 4

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/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-508-734-4
Query Match          92.9%; Score 65; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12
   |||||
Db 2 CFQWQRNNAKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match          92.9%; Score 65; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12
   |||||
Db 3 CFQWQRNNAKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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```
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek Jr.
/ REGISTRATION NUMBER: 33,367
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-8850
/ TELEFAX: 202-371-8856
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ HYPOTHETICAL:
/ ANTI-SENSE:
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM:
/ STRAIN:
/ INDIVIDUAL ISOLATE:
/ DEVELOPMENTAL STAGE:
/ HAPLOTYPE:
/ TISSUE TYPE:
/ CELL TYPE:
/ CELL LINE:
/ ORGANELLE:
/ IMMEDIATE SOURCE:
/ LIBRARY:
/ CLONE:
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ UNITS:
/ FEATURE:
/ NAME/KEY: modified site
/ LOCATION: 4
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "thiol group of
/ OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
/ OTHER INFORMATION: thiol group of Cys residue at location 21"
/ FEATURE:
/ NAME/KEY: modified site
/ LOCATION: 21
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "thiol group of
/ OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
/ OTHER INFORMATION: thiol group of Cys residue at location 4"
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ TITLE:
/ JOURNAL:
/ VOLUME:
/ ISSUE:
/ PAGES:
/ DATE:
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE:
/ RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

Query Match          92.9%; Score 65; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12
   |||||
Db 4 CFQWQRNNAKVR 15
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## RESULT 15

US-07-891-174-10  
; Sequence 10, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 4  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 21"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 21

## IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 4"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-10  
Query Match 92.9%; Score 65; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 2.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQRNNAKVR 12  
Db 4 CFQWQRNNAKVR 15  
Search completed: February 21, 2003, 07:50:34  
Job time : 8.7 secs

GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107b-76  
Perfect score: 70  
Sequence: 1 CFQWQRNNAKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08 NEW PUB.pap.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06 NEW PUB.pap.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06 PUBCOMB.pap.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07 NEW PUB.pap.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07 PUBCOMB.pap.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS PUBCOMB.pap.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08 PUBCOMB.pap.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09 NEW PUB.pap.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09 PUBCOMB.pap.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10 NEW PUB.pap.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10 PUBCOMB.pap.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60 NEW PUB.pap.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60 PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	40	57.1	15	9	US-09-798-869-7
8	39	55.7	15	9	US-09-798-869-4
9	39	55.7	15	9	US-09-798-869-29
10	39	55.7	15	9	US-09-798-869-30
11	39	55.7	25	9	US-09-798-869-22
12	39	55.7	1617	9	US-10-090-453A-2
13	37	52.9	21	10	US-09-864-761-47985
14	36	51.4	15	9	US-09-798-869-8
15	35	50.0	846	9	US-10-051-409-4
16	34	48.6	95	10	US-09-764-864-1031
17	34	48.6	312	10	US-09-935-428A-4
18	34	48.6	1564	10	US-09-801-368-244
19	33	47.1	26	10	US-09-864-761-46809

20	33	47.1	77	10	US-09-864-761-41002	Sequence 41002, A
21	33	47.1	78	10	US-09-820-893-136	Sequence 136, App
22	33	47.1	199	9	US-09-764-868-963	Sequence 963, App
23	33	47.1	331	9	US-10-099-275-2	Sequence 2, Appli
24	33	47.1	331	10	US-09-953-956-8	Sequence 8, Appli
25	33	47.1	331	12	US-10-114-464-8	Sequence 8, Appli
26	33	47.1	332	9	US-09-738-626-5674	Sequence 5674, Ap
27	33	47.1	333	9	US-09-796-753-26	Sequence 119, App
28	33	47.1	338	9	US-09-978-295A-119	Sequence 119, App
29	33	47.1	338	9	US-09-978-697-119	Sequence 119, App
30	33	47.1	338	9	US-09-978-192A-119	Sequence 119, App
31	33	47.1	338	9	US-09-999-832A-119	Sequence 119, App
32	33	47.1	338	9	US-09-978-189-119	Sequence 119, App
33	33	47.1	553	9	US-09-796-753-14	Sequence 14, Appli
34	33	47.1	553	10	US-09-981-649A-6	Sequence 6, Appli
35	33	47.1	553	10	US-09-981-649A-24	Sequence 24, Appli
36	33	47.1	554	10	US-09-981-649A-30	Sequence 30, Appli
37	33	47.1	554	10	US-09-981-649A-32	Sequence 32, Appli
38	33	47.1	559	10	US-09-981-649A-28	Sequence 28, Appli
39	33	47.1	782	10	US-09-841-739-9	Sequence 9, Appli
40	33	47.1	1403	8	US-08-913-322-22	Sequence 22, Appli
41	33	47.1	1403	8	US-08-913-322-24	Sequence 24, Appli
42	33	47.1	1579	10	US-09-801-368-368	Sequence 368, App
43	33	47.1	2273	10	US-09-995-542-12	Sequence 12, Appli
44	33	47.1	2310	10	US-09-995-542-10	Sequence 10, Appli
45	32	45.7	56	10	US-09-864-761-44710	Sequence 44710, A

## ALIGNMENTS

RESULT 1  
US-09-798-869-2  
; Sequence 2, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ/RNNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GS99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;  
Best Local Similarity 91.7%; Pred. No. 2.7e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNNAKVR 12  
| | | | | | | | | | | | | | | |  
Db 3 CFQWQRNNAKVR 14

RESULT 2  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ/RNNSON  
US-09-798-869-20



Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|||||:  
Db 3 CYQWQRMNKL 13

RESULT 6  
US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ(RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 68.6%; Score 48; DB 9; Length 25;  
Best Local Similarity 63.6%; Pred. No. 0.037;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|||||:  
Db 3 CYQWQRMNKL 13

RESULT 7  
US-09-798-869-7  
; Sequence 7, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ(RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.53;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|||||:  
Db 3 CYQWQRMNKL 13

RESULT 8  
US-09-798-869-4  
; Sequence 4, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ(RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.78;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|||||:  
Db 3 CLRWQNMNKL 13

RESULT 9  
US-09-798-869-29  
; Sequence 29, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ(RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-29

Query Match 55.7%; Score 39; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.78;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|||||:  
Db 3 CFRWQNMNKL 13

## RESULT 10

US-09-798-869-30  
; Sequence 30, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-30

Query Match 55.7%; Score 39; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.78;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|:|:|:|:  
DB 3 CFQWQRMNAKV 13

## RESULT 11

US-09-798-869-22  
; Sequence 22, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;  
Best Local Similarity 54.5%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|:|:|:|:  
DB 3 CFQWQRMNAKV 13

## RESULT 12

US-10-090-453A-2  
; Sequence 2, Application US/10090453A  
; Patent No. US20020173004A1  
; GENERAL INFORMATION:

; APPLICANT: Chen, Hongyun  
; APPLICANT: Le Bihan, Stephane  
; APPLICANT: Kulhanek, Barbara  
; TITLE OF INVENTION: NOVEL ABCA6 TRANSPORTER AND USES THEREOF  
; FILE REFERENCE: 100103.404  
; CURRENT APPLICATION NUMBER: US/10/090,453A  
; CURRENT FILING DATE: 2002-05-29  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1617  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-090-453A-2

Query Match 55.7%; Score 39; DB 9; Length 1617;  
Best Local Similarity 72.7%; Pred. No. 81;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11  
|:|:|:|:|:  
DB 440 CFQWQRMNAKV 450

## RESULT 13

US-09-864-761-47985  
; Sequence 47985, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203



; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 47985  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL096701.14  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6  
; OTHER INFORMATION: EST\_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06  
US-09-864-761-47985

Query Match 52.9%; Score 37; DB 10; Length 21;  
Best Local Similarity 83.3%; Pred. No. 2.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6  
Db 16 CFQWRR 21

RESULT 14  
US-09-798-869-8  
; Sequence 8, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINEJ(RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine  
; OTHER INFORMATION: sequence)  
US-09-798-863-8

Query Match 51.4%; Score 36; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 2.6;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMAKV 11  
Db 3 CLRQWQEMKV 13

RESULT 15  
US-10-051-409-4  
; Sequence 4, Application US/10051409  
; Publication No. US20030027171A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Chu-Wen  
; APPLICANT: Tsou, Ann-Ping  
; APPLICANT: Chi, Chin-Wen  
; APPLICANT: Fann, Ming-Ji  
; APPLICANT: Chou, Chen-Kung  
; TITLE OF INVENTION: CELL CYCLE REGULATOR PROTEIN  
; FILE REFERENCE: 12005-003001

; CURRENT APPLICATION NUMBER: US/10/051,409  
; CURRENT FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/262,885  
; PRIOR FILING DATE: 2001-01-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 846  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-051-409-4

Query Match 50.0%; Score 35; DB 9; Length 846;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNM 8  
Db 448 CFQWDRKL 455

Search completed: February 21, 2003, 08:08:05  
Job time : 10.55 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-76

Perfect score: 70

Sequence: 1 CFQWQNNMAKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.\*

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 J2323	lactoferrin - goat
3	47	67.1	511	2 AB0858	hypothetical prote
4	45	64.3	33	2 S52107	lactoferrin - shee
5	42	60.0	749	2 A45687	outer capsid prote
6	40	57.1	205	2 E90094	26S proteasome SU
7	40	57.1	317	2 T47233	cysteine synthase
8	39	55.7	707	1 A28438	lactoferrin precu
9	38	54.3	515	2 T00510	probable cytochrom
10	38	54.3	543	2 T00513	cytochrome P450 ho
11	38	54.3	584	2 C84325	hypothetical prote
12	38	54.3	4568	2 T08030	dyein beta heavy
13	37	52.9	742	2 T25415	hypothetical prote
14	37	52.9	2517	2 S58380	probable RNA-direc
15	36.5	52.1	290	2 C97414	hypothetical prote
16	36	51.4	57	2 D81949	hypothetical prote
17	36	51.4	298	2 AD2346	hypothetical prote
18	36	51.4	405	2 AB1461	B. subtilis YabE p
19	36	51.4	408	2 AC1098	B. subtilis YabE p
20	36	51.4	435	2 S52784	ornithine decarbox
21	36	51.4	496	2 T50146	probable era/thdtr
22	36	51.4	501	2 T39801	hypothetical sh3-c
23	36	51.4	518	2 B84514	probable cytochrom
24	36	51.4	628	2 S77374	cell division prot
25	36	51.4	710	2 T49516	Atu related protei
26	36	51.4	717	2 T33295	hypothetical prote
27	36	51.4	820	2 G82168	trimethylamine-N-o
28	36	51.4	1274	2 T04018	hypothetical prote
29	36	51.4	1767	2 T00458	hypothetical prote

30 35.5 50.7 451 2 AB2296  
31 35 50.0 145 2 F84496  
32 35 50.0 275 2 T22597  
33 35 50.0 282 2 F90580  
34 35 50.0 283 2 D72378  
35 50.0 447 2 S53309  
36 35 50.0 481 2 B96691  
37 35 50.0 492 2 B85441  
38 35 50.0 499 2 T04730  
39 35 50.0 500 2 C85441  
40 35 50.0 500 2 T52174  
41 35 50.0 649 2 AB2154  
42 35 50.0 665 2 T34079  
43 35 50.0 668 2 C71868  
44 35 50.0 708 2 B84950  
45 35 50.0 728 2 S71467

## ALIGNMENTS

## RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence, revision 21-Nov-1997 #text, change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S741

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GE/EMBL/DBU

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AA560324.1; PID:G467237

R:Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148 'T', 150-422 'C', 424-711 <REY>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52559; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A:Note: sequence extracted from NCBI backbone (NCBIIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326545; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70, 989-993, 1987  
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A;Reference number: S07160; MUID:88001031; PMID:3477300  
 A;Accession: S07160  
 A;Molecule type: mRNA  
 A;Residues: 436-487, 'A', 489-711 <RAD>  
 A;Cross-references: EXBL:M18642; PIDN:AAA86665.1; PID:G386855  
 R;Panella, T.J.; Liu, X.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51, 3037-3043, 1991  
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A;Reference number: A61169; MUID:91235214; PMID:1674448  
 A;Accession: A61169  
 A>Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 3-701, 'SWKPVN' <PAN>  
 A;Experimental source: normal breast tissue  
 R;Mets-Buttigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;  
 Eur. J. Biochem. 145, 659-666, 1984  
 A>Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth  
 A;Reference number: A31000; MUID:85076667; PMID:6510420  
 A;Accession: A31000  
 A;Molecule type: protein  
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4  
 A;Note: this is the final paper in a series  
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.  
 Eur. J. Biochem. 241, 303-308, 1996  
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affini  
 A;Reference number: S74119; MUID:97054624; PMID:8898921  
 A;Accession: S74119  
 A;Molecule type: protein  
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A;Experimental source: neutrophil granulocytes  
 C;Genetics:  
 A;Gene: GDB:LTF  
 A;Cross-references: GDB:119368; OMIM:150210  
 A;Map position: 3q21-3q23  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein; iron binding; milk  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-711/Product: lactotransferrin #status experimental <MAT>  
 F;21-356/Domain: transferrin repeat homology <TRH1>  
 F;360-699/Domain: transferrin repeat homology <TRH2>  
 F;729-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e  
 F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;368-400, 378-391, 425-706, 647-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat  
 Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00068;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNNAKVR 12  
 Db 39 CFQWQRNNAKVR 50  
 RESULT 2  
 JC2323  
 lactoferrin - goat  
 C;Species: Capra aegagrus hircus (domestic goat)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C;Accession: JC2323  
 R;Lue Provost, F.; Nocard, M.; Guerin, G.; Martin, P.  
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994  
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus  
 A;Reference number: JC2323; MUID:94380047; PMID:8093048  
 A;Accession: JC2323  
 A;Molecule type: mRNA  
 A;Residues: 1-708 <LEP>  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication; glycoprotein  
 F;359-696/Domain: transferrin repeat homology <TRH2>  
 F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.6%; Score 48; DB 2; Length 708;  
 Best Local Similarity 63.8%; Pred. No. 0.87;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 11  
 Db 38 CYQWQRNNAKVR 48

RESULT 3  
 AB0858  
 hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typh  
 C;Species: Salmonella enterica subsp. enterica serovar Typhi  
 A;Note: this species has also been called Salmonella typhi  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
 C;Accession: AB0858  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A;Reference number: AB0502; PMID:11677608  
 A;Accession: AB0858  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-511 <PAR>  
 A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:G16504016; GSPDB:GN00176  
 C;Genetics:  
 A;Gene: STY3070

Query Match 67.1%; Score 47; DB 2; Length 511;  
 Best Local Similarity 66.7%; Pred. No. 0.96;  
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 12  
 Db 350 CFQWQRNNAKVR 361

RESULT 4  
 S52107  
 lactoferrin - sheep (fragment)  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 14-Jul-1995 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997  
 C;Accession: S52107  
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.  
 Biochim. Biophys. Acta 1243, 25-32, 1995  
 A>Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a  
 A;Reference number: S52107; MUID:95127729; PMID:7827104  
 A;Accession: S52107  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-33 <QIA>  
 C;Superfamily: transferrin; transferrin repeat homology  
 C;Keywords: duplication

Query Match 64.3%; Score 45; DB 2; Length 33;  
 Best Local Similarity 54.5%; Pred. No. 0.14;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNNAKVR 11  
 Db 19 CYQWQRNNAKVR 29

RESULT 5  
 A45687  
 outer capsid protein VP4 - human rotavirus B  
 C;Species: human rotavirus B  
 C;Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 19-Feb-1999  
 C;Accession: A45687

R.Mackow, E.R.; Werner-Eckert, R.; Fay, M.B.; Tao, H.; Chen, G.  
 J. Virol. 67, 2730-2738, 1993  
 A:Title: Identification and baculovirus expression of the VP4 protein of the human group  
 A:Reference number: A45687; MUID:93233240; PMID:9386274  
 A:Accession: A45687  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-749 <MAC>  
 A:Note: sequence inconsistent with the nucleotide translation  
 A:Note: sequence extracted from NCBI backbone (NCBIN:130353, NCBI:130355)  
 C:Superfamily: rotavirus core protein

Query Match 60.0%; Score 42; DB 2; Length 749;  
 Best Local Similarity 58.3%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQNMAYR 12  
 |||:|:|:  
 Db 195 CFTWDMNCANVR 206

RESULT 6  
 E90094  
 26S proteasome SU B5 [imported] - Guillardia theta nucleomorph  
 C:Species: nucleomorph Guillardia theta  
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
 R:Accession: E90094  
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reil  
 Nature 410, 1091-1096, 2001  
 A:Title: The highly reduced genome of an enslaved algal nucleus.  
 A:Reference number: A99082; MUID:11323671; PMID:11323671  
 A:Accession: E90094  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-205 <DOU>  
 A:Cross-references: GB:AF165818; NID:gl3794510; PIDN:AAK39885.1; GSPDB:GN00150  
 C:Genetics:  
 A:Gene: prSB5  
 A:Map position: 1  
 A:Genome: nucleomorph  
 C:Keywords: nucleomorph

Query Match 57.1%; Score 40; DB 2; Length 205;  
 Best Local Similarity 45.5%; Pred. No. 7.3;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQNMAYR 11  
 |||:|:|:  
 Db 63 CFTWERNLSSL 73

RESULT 7  
 T47233  
 cysteine synthase (EC 4.2.99.8) cysK - Lactococcus lactis subsp. cremoris  
 N:Alternate names: O-acetylserine sulfhydrylase  
 C:Species: Lactococcus lactis subsp. cremoris  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 03-Nov-2000  
 R:Accession: T47233  
 R:Fernandez, M.; van Doesburg, W.; Rutten, G.A.M.; Marugg, J.D.; Altling, A.C.; van Kran  
 Appl. Environ. Microbiol. 66, 42-48, 2000  
 A:Title: Molecular and functional analysis of the metC gene of Lactococcus lactis, encod  
 A:Reference number: Z24409; MUID:20087515; PMID:10618201  
 A:Accession: T47233  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-317 <PER>  
 A:Cross-references: EMBL:AF131880; NID:g6513594; PIDN:AAF14694.1; PID:g6513596  
 A:Experimental source: strain MG1363; asp. cremoris  
 C:Genetics:  
 A:Gene: cysK  
 C:Superfamily: threonine dehydratase  
 C:Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate

F:44/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted  
 Query Match 57.1%; Score 40; DB 2; Length 317;  
 Best Local Similarity 55.6%; Pred. No. 11;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WQNNMAKVR 12  
 |||:|:|:  
 Db 277 WQNNMAKVR 285

RESULT 8  
 A28438  
 lactoferrin precursor - mouse  
 N:Alternate names: lactotransferrin  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A28438; A41205  
 R:Pentecost, B.T.; Teng, C.T.  
 J. Biol. Chem. 262, 10134-10139, 1987  
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret  
 A:Reference number: A92596; MUID:87280033; PMID:3611056  
 A:Accession: A28438  
 A:Molecule type: mRNA  
 A:Residues: 3-707 <PEN>  
 A:Cross-references: EMBL:J03298  
 R:Liu, Y.; Teng, C.T.  
 J. Biol. Chem. 266, 21880-21885, 1991  
 A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.  
 A:Reference number: A41205; MUID:92042099; PMID:1939212  
 A:Accession: A41205  
 A:Molecule type: DNA  
 A:Residues: 1-15 <LIU>  
 A:Cross-references: GB:M74778  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-707/Product: lactotransferrin #status predicted <MAT>  
 F:338-695/Domain: transferrin repeat homology <TRH2>  
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 707;  
 Best Local Similarity 54.5%; Pred. No. 38;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNMAYR 11  
 |||:|:|:  
 Db 37 CLRWQNMAYR 47

RESULT 9  
 T00510  
 probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 23-Mar-2001  
 C:Accession: T00510; A84622  
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,  
 submitted to the EMBL Data Library, November 1997  
 A:Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.  
 A:Reference number: Z14164  
 A:Accession: T00510  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-515 <ROU>  
 A:Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642441  
 A:Experimental source: cultivar Columbia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N  
 m.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: A84622

A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-515 <STO>

A:Cross-references: GB:AE002093; NID:G2642441; PIDN:AA887109.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g23220; T20D16.15

A:Map position: 2

A:Introns: 182/3; 310/3

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:312-471/Domain: cytochrome P450 homology <P45>

F:449/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 54.3%; Score 38; DB 2; Length 515;

Best Local Similarity 83.3%; Pred. No. 43;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6

DB 469 CFEWQR 474

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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.F.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: C84325

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-584 <STO>

A:Cross-references: GB:AE004437; NID:G10581192; PIDN:AAG19967.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG1732C

Query Match 54.3%; Score 38; DB 2; Length 584;

Best Local Similarity 41.7%; Pred. No. 48;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWRNMAKVR 12

DB 445 CFTWRKDMERK 456

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RESULT 12

T08030

C:Species: Chlamydomonas reinhardtii

C:Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 02-Feb-2001

C:Accession: T08030

R;Mitchell, D.R.; Brown, K.S.

J. Cell Sci. 107, 635-644, 1994

A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.

A:Reference number: Z16302; MUID:94274778; PMID:8006077

A:Accession: T08030

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-4568 <MIT>

A:Cross-references: EMBL:U02963; NID:G409965; PIDN:AAA19956.1; PID:G514215

A:Experimental source: strain 21gr

C:Genetics:

A:Gene: ODA4

A:Map position: IX

A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;

3334/3; 3686/3; 3882/3; 4240/3

C:Superfamily: dynein heavy chain, ciliary

C:Keywords: nucleotide binding; P-loop

F:1919-1926/Region: nucleotide-binding motif A (P-loop)

F:2202-2209/Region: nucleotide-binding motif A (P-loop)

F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 54.3%; Score 38; DB 2; Length 4568;

Best Local Similarity 41.7%; Pred. No. 3.8e+02;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWRNMAKVR 12

DB 1852 CFQWQSLRYIQ 1863

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RESULT 13

T25415

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000

C:Accession: T25415

R;Wilkinson, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z20031

A:Accession: T25415

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-742 <WIL>

hypothetical protein T28D6.5 - Caenorhabditis elegans

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: C84325

hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: C84325

A;Cross-references: EMBL:281134; PIDN:CAB03450.1; GSPDB:GN00021; CESP:T28D6.5

A;Experimental source: clone T28D6

C;Genetics:

A;Gene: CESP:T28D6.5

A;Map position: 3

A;Introns: 9/3; 36/3; 70/3; 112/3; 258/3; 319/3; 468/2; 586/1; 638/3; 671/1

C;Superfamily: Caenorhabditis elegans hypothetical protein T28D6.5

#### Query Match

Best Local Similarity 52.9%; Score 37; DB 2; Length 742;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 CFQWQRMNAKVR 12

Db 193 CFWVRKSKAK 204

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#### RESULT 14

S58380

probable RNA-directed DNA polymerase (EC 2.7.7.49) - Crithidia fasciculata retrotransposon

N;Alternate names: probable reverse transcriptase

C;Species: Crithidia fasciculata

C;Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Sep-1997

C;Accession: S58380; S58381

R;Gabriel, A.

submitted to the EMBL Data Library, December 1994

A;Reference number: S58380

A;Accession: S58380

A;Molecule type: DNA

A;Residues: 1-2517 <GAB>

A;Cross-references: EMBL:U19151; NID:G624680; PID:G624681

R;Teng, S.C.; Wang, S.X.; Gabriel, A.

Nucleic Acids Res. 23, 2929-2936, 1995

A;Title: A new non-LTR retrotransposon provides evidence for multiple distinct site-spec

A;Reference number: S58381; MUID:95388509; PMID:7659515

A;Accession: S58381

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1825-2116 <TEN>

A;Cross-references: EMBL:U19151

A;Experimental source: retrotransposon CRE2

C;Genetics:

A;Mobile element: retrotransposon CRE2

C;Keywords: nucleotidyltransferase

#### Query Match

Best Local Similarity 52.9%; Score 37; DB 2; Length 2517;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 CFQWQRMNAKVR 12

Db 2457 FQWRRLAGVK 2467

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#### RESULT 15

C97414

hypothetical protein AGR\_C 800 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002

C;Accession: C97414

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; PMID:11743194

A;Accession: C97414

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-230 <KUR>

A;Cross-references: GB:AB007869; PIDN:AAK86268.1; PID:gl5155378; GSPDB:GN00169

C;Genetics:

A;Gene: AGR\_C 800

A;Map position: circular chromosome

#### Query Match

Best Local Similarity 52.1%; Score 36.5; DB 2; Length 290;

Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 FQWQRMNAK 10

Db 40 FQWQRMNAK 49

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Search completed: February 21, 2003, 07:47:48

Job time : 10.65 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107B-76  
Perfect score: 70  
Sequence: 1 CFQWQENMAKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	65	92.9	711	1 TRFL_HUMAN	P02788 homo sapien
2	51	72.9	708	1 TRFL_CAMDR	Q9tum0 camelus dro
3	48	68.6	708	1 TRFL_CAPHI	Q29477 capra hircu
4	43	61.4	695	1 TRFL_HORSE	O77811 equus caball
5	42	60.0	749	1 VP4_ROTGA	Q04916 rotavirus (
6	39	55.7	707	1 TRFL_MOUSE	P08071 mus musculu
7	38	54.3	4568	1 DYHE_CHIRE	Q39565 chlamydomon
8	36	51.4	435	1 DCOE_PANRE	P49725 panagrellus
9	36	51.4	496	1 MSS1_SCHPO	Q9ute7 schizosacch
10	36	51.4	628	1 FTH3_SYNY3	P73437 synectocyst
11	36	51.4	663	1 PDII_HUMAN	Q9ulc6 homo sapien
12	35	50.0	447	1 PD6C_SPIOL	P48629 spinacia ol
13	35	50.0	502	1 C911_ARATH	Q9f965 arabidopsis
14	35	50.0	665	1 YL14_CABEL	Q11100 caenorhabdi
15	35	50.0	708	1 FTA_EUCAI	P57273 buchnera ap
16	35	50.0	728	1 KDGI_ARATH	Q39017 arabidopsis
17	35	50.0	765	1 Y008_HUMAN	P27314 seoul virus
18	35	50.0	2151	1 RRPL_SEOU8	P27314 seoul virus
19	34	48.6	137	1 YEDD_ECOLI	P31063 escherichia
20	34	48.6	141	1 YEDD_SALTY	Q06399 salmonella
21	34	48.6	172	1 Y708_METJA	Q58118 methanococc
22	34	48.6	238	1 RNPH_AGRT5	Q8u198 agrobacteri
23	34	48.6	246	1 Y495_SYNY3	Q55185 synectocyst
24	34	48.6	275	1 IL2A_BOVIN	P12342 bos taurus
25	34	48.6	275	1 IL2A_SHEEP	P26898 ovis aries
26	34	48.6	324	1 RADA_SULSO	Q55075 sulfolobus
27	34	48.6	401	1 O88A_DROME	Q9vfn2 drosophila
28	34	48.6	422	1 PAPA_CHICK	Q90678 g platelet-
29	34	48.6	552	1 PYRG_SYNY3	P74208 synectocyst
30	34	48.6	566	1 YJ19_SYNY3	P73121 synectocyst
31	34	48.6	1135	1 PHYC_SORBI	P93528 sorghum bic
32	34	48.6	1564	1 PDRA_YEAST	P51533 saccharomyc
33	34	48.6	3680	1 DMD_CANFA	O97592 canis famli

34 33 47.1 128 1 YQ82\_CABEL Q9237 caenorhabdi  
35 33 47.1 154 1 YSCO\_YERPS P40294 yersinia ps  
36 33 47.1 164 1 DNAT\_BUCAI P57135 buchnera ap  
37 33 47.1 211 1 LOLE\_VIBCH P57070 vibrio chol  
38 33 47.1 274 1 APAH\_BUCAI P57242 buchnera ap  
39 33 47.1 285 1 YX47\_STRCO Q9x8h0 streptomyce  
40 33 47.1 292 1 NLA\_DROME Q9xzl8 drosophila  
41 33 47.1 303 1 UL24\_HSVSA Q01005 herpesvirus  
42 33 47.1 312 1 CCSA\_ODOSI P49523 odontella s  
43 33 47.1 331 1 CATS\_HUMAN P25774 homo sapien  
44 33 47.1 399 1 XYLR\_CALSR P40981 caldicellul  
45 33 47.1 407 1 YKAD\_CABEL P34263 caenorhabdi

## ALIGNMENTS

RESULT 1  
TRFL\_HUMAN STANDARD; PRJ: 711 AA.  
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;  
AC Q96KZ5;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;  
DE Lactoferrin B; Lactoferrin C].  
GN LTF OR LF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90384839; PubMed=2402455;  
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;  
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";  
RL Nucleic Acids Res. 18:5288-5288(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cho Y.Y.;  
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Conneely O.M.;  
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Liang Q., Jimenez-Flores R., Richardson T.;  
RL "Molecular cloning and sequence analysis of human lactoferrin.";  
RT Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Wei X., Han J., Rado T.A.;  
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA  
sequences";  
RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Chang H., Chen X., Huan L.;  
RL "cDNA cloning and sequence analysis of human lactoferrin.";  
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE=Mammary Gland.  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Ogden J.E.;  
RT "Nucleotide sequence of human lactoferrin cDNA.";  
RL Nucleic Acids Res. 18:4013-4013(1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
RA Legrand D., Spik G., Montreuil J., Jolles P.;  
RT "Human lactotransferrin: amino acid sequence and structural  
RT comparisons with other transferrins.";  
RL Eur. J. Biochem. 145:659-666(1984).  
RN [10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
RA Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
RT alignment of the cyanogen bromide fragments and characterization of  
RT N- and C-terminal domains.";  
RL Biochim. Biophys. Acta 670:243-254(1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
RA Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
RT lactotransferrin.";  
RL FEBS Lett. 142:107-110(1982).  
RN [12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
RT expression of mRNA during normal and leukemic myelopoiesis.";  
RL Blood 70:989-993(1987).  
RN [13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Chao L., la Bastide M., Kaplan N., Greco T., Touchman J., Mazny D.,  
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RA Sagripanti J.L.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2585506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
RT and refinement at 2.8-A resolution.";  
RL J. Mol. Biol. 209:711-734(1989).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
RT resolution.";  
RL Acta Crystallogr. D 51:629-646(1995).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
RA Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
RT binding properties and crystal structure of the histidine-  
RT 253->methionine mutant.";  
RL Biochemistry 36:341-346(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in Aspergillus  
RT awamori.";  
RL Acta Crystallogr. D 55:403-407(1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
RT and analysis of ligand-induced conformational change.";  
RL Acta Crystallogr. D 54:1319-1335(1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioic antagonist peptides derived  
RT from human lactoferrin.";  
RL Agric. Biol. Chem. 54:1803-1810(1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Clintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,  
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejtmancik J.F., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RL Mol. Vision 4:31-32(1998).  
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
CC OF AN ANION, USUALLY BICARBONATE.  
CC -1- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPTOID ANTAGONIST  
CC ACTIVITY. LACTOFERRONIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERRONIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X53961; CAA37914.1; -  
CC EMBL; U07643; AAB60324.1; -  
CC EMBL; M9150; AAA36159.1; -  
CC EMBL; M83202; AAA59511.1; -  
CC EMBL; M83205; AAA58656.1; -  
CC EMBL; M18642; AAA86665.1; -  
CC EMBL; AE332168; AAG48753.1; -  
CC EMBL; BC015822; AAH15822.1; -  
CC EMBL; BC015823; AAH15823.1; -  
CC EMBL; M73700; AAA59479.1; -  
CC EMBL; X52941; CAA37116.1; -  
CC EMBL; U95626; AAB57795.1; -  
CC PIR; S11228; TFFUL.  
CC PDB; 1LCE; 31-AUG-94.  
CC PDB; 1LCT; 31-OCT-93.  
CC PDB; 1LFG; 31-JUL-94.  
CC PDB; 1LPH; 31-OCT-93.  
CC PDB; 1LFI; 31-OCT-93.  
CC PDB; 1LGB; 31-AUG-94.  
CC PDB; 1LGC; 31-AUG-94.  
CC PDB; 1LGA; 08-NOV-96.  
CC PDB; 1DSN; 08-MAR-96.  
CC PDB; 1HSE; 12-MAR-97.  
CC PDB; 1VFD; 21-APR-97.



Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00048; Mismatches 1; Indels 0; Gaps 0;  
 Matches 11; Conservative 0;

QY 1 CFQWQRMKVR 12  
 DB 39 CFQWQRMKVR 50

RESULT 2  
 ID TRFL CAMDR STANDARD; PRT; 708 AA.  
 AC O9TUN0; Q9WZ55;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhon Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC  
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 CC -----  
 CC EMBL; AJ131674; CAB53387.1; -;  
 CC EMBL; AF165879; AAF82241.1; -;  
 CC HSP; O77811; 1B1X.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SM00094; TR\_FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN 1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN 2; 2.  
 CC PROSITE; PS00207; TRANSFERRIN 3; 2.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW Signal.  
 FT SIGNAL. 1 19 BY SIMILARITY.  
 FT CHAIN 20 708 LACTOTRANSFERRIN.  
 FT REPEAT 20 363 1.  
 FT REPEAT 364 708 2.  
 FT DISULFID 28 64 BY SIMILARITY.  
 FT DISULFID 38 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .)  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;  
 Query Match 72.9%; Score 51; DB 1; Length 708;  
 Best Local Similarity 75.0%; Pred. No. 0.14;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12  
 DB 38 CAQWQRMKVR 49

RESULT 3  
 ID TRFL CAPHI STANDARD; PRT; 708 AA.  
 AC Q29477; Q29479;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA MEDLINE=9438004; PubMed=8093048;  
 RA le Provost F.; Nocart M.; Guerin G.; Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the  
 RT relevant locus to bovine U12 syntenic group.";  
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.



FT DISULFID 463 538  
 FT DISULFID 487 681  
 FT DISULFID 497 511  
 FT DISULFID 508 521  
 FT DISULFID 579 593  
 FT DISULFID 631 636  
 FT METAL 66 66  
 FT METAL 98 98  
 FT METAL 138 198  
 FT METAL 239 259  
 FT METAL 401 401  
 FT METAL 439 439  
 FT METAL 532 532  
 FT METAL 601 601  
 FT BINDING 127 127  
 FT BINDING 469 469  
 FT CARBOHYD 143 143  
 FT CARBOHYD 287 287  
 FT CARBOHYD 482 482  
 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 61.4%; Score 43; DB 1; Length 695;  
 Best Local Similarity 66.7%; Pred. No. 3.7; Indels 2; Mismatches 2; Gaps 0;  
 Matches 8; Conservative 2; Indels 2; Gaps 0;

QY 1 CFOWQRMNAKVR 12  
 | : ||||| |  
 Db 25 CAKFQRMNAKVR 36

RESULT 5  
 VP4\_ROTGA STANDARD; PRT; 749 AA.  
 ID VP4\_ROTGA  
 AC Q04916;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).  
 GN S4.  
 OS Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).  
 OC Viruses; deRNA viruses; Reoviridae; Rotavirus.  
 OX NCBI\_TaxID=12705;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93233240; PubMed=8386274;  
 RA Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;  
 RT "Identification and baculovirus expression of the VP4 protein of the  
 human group B rotavirus ADRV";  
 RL J. Virol. 67:2730-2738(1993).  
 CC -!- SUBCELLULAR LOCATION: Outer capsid.  
 CC -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.  
 CC  
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 CC  
 CC EMBL; M51434; AAA47338.1; -  
 CC InterPro; IPR000416; Cap\_VP4.  
 CC Pfam; PF00426; VP4; 1.  
 CC  
 KW Coat protein; Glycoprotein.  
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 749 AA; 84362 MW; D123527DEAE0F21 CRC64;

Query Match 60.0%; Score 42; DB 1; Length 749;  
 Best Local Similarity 58.3%; Pred. No. 6;  
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFOWQRMNAKVR 12  
 | : ||||| |  
 Db 195 CFTWDMNCANVR 206

RESULT 6  
 TRPL\_MOUSE STANDARD; PRT; 707 AA.  
 ID TRPL\_MOUSE  
 AC P08071; P70690; Q61799; Q922P2;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87280033; PubMed=3611056;  
 RA Pentecost B.T., Teng C.T.;  
 RT "Lactotransferrin is the major estrogen inducible protein of mouse  
 uterine secretions";  
 RL J. Biol. Chem. 262:10134-10139(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Morishita K.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-14 FROM N.A.  
 RX MEDLINE=92042099; PubMed=1939212;  
 RA Liu Y., Teng C.T.;  
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter";  
 RL J. Biol. Chem. 266:21880-21885(1991).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 CC OF AN ANION, USUALLY BICARBONATE.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC  
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 CC  
 CC EMBL; J03298; AAA40525.1; -  
 CC EMBL; D88510; BAA1363.1; -  
 CC EMBL; BC006904; AAH06904.1; -  
 CC EMBL; M74778; AAA39427.1; -  
 CC PIR; A28438; A28438.  
 CC HSP; P02788; 1CB6.  
 CC MGD; MGI:96837; Ltf.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.

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DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR PER; 2
DR PROSITE: PS00205; TRANSFERRIN_1; 1.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
  1 19 BY SIMILARITY.
  FT SIGNAL.
  FT CHAIN.
  FT REPEAT 20 707 LACTOTRANSFERRIN.
  FT REPEAT 20 357 1.
  FT REPEAT 358 707 2.
  FT DISULFID 27 53 BY SIMILARITY.
  FT DISULFID 37 54 BY SIMILARITY.
  FT DISULFID 133 216 BY SIMILARITY.
  FT DISULFID 175 191 BY SIMILARITY.
  FT DISULFID 188 199 BY SIMILARITY.
  FT DISULFID 249 263 BY SIMILARITY.
  FT DISULFID 366 398 BY SIMILARITY.
  FT DISULFID 376 389 BY SIMILARITY.
  FT DISULFID 423 702 BY SIMILARITY.
  FT DISULFID 443 665 BY SIMILARITY.
  FT DISULFID 475 550 BY SIMILARITY.
  FT DISULFID 499 693 BY SIMILARITY.
  FT DISULFID 509 523 BY SIMILARITY.
  FT DISULFID 520 533 BY SIMILARITY.
  FT DISULFID 591 605 BY SIMILARITY.
  FT DISULFID 643 648 BY SIMILARITY.
  FT METAL 78 78 IRON 1 (BY SIMILARITY).
  FT METAL 110 110 IRON 1 (BY SIMILARITY).
  FT METAL 210 210 IRON 1 (BY SIMILARITY).
  FT METAL 271 271 IRON 2 (BY SIMILARITY).
  FT METAL 413 413 IRON 2 (BY SIMILARITY).
  FT METAL 451 451 IRON 2 (BY SIMILARITY).
  FT METAL 544 544 IRON 2 (BY SIMILARITY).
  FT METAL 613 613 ANION (POTENTIAL).
  FT BINDING 139 139 ANION (POTENTIAL).
  FT BINDING 481 481 ANION (POTENTIAL).
  FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
  FT CONFLICT 494 494 N-LINKED (GLCNAC. .) (POTENTIAL).
  FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
  FT CONFLICT 25 25 R -> Q (IN REF. 2).
  FT CONFLICT 82 82 M -> L (IN REF. 2).
  FT CONFLICT 359 359 S -> T (IN REF. 2).
  FT CONFLICT 382 382 A -> D (IN REF. 1).
  FT CONFLICT 449 449 E -> G (IN REF. 2).
  FT CONFLICT 629 629 L -> V (IN REF. 1).
  SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;

Query Match 55.7%; Score 39; DB 1; Length 707;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 11
Db 37 CLRQWQRMNAKV 47

RESULT 7
DYHB_CHLRE STANDARD; PRT; 4568 AA.
ID DYHB_CHLRE
AC Q39565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
CC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21gr;

RX MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes."
RL J. Cell Sci. 107:635-644(1994).
CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA). 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC
CC EMBL; U02963; AAA19956.1; -
CC InterPro; IPR004273; Dynein heavy.
CC Pfam; PF03028; Dynein heavy; 1.
CC Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 54.3%; Score 38; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMNAKV 12
Db 1852 CFQWQSQLRYIQ 1863

RESULT 8
DCOR_PANRE STANDARD; PRT; 435 AA.
ID DCOR_PANRE
AC P49725;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Ornithine decarboxylase (EC 4.1.1.17) (ODC).
GN ODC.
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
CC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95290001; PubMed=7772052;
RA von Besser H., Niemann G., Domdey B., Walter R.D.;
RT "Molecular cloning and characterization of ornithine decarboxylase
cDNA of the nematode Panagrellus redivivus."
RL Biochem. J. 308:635-640(1995).
CC -!- CATALYTIC ACTIVITY: L-ornithine = putrescine + CO(2).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY

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CC OF POLYAMINE BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGinine
CC DECARBOXYLASES.
CC
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CC -----
CC EMBL; X82199; CAA57683.1; -
CC DR EMBL; X95719; CAA65024.1; -
CC DR HSSP; P07805; 1F3T.
CC DR InterPro; IPR000183; Decarboxylase2.
CC DR Pfam; PF00278; Orn_DAP_Arg_deC; 1.
CC DR Pfam; PF02784; Orn_Arg_Gec_N; 1.
CC DR PRINTS; PR01179; ODACRBLXASE.
CC DR PROSITE; PS00878; ODR_DC_2_1; 1.
CC DR PROSITE; PS00879; ODR_DC_2_2; 1.
CC KW Lyase; Decarboxylase; Pyridoxal phosphate; Polyamine biosynthesis.
CC FT BINDING 76 PRIDOXAL PHOSPHATE (BY SIMILARITY).
CC FT ACT_SITE 368 368 BY SIMILARITY.
CC SQ SEQUENCE 435 AA; 47110 MW; BB093C1EF7FEFA4 CRC64;
CC
CC Query Match 51.4%; Score 36; DB 1; Length 435;
CC Best Local Similarity 66.7%; Pred. No. 40;
CC Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 3 QWQORNMAKV 11
CC Db 61 QWQORTMPRV 69
CC
CC RESULT 9
CC MSS1_SCHPO STANDARD; PRT; 496 AA.
CC ID MSS1_SCHPO STANDARD; PRT; 496 AA.
CC AC Q9UTE7;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE GTPase MSS1 homolog, mitochondrial precursor.
CC GN SPAC222.05C.
CC OS Schizosaccharomyces pombe (Fission yeast).
CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
CC OC Schizosaccharomycetes.
CC OX NCBI_TaxID=4895;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=972;
CC RX MEDLINE=21848401; PubMed=11859360;
CC RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
CC RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
CC RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
CC RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
CC RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
CC RA Holroyd S., Hohnsby T., Howarth S., Ruckie E.J., Hunt S., Jagels K.,
CC RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
CC RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
CC RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
CC RA Rutherford K., Rutter S., Saunders D., Seeger K., Stevens K.,
CC RA Skellern J., Simmonds M., Squares R., Squares S., Sharns K.,
CC RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
CC RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
CC RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
CC RA Gabel C., Fuchs M., Pritcz C., Holzer E., Moestl D., Hilbert H.,
CC RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
CC RA Eger P., Zimmermann W., Wedler H., Wambutt R., Fournelle B.,
CC RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
CC RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

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RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
RA Cerutti L., Lowe I., McCombie W.R., Paulsen I., Potashkin J.,
RA Spakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
CC PROTEINS. TRME SUBFAMILY.
CC
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CC
CC -----
CC EMBL; AL132798; CAB60697.1; -
CC DR InterPro; IPR005289; GTP-binding_dom.
CC DR InterPro; IPR002917; MWR_HSR1.
CC DR InterPro; IPR005225; Small_GTP.
CC DR InterPro; IPR004520; ThdF.
CC DR Pfam; PF01926; MWR_HSR1; 1.
CC DR TIGRFAMs; TIGR00231; small_GTP; 1.
CC DR TIGRFAMs; TIGR00450; thdF; 1.
CC DR TIGRFAMs; TIGR00650; MG442; 1.
CC KW trNA processing; Mitochondrion; GTP-binding; Transit peptide.
CC FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
CC FT CHAIN 246 253 GTP (POTENTIAL).
CC FT NP_BIND 246 253 GTP (POTENTIAL).
CC SQ SEQUENCE 496 AA; 55315 MW; 092F7E1E1CDD80D2 CRC64;
CC
CC Query Match 51.4%; Score 36; DB 1; Length 496;
CC Best Local Similarity 33.3%; Pred. No. 46;
CC Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 CFQWQORNMAKV 12
CC Db 178 CFWWRKKLIEYR 189
CC
CC RESULT 10
CC FTH3_SYNY3 STANDARD; PRT; 628 AA.
CC ID FTH3_SYNY3 STANDARD; PRT; 628 AA.
CC AC P73437;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Cell division protein ftsH homolog 3 (EC 3.4.24.-).
CC GN SLL1463.
CC OS Synechocystis sp. (strain PCC 6803).
CC OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
CC OX NCBI_TaxID=1148;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=97061201; PubMed=8905231;
CC RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
CC RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
CC RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
CC RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
CC RA Yanada M., Yasuda M., Tabata S.;
CC RT "Sequence analysis of the genome of the unicellular cyanobacterium
CC Synechocystis sp. strain PCC6803. II. Sequence determination of the
CC entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
CC (BY SIMILARITY).
CC -!- COPACITOR. BINDS 1 ZINC ION (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41.

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DR EMBL; D90906; BAA17477.1; -  
 DR MEMOPS; M41.009; -  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003959; AAA\_ATPase\_cent.  
 DR InterPro; IPR003960; AAA\_sub.  
 DR InterPro; IPR000642; Peptidase\_M41.  
 DR InterPro; IPR000130; Zn\_Mpeptidase.  
 DR Pfam; PF00004; AAA; 1.  
 DR Pfam; PF01434; Peptidase\_M41; 1.  
 DR SMART; SMO0382; AAA; 1.  
 DR TIGRfam; TIGR01241; FtsH\_fam; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR PROSITE; PS00674; AAA; 1.  
 KW Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;  
 KW Zinc; Multigene family; Complete proteome.  
 KW Zinc; Multigene family; Complete proteome.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 31 POTENTIAL.  
 FT DOMAIN 32 119 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 120 142 POTENTIAL.  
 FT DOMAIN 143 221 CYTOPLASMIC (POTENTIAL).  
 FT NP\_BIND 214 221 ATP (POTENTIAL).  
 FT METAL 438 439 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT\_SITE 439 439 BY SIMILARITY.  
 FT METAL 442 442 ZINC (CATALYTIC) (BY SIMILARITY).  
 SQ SEQUENCE 628 AA; 68199 MW; 8B2563000F73EBA CRC64;

Query Match 51.4%; Score 36; DB 1; Length 628;  
 Best Local Similarity 66.7%; Pred. No. 58;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQRNMAKV 11  
 DB 8 QWQRRLASV 16

RESULT 11  
 PD11 HUMAN STANDARD; PRT; 663 AA.  
 AC Q2ULC6.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-arginine deiminase type I (EC 3.5.3.15) (Peptidylarginine  
 DE deiminase I).  
 GN PD11 OR PD11.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 RC TISSUE=Epidermis;  
 RC TISSUE=Epidermis;  
 RA Tishigami A., Guerrin-Weber M., Sebbag M., Serre G., Senshu T.;  
 RA "Molecular cloning of peptidylarginine deiminase type I cDNA from a  
 RT human epidermis.";  
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: CATALYZES THE DEIMINATION OF ARGININE RESIDUES OF  
 CC PROTEINS (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: Protein L-arginine + H(2)O = protein L-  
 CC citrulline + NH(3).  
 CC -!- COFACTOR: REQUIRES CALCIUM IONS (BY SIMILARITY).  
 CC -!- SIMILARITY: SOME SIMILARITY WITH ARGINASE AND TO ARGININE  
 CC DEIMINASE.

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DR EMBL; AB033768; BAA85771.1; -  
 DR Genew; HGNC; 18367; PAD11.  
 DR InterPro; IPR004303; Prot\_arg\_deim.  
 DR Pfam; PF03068; PAD; 1.  
 KW Hydrolase; Calcium-binding; Multigene family.  
 FT CA\_BIND 506 517 EF-HAND (POTENTIAL).  
 SQ SEQUENCE 663 AA; 74607 MW; 0BD8D460634EE2D9 CRC64;

Query Match 51.4%; Score 36; DB 1; Length 663;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQQRNMAK 10  
 DB 546 CIDWNRNVLK 555

RESULT 12  
 FD6C SPIOL STANDARD; PRT; 447 AA.  
 ID PD6C SPIOL  
 AC P48629;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).  
 GN FAD6.  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 [1]  
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.  
 RP STRAIN=cv. Subito; TISSUE=Leaf;  
 RC MEDLINE=95036044; PubMed=7948918;  
 RX Schmidt H., Dresselhaus T., Buck F., Heinz E.;  
 RA "Purification and PCR-based cDNA cloning of a plastidial n-6  
 RT desaturase.";  
 RL Plant Mol. Biol. 26:631-642(1994).  
 CC -!- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES  
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY  
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT  
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS  
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.  
 CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).  
 CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE  
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 CC  
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DR EMBL; X78311; CAA55121.1; -  
 DR InterPro; IPR001225; FA\_Desaturase.  
 DR Pfam; PF00487; FA\_Desaturase; 1.  
 DR ProDom; PD001081; FA\_Desaturase; 1.  
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
 KW Transit peptide.  
 FT TRANSIT 1 65 CHLOROPLAST.

FT CHAIN 66 447 OMEGA-6 FATTY ACID DESATURASE.  
 FT DOMAIN 171 175 HISTIDINE BOX-1.  
 FT DOMAIN 207 211 HISTIDINE BOX-2.  
 FT DOMAIN 367 371 HISTIDINE BOX-3.  
 SQ SEQUENCE 447 AA; 51306 MW; 2BA7C87FF9F5350E CRC64;  
 Query Match 50.0%; Score 35; DB 1; Length 447;  
 Best Local Similarity 43.8%; Pred. No. 62;  
 Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;  
 QY 1 CFOWQ---RNNAKVR 12  
 Db 33 CIKQKPCRLNLGHVR 48  
 RESULT 13  
 C911 ARATH STANDARD; PRT; 502 AA.  
 AC Q9FG65; O65789;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cytochrome P450 91A1 (EC 1.14.1.1).  
 GN CYP91A1 OR AT5G36220 OR T3066.3.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016721; PubMed=11130714;  
 RA Tabata S., Kaneo T., Nakamura Y., Kotani H., Kato T., Asamizu E.,  
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,  
 RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,  
 RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,  
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,  
 RA Habermann K., Murray J., Johnson D., Rohlfing J., Nelson R.,  
 RA Stoenkang T., Pepin K., Speith J., Sekhon M., Armstrong J., Becker M.,  
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,  
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,  
 RA Leonard S., Meyer R., Mulvaney E., Ozerky P., Riley A., Stromatt C.,  
 RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,  
 RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,  
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,  
 RA Martensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,  
 RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,  
 RA Entian K.-D., Terry N., Hartley N., Bent E., Johnson S.,  
 RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,  
 RA Rampertger U., Wedler H., Balke K., Wedler E., Peters S.,  
 RA van Staveren M., Dirks W., Mooijman P., Klein Lankhorst R.,  
 RA Weizsaecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,  
 RA Feldpausch M., Lamberth S., Villarroel R., Giesen J., Ardiles W.,  
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,  
 RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,  
 RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis  
 thaliana."  
 RL Nature 408:823-826 (2000).  
 RN [2]  
 RP SEQUENCE OF 3-502 FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=98281573; PubMed=9620263;  
 RA Mizutani M., Ward E., Ohta D.,  
 RT "Cytochrome P450 superfamily in Arabidopsis thaliana: isolation of  
 cDNAs, differential expression, and RFLP mapping of multiple  
 cytochromes P450."  
 RL Plant Mol. Biol. 37:39-52 (1998).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
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 CC -----  
 DR EMBL; AB026661; BAB09361.1; -.  
 DR EMBL; D78606; BAA28538.1; -.  
 DR HSP; P14779; IJPZ.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450.1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.  
 FT TRANSMEM 6  
 FT BINDING 440 440 HEME (BY SIMILARITY).  
 FT SEQUENCE 502 AA; 56723 MW; 1A348ABDD76A41B0 CRC64;  
 Query Match 50.0%; Score 35; DB 1; Length 502;  
 Best Local Similarity 66.7%; Pred. No. 70;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFOWQ 6  
 Db 460 CFWEHR 465  
 RESULT 14  
 YL14 CAEL STANDARD; PRT; 665 AA.  
 ID YL14 CAEL  
 AC Q11100;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein C02F12.4 in chromosome X.  
 GN C02F12.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Paloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2.  
 RA Miller N.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; U41545; AAK39134.1; -.  
 DR WormPep; C02F12.4; CE03899.  
 DR InterPro; IPR001331; GDS\_CDC24.  
 DR InterPro; IPR001849; PH\_  
 DR InterPro; IPR001230; Prenyl\_site.  
 DR InterPro; IPR000219; RhogEF.  
 DR Pfam; PF00621; RhogEF; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RhogEF; 1.  
 DR PROSITE; PS00741; DH\_1; FALSE\_NEG.  
 DR PROSITE; PS50010; DH\_2; 1.  
 KW Hypothetical protein.  
 FT DOMAIN 54 227 DH.  
 SQ SEQUENCE 665 AA; 76818 MW; 909FB2E03EA76AA6 CRC64;  
 Query Match 50.0%; Score 35; DB 1; Length 665;  
 Best Local Similarity 66.7%; Pred. No. 92;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WORNMAKVR 12  
 DB 380 WORNDRKLR 388

RESULT 15  
 ID\_PTA\_BUCAI STANDARD; PRT; 708 AA.  
 AC P57273;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phosphate acetyltransferase (EC 2.3.1.8) (Phosphotransacetylase).  
 GN PTA OR BUL76;  
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
 symbiotic bacterium).  
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
 ON NCBI TaxID=118099;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Tokyo 1998;  
 RX MEDLINE=20445173; PubMed=10993077;  
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
 RT "Genome sequence of the endocellular bacterial symbiont of aphids  
 Buchnera sp. APS.";  
 RL Nature 407:81-86(2000).  
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + phosphate = CoA + acetyl  
 phosphate  
 CC -!- PATHWAY: LAST OF TWO STEPS IN THE CONVERSION OF ACETATE TO  
 ACETYL-COA.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; CONTAINS A DOMAIN WITH SOME  
 SIMILARITIES WITH COBQ/BIOD.  
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PHOSPHATE  
 ACETYLTRANSFERASE AND BUTYRYLTRANSFERASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF001118; BAB12893.1; -;  
 DR InterPro; IPR002505; PTA\_PTB.  
 DR InterPro; IPR004614; Pta\_  
 DR Pfam; PF01515; PTA\_PTB; 1.  
 DR TIGRFAMs; TIGR00651; Pta; 1.  
 KW Transferase; Acyltransferase; Complete proteome.  
 FT DOMAIN 388 708 PHOSPHATE ACETYLTRANSFERASE.  
 SQ SEQUENCE 708 AA; 80770 MW; 1EDC4394824ED89A CRC64;

Query Match 50.0%; Score 35; DB 1; Length 708;  
 Best Local Similarity 41.7%; Pred No. 98;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CFQWORNMAKVR 12  
 DB 217 CIPWNRNIVTR 228

Search completed: February 21, 2003, 07:27:51  
 Job time : 6.6 secs



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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107B-76  
Perfect score: 70  
Sequence: 1 CFQWQRNMAKVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.\*  
1: sp\_archea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_proteob.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacterioph.\*  
17: sp\_archesp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	85.7	711	4 Q8TCD2	Q8tcd2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9ucy5 homo sapien
3	47	67.1	511	16 Q82462	Q82462 salmonella
4	45	64.3	33	6 Q9TR80	Q9tr80 ovis aries
5	41	58.6	469	9 Q38115	Q38115 bacterioph
6	40	57.1	205	8 Q98RR2	Q98rr2 guillardia
7	40	57.1	1376	3 Q8X1P2	Q8xip2 podospora a
8	40	57.1	2186	5 Q9N306	Q9n306 trypanosoma
9	39	55.7	372	10 Q81653	Q81653 hemerocalli
10	39	55.7	1617	4 Q8WNZ6	Q8wnz6 homo sapien
11	38	54.3	105	10 Q9XFD5	Q9xfds oryza sativ
12	38	54.3	515	10 Q22185	Q22185 arabidopsis
13	38	54.3	543	10 Q22188	Q22188 arabidopsis
14	38	54.3	584	17 Q9HPA3	Q9hpa3 halobacteri
15	38	54.3	750	12 Q9E8I8	Q9e8i8 human rotav
16	37	52.9	212	5 Q9BID5	Q9bid5 heterodera

17	37	52.9	212	5	Q967C4	Q967c4 heterodera
18	37	52.9	444	10	Q9AX10	Q9ax10 oryza sativ
19	37	52.9	730	12	Q83343	Q83343 murid herpe
20	37	52.9	742	5	Q18151	Q18151 caenorhabdi
21	36.5	52.1	290	16	Q8U5K9	Q8u5k9 agrobacteri
22	36	51.4	57	16	Q9JV34	Q9jv34 neisseria m
23	36	51.4	91	15	Q77855	Q77855 human immun
24	36	51.4	91	15	Q77856	Q77856 human immun
25	36	51.4	119	15	Q8Q454	Q8q454 human immun
26	36	51.4	148	10	Q9XHP1	Q9xhp1 sesamum ind
27	36	51.4	298	16	Q8YP77	Q8yp77 anabaena sp
28	36	51.4	341	11	Q8R2A4	Q8r2a4 mus musculu
29	36	51.4	405	16	Q92F81	Q92f81 listeria in
30	36	51.4	408	16	Q8YAE4	Q8yae4 listeria mo
31	36	51.4	501	3	Q9UUD0	Q9uud0 schizosacch
32	36	51.4	518	10	Q9SI49	Q9si49 arabidopsis
33	36	51.4	602	10	Q8S013	Q8s013 oryza sativ
34	36	51.4	753	5	Q9NDT2	Q9ndt2 plasmodium
35	36	51.4	820	16	Q9KEF0	Q9kef0 vibrio chol
36	36	51.4	1049	10	Q9FVG3	Q9fvg3 arabidopsis
37	36	51.4	1055	10	Q9LIV9	Q9liv9 oryza sativ
38	36	51.4	1137	5	Q9VSA6	Q9vsa6 drosophila
39	36	51.4	1274	10	Q9S287	Q9s287 arabidopsis
40	36	51.4	1767	10	Q8O663	Q8o663 arabidopsis
41	35.5	50.7	451	16	Q8YQB2	Q8yqb2 anabaena sp
42	35	50.0	99	15	Q8Q2M7	Q8q2m7 human immun
43	35	50.0	145	10	Q9ZQM4	Q9zqm4 arabidopsis
44	35	50.0	160	5	Q9VIY2	Q9viy2 drosophila
45	35	50.0	185	10	Q9SW68	Q9sw68 arabidopsis

#### ALIGNMENTS

#### RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.  
 ID Q8TCD2;  
 AC Q8TCD2;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Lactotransferrin.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PROSTATE;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC022347; AAH22347.1; -- 1B9CTEE097C45PAP CRC64;  
 SQ SEQUENCE 711 AA; 78327 MW; 1B9CTEE097C45PAP CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;  
 Best Local Similarity 90.9%; Pred.No. 0.0052;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMAKV 11  
 DB 39 CFQWQRNMAKV 49

#### RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.  
 ID Q9UCY5  
 AC Q9UCY5;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE Lactoferrin homolog (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RA Sato I.;  
 RT "Characterization of the 84-kDa protein with ABH activity in human  
 RT seminal plasma";  
 RL Jpn. J. Legal Med. 49:281-293(1995).  
 DR HSP; P02788; 1BKA.  
 DR InterPro: IPR001156; Transferrin.  
 DR Pfam: PF00405; transferrin; 1.  
 SQ SEQUENCE 38 AA; 4459 MW; 0402P490B5EBDEB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;  
 Best Local Similarity 90.9%; Pred. No. 0.0012;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNRKVR 12  
 Db 21 FQWQNRKVR 31

RESULT 3  
 Q82462  
 ID Q82462 PRELIMINARY; PRT; 511 AA.  
 AC Q82462;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein ST3070.  
 GN STY3070.  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11577608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18";  
 RL Nature 413:848-852(2001).  
 DR EMBL; AL622276; CAD06049.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match 67.1%; Score 47; DB 16; Length 511;  
 Best Local Similarity 66.7%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 12  
 Db 350 CFQWQNRKVR 361

RESULT 4  
 Q9TR80  
 ID Q9TR80 PRELIMINARY; PRT; 33 AA.  
 AC Q9TR80;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Lactoferrin (Fragment).  
 OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=95127729; PubMed=7827104;  
 RA Qian Z.Y., Jolles P., Migliore-Samouri D., Fiat A.M.;  
 RL Biochim. Biophys. Acta 1243:25-32(1995).  
 DR HSP; O77698; ICE2.  
 DR InterPro: IPR001156; Transferrin.  
 DR Pfam: PF00405; transferrin; 1.  
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;  
 Best Local Similarity 54.5%; Pred. No. 0.13;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 11  
 Db 19 CYQWQNRKVR 29

RESULT 5  
 Q38115  
 ID Q38115 PRELIMINARY; PRT; 469 AA.  
 AC Q38115;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE ORF29.  
 OS Bacteriophage rlt.  
 OC Viruses.  
 OX NCBI\_TaxID=43695;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96332668; PubMed=8730874;  
 RA Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;  
 RT "Inducible gene expression mediated by a repressor-operator system  
 RT isolated from *Lactococcus lactis* bacteriophage rlt.";  
 RL Mol. Microbiol. 19:1331-1341(1996).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96332669; PubMed=8730875;  
 RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,  
 RA Venema G., Nauta A.;  
 RT "Sequence analysis and molecular characterization of the temperate  
 RT lactococcal bacteriophage rlt.";  
 RL Mol. Microbiol. 19:1343-1355(1996).  
 DR EMBL; U38906; AAB18704.1; -;  
 SQ SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;

Query Match 58.6%; Score 41; DB 9; Length 469;  
 Best Local Similarity 50.0%; Pred. No. 14;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKVR 10  
 Db 39 CYPWQNRKVR 48

RESULT 6  
 Q98RR2  
 ID Q98RR2 PRELIMINARY; PRT; 205 AA.  
 AC Q98RR2;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE 26S proteasome SU B5.  
 GN PRS5.  
 OS Guillardia theta (Cryptomonas phi).  
 OC Nucleomorph.  
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

OX NCBI\_TaxID=55529;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2123349; PubMed=11323671;

RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,

RT Wu X., Reich M., Cavalier-Smith T., Maier U.G.;

RL "The highly reduced genome of an enslaved algal nucleus.";

DR EMBL; AF165818; AAK39885.1; -

DR InterPro; IPR000243; Proteasome B.

DR Pfam; PF00227; Proteasome; 1.

DR PRINTS; PR00141; PROTEASOME.

DR Proteasome.

SQ SEQUENCE 205 AA; 22691 MW; D30F5289C8C85049 CRC64;

Query Match 57.1%; Score 40; DB 8; Length 205;

Best Local Similarity 45.5%; Pred. No. 9;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNMAKV 11

|||:|:|:|

Db 63 CFWEENLSSL 73

RESULT 7

Q8X1P2

ID Q8X1P2 PRELIMINARY; PRT; 1376 AA.

AC Q8X1P2

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Beta transducin-like protein HET-D2Y.

GN HET-D.

OS Podospora anserina.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariales; Lasiosphaeriaceae; Podospora.

OX NCBI\_TaxID=5145;

RN [1]

RP SEQUENCE FROM N.A.

RA Espagne E., Balhadere P., Begueret J., Turcq B.;

RT "A new family of WD40 proteins implicated in vegetative

RT incompatibility; evidence for a major role of WD40 repeat domain in

RT the specificity of het-e and het-d genes.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AF232585; AAL37301.1; -

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 12.

DR PRINTS; PR00320; GPROTEINRPT.

DR ProDom; PD000018; WD40; 9.

DR SMART; SM00320; WD40; 12.

DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_11.

DR PROSITE; PS00682; WD\_REPEATS\_2; 11.

DR PROSITE; PS0294; WD\_REPEATS\_REGION; 1.

SQ SEQUENCE 1376 AA; 152068 MW; 2191826AA5C62D97 CRC64;

Query Match 57.1%; Score 40; DB 3; Length 1376;

Best Local Similarity 77.8%; Pred. No. 72;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNNMAKV 10

|||:|:|:|

Db 95 FQWYRNAAK 103

RESULT 8

Q9N906

ID Q9N906 PRELIMINARY; PRT; 2186 AA.

AC Q9N906;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Conserved hypothetical protein CHRI.67.

GN

OS Trypanosoma brucei.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

OX NCBI\_TaxID=5691;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TREU927;

RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,

RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,

RA Gerrard C., Rajandream M.A., Barrell B.G.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AL359782; CAB95377.1; -

DR InterPro; IPR002035; VWF\_A.

DR SMART; SM00327; VWA; 1.

DR PROSITE; PS0234; VWF; 1.

KW Hypothetical protein.

SQ SEQUENCE 2186 AA; 245737 MW; 78BB75505012005A CRC64;

Query Match 57.1%; Score 40; DB 5; Length 2186;

Best Local Similarity 40.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMAKV 10

|||:|:|:|

Db 588 CYWERNASR 597

RESULT 9

O81653

ID O81653 PRELIMINARY; PRT; 372 AA.

AC O81653;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Senescence-associated protein 3 (Fragment).

GN SA3.

OS Hemerocallis hybrid cultivar.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;

OC Hemerocallidaceae; Hemerocallis.

OX NCBI\_TaxID=80862;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;

RX MEDLINE=99339249; PubMed=10412903;

RA Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker E.L.;

RT "Identification of senescence-associated genes from daylily petals.";

RL Plant Mol. Biol. 40:237-248(1999).

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

DR EMBL; AF082028; AAC34853.1; -

DR InterPro; IPR001128; Cytochrome\_P450.

DR Pfam; PF00067; P450; 1.

DR PRINTS; PR00385; P450.

DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN\_1.

KW Heme; Monooxygenase; Oxidoreductase.

FT NON TER 1

SQ SEQUENCE 372 AA; 41909 MW; 55FB3EAF9699595E CRC64;

Query Match 55.7%; Score 39; DB 10; Length 372;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNN 7

|||:|:|:|

Db 328 CFWDNRN 334

RESULT 10

Q8WZ6

ID Q8WZ6 PRELIMINARY; PRT; 1617 AA.

AC Q8WZ6;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ATP-binding cassette A6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schriem L.M., Arnould I., Prades C., Lachtermacher-Rocha M.,
RA Schneider T., Maitoux C., Lemoine C., Debono D., Devaud C.,
RA Naudin L., Bauche S., Annat M., Alimets R., Deneffe P., Rosier M.,
RA Dean M.;
RT "Identification and characterization of a cluster of five new ATP-
RT binding cassette transporter genes on human chromosome 17q24: a novel
RT sub-group within the ABCA sub-family.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY028898; AAC30023.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR004881; DUF258.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF03193; DUF258; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SMC0382; AAA; 2.
KW ATP-binding.
SQ SEQUENCE 1617 AA; 184254 MW; E7A9641621045DC1 CRC64;
Query Match 55.7%; Score 39; DB 4; Length 1617;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNNAKV 11
DB 440 CFQHQRTNAKV 450
|||||

RESULT 11
Q9XFD5 PRELIMINARY; PRT; 105 AA.
AC Q9XFD5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=PANICLE;
RA Liu J., Yang J.;
RT "Suppression subtractive hybridization (SSH) identified candidate
RT genes that are differentially expressed at rice young panicle.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF140486; RAD3699.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON TER
SQ SEQUENCE 105 AA; 11912 MW; B0EEFCD487819F9 CRC64;
Query Match 54.3%; Score 38; DB 10; Length 105;
Best Local Similarity 83.3%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6
DB 61 CFQWR 66
|||||

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RESULT 12
O22185 PRELIMINARY; PRT; 515 AA.
AC O22185;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative cytochrome P450.
GN AT2G23220.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Gruell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AC002391; AAB87109.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 515 AA; 59089 MW; 3177CC439269D15B CRC64;
Query Match 54.3%; Score 38; DB 10; Length 515;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6
DB 469 CFQWR 474
|||||

RESULT 13
O22188 PRELIMINARY; PRT; 543 AA.
AC O22188;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative cytochrome P450.
GN AT2G23190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

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RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,  
RA Copenhagen G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,  
RA Salzberg S.L., Fraser C.M., Venter J.C.;  
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana.";  
RL Nature 402:761-768(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
DR EMBL; AC002391; AAB87112.1; -.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PF00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Heme; Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 543 AA; 62777 MW; 06332D6C090FDB12 CRC64;  
Query Match 54.3%; Score 38; DB 10; Length 543;  
Best Local Similarity 83.3%; Pred. No. 63;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CFQWQR 6  
DB 498 CFQWQR 503  
RESULT 14  
ID Q9HPA3 PRELIMINARY; PRT; 584 AA.  
AC Q9HPA3;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Vng1732c.  
GN VNG1732C.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
OX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20504483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
RA Isenbarger T.A., Peck R.F., Pohlischer M., Spudich J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;  
RT "Genome sequence of Halobacterium species NRC-1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL; AE005078; AAG19987.1; -.  
DR InterPro; IPR001646; Septicide\_repeat.  
DR InterPro; IPR001622; K-channel\_pore.  
DR Pfam; PF00805; Pentapeptide; 2.  
KW Complete proteome.  
SQ SEQUENCE 584 AA; 65151 MW; 21BF5D5F0486CC06 CRC64;

Query Match 54.3%; Score 38; DB 17; Length 584;  
Best Local Similarity 41.7%; Pred. No. 68;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNMAKVR 12  
DB 445 CFQWQRNMAKVR 456

RESULT 15  
Q9B8I8 PRELIMINARY; PRT; 750 AA.  
ID Q9B8I8;  
AC Q9B8I8;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Outer capsid protein VP4.  
OS Human rotavirus B.  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
OX NCBI\_TaxID=10942;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CAL;  
RX MEDLINE=21080727; PubMed=11213100;  
RA Sen A., Kobayashi N., Das S., Krishnan T., Bhattacharya S.K.,  
RA Naik T.N.;  
RT "The evolution of human group B rotaviruses.";  
RL Lancet 357:198-199(2001).  
DR EMBL; AF184084; AAG16961.1; -.  
DR InterPro; IPR000416; Cap\_VP4.  
DR Pfam; PF00426; VP4; 1.  
SQ SEQUENCE 750 AA; 84727 MW; AF2F7BADE93BF9E8 CRC64;  
Query Match 54.3%; Score 38; DB 12; Length 750;  
Best Local Similarity 50.0%; Pred. No. 89;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 CFQWQRNMAKVR 12  
DB 196 CFQWQRNMAKVR 207

Search completed: February 21, 2003, 07:44:30  
Job time : 21.8 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56,502 Million cell updates/sec

Title: US-09-743-107b-77  
Perfect score: 70  
Sequence: 1 CFQWQNRRAVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
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6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
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11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	70	100.0	12	21	AAV78077 Human lactoferrin
2	65	92.9	12	21	AAV78038 Human lactoferrin
3	65	92.9	12	21	AAV78046 Human lactoferrin
4	65	92.9	12	21	AAV78047 Human lactoferrin
5	65	92.9	13	21	AAV78037 Human lactoferrin
6	65	92.9	13	21	AAV78048 Human lactoferrin
7	65	92.9	13	21	AAV78049 Human lactoferrin
8	65	92.9	14	21	AAV78036 Human lactoferrin
9	65	92.9	14	21	AAV78050 Human lactoferrin
10	65	92.9	14	21	AAV78051 Human lactoferrin

11	65	92.9	15	17	AAV98854 Peptide for anti-u
12	65	92.9	15	21	AAV78035 Human lactoferrin
13	65	92.9	15	21	AAV78052 Human lactoferrin
14	65	92.9	15	21	AAV78063 Human lactoferrin
15	65	92.9	16	21	AAV78031 Human lactoferrin
16	65	92.9	16	21	AAV78064 Human lactoferrin
17	65	92.9	16	21	AAV78065 Human lactoferrin
18	65	92.9	17	21	AAV78034 Human lactoferrin
19	65	92.9	17	21	AAV78066 Human lactoferrin
20	65	92.9	17	21	AAV78067 Human lactoferrin
21	65	92.9	18	15	AAV69352 Human lactoferrin
22	65	92.9	18	17	AAV13397 Advanced glycosyla
23	65	92.9	18	21	AAV78033 Human lactoferrin
24	65	92.9	19	21	AAV68867 Amino acid sequenc
25	65	92.9	19	21	AAV78032 Human lactoferrin
26	65	92.9	20	13	AAV21810 Anti microbial pep
27	65	92.9	20	14	AAV44841 Lactoferrin-relate
28	65	92.9	20	15	AAV48530 Lactoferrin derive
29	65	92.9	20	15	AAV48531 Lactoferrin derive
30	65	92.9	20	15	AAV57461 Lactoferrin derive
31	65	92.9	20	15	AAV57462 Lactoferrin derive
32	65	92.9	20	16	AAV84698 Bovine lactoferrin
33	65	92.9	20	16	AAV84699 Bovine lactoferrin
34	65	92.9	20	16	AAV80283 Anti-parasitic lac
35	65	92.9	20	16	AAV80284 Anti-parasitic lac
36	65	92.9	20	17	AAV98553 Peptide for anti-u
37	65	92.9	20	17	AAV91852 Lactoferrin-derive
38	65	92.9	20	17	AAV03045 Lactoferrin-derive
39	65	92.9	20	17	AAV90607 Lactoferrin-derive
40	65	92.9	20	17	AAV87621 Lactoferrin-derive
41	65	92.9	20	17	AAV87622 Lactoferrin-derive
42	65	92.9	20	18	AAV26150 Lactoferrin derive
43	65	92.9	20	18	AAV14036 Anti-parasitic pep
44	65	92.9	20	19	AAV70310 Thrombus formation
45	65	92.9	20	19	AAV53224 Lactoferrin hydrol

#### ALIGNMENTS

RESULT 1  
AAV78077  
ID AAV78077 standard; Peptide; 12 AA.  
XX AC AAV78077;  
XX DT 25-APR-2000 (first entry)  
XX DE Human lactoferrin derived peptide SEQ ID NO:77.  
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX OS Homo sapiens.  
OS Synthetic.  
XX PN WO200001730-A1.  
XX PD 13-JAN-2000.  
XX PF 06-JUL-1999; 99WO-SE01230.  
XX PR 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX PA (ASCI-) A+ SCI INVEST AB.  
XX PI Hanson LA; Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX SQ Sequence 12 AA;  
Query Match 100.0%; Score 70; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRVR 12  
DB 1 CFQWQRNMRVR 12  
|||||

RESULT 2  
AAY78038  
ID AAY78038 standard; Peptide; 12 AA.  
XX AC AAY78038;  
XX DT 25-APR-2000 (first entry)  
XX DE Human lactoferrin derived peptide SEQ ID NO:38.  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200001730-A1.  
XX PD 13-JAN-2000.  
XX PF 06-JUL-1999; 99WO-SE01230.  
XX PR 06-JUL-1998; 98SE-0002441.  
XX PR 17-JUL-1998; 98SE-0002562.  
XX PR 29-DEC-1998; 98SE-0004614.  
XX PA (ASCI-) A+ SCI INVEST AB.  
XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.

XX SQ Sequence 12 AA;  
Query Match 92.9%; Score 65; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 9.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRVR 12  
DB 1 CFQWQRNMRVR 12  
|||||

RESULT 3  
AAY78046  
ID AAY78046 standard; Peptide; 12 AA.  
XX AC AAY78046;  
XX DT 25-APR-2000 (first entry)  
XX DE Human lactoferrin derived peptide SEQ ID NO:46.  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200001730-A1.  
XX PD 13-JAN-2000.  
XX PF 06-JUL-1999; 99WO-SE01230.  
XX PR 06-JUL-1998; 98SE-0002441.  
XX PR 17-JUL-1998; 98SE-0002562.  
XX PR 29-DEC-1998; 98SE-0004614.  
XX PA (ASCI-) A+ SCI INVEST AB.  
XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 9.6e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNNRRAVR 12  
 |||||  
 DB 1 CFQWQNNRRAVR 12

RESULT 4  
 AAY78047  
 ID AAY78047 standard; Peptide; 12 AA.  
 XX AC AAY78047;  
 XX DT 25-APR-2000 (first entry)  
 XX Human lactoferrin derived peptide SEQ ID NO:47.  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX urinary tract infection; colitis; Candida infection; fungicidal;  
 XX bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.  
 OS WO200001730-A1.  
 XX PD 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 XX 17-JUL-1998; 98SE-0002562.  
 XX 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 XX lactoferrin. The peptides are taken up in the intestine through  
 XX binding to specific lactoferrin receptors and are then transported  
 XX through the circulation. A medicinal product of the peptide or fragment  
 XX can be used for treating and/or prevention of infections (such as  
 XX urinary tract infections, colitis, and Candida infection on a mucosal  
 XX membrane), inflammations and/or tumors. The peptides can also be used  
 XX in food stuffs such as infant formula food. The peptides are also  
 XX fungicidal and bactericidal and may also be used as preservatives.  
 XX Even though native human lactoferrin have been shown to have desired  
 XX anti-inflammatory anti-infectious and anti-tumoural properties they  
 XX cannot be used clinically on a broad basis because of high production  
 XX costs. Therefore, provision of peptides based on lactoferrin would  
 XX enable them to be used for the same purposes as lactoferrin at lower  
 XX cost.

XX SQ Sequence 12 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 9.6e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWQNNRRAVR 12  
 |||||  
 DB 1 CFQWQNNRRAVR 12

RESULT 5  
 AAY78037  
 ID AAY78037 standard; Peptide; 13 AA.  
 XX AC AAY78037;  
 XX DT 25-APR-2000 (first entry)  
 XX Human lactoferrin derived peptide SEQ ID NO:37.  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX urinary tract infection; colitis; Candida infection; fungicidal;  
 XX bactericidal; preservative.

XX Homo sapiens.  
 XX Synthetic.  
 XX WO200001730-A1.  
 XX PD 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 XX 17-JUL-1998; 98SE-0002562.  
 XX 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 XX lactoferrin. The peptides are taken up in the intestine through  
 XX binding to specific lactoferrin receptors and are then transported  
 XX through the circulation. A medicinal product of the peptide or fragment  
 XX can be used for treating and/or prevention of infections (such as  
 XX urinary tract infections, colitis, and Candida infection on a mucosal  
 XX membrane), inflammations and/or tumors. The peptides can also be used  
 XX in food stuffs such as infant formula food. The peptides are also  
 XX fungicidal and bactericidal and may also be used as preservatives.  
 XX Even though native human lactoferrin have been shown to have desired  
 XX anti-inflammatory anti-infectious and anti-tumoural properties they  
 XX cannot be used clinically on a broad basis because of high production  
 XX costs. Therefore, provision of peptides based on lactoferrin would  
 XX enable them to be used for the same purposes as lactoferrin at lower  
 XX cost.

XX SQ Sequence 13 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 0.0001;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 CFQWQNNRAVR 12  
 |||||  
 Db 2 CFQWQNNRKVR 13

## RESULT 6

ID AAY78048  
 ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.0001; 1; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0;

QY 1 CFQWQNNRAVR 12

|||||

Db 2 CFQWQNNRKVR 13

## RESULT 7

AAY78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 13 AA;

Query Match 92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.0001; 1; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0;

QY 1 CFQWQNNRAVR 12

|||||

Db 2 CFQWQNNRKVR 13

## RESULT 8

AAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AAY78036;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:36.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 12; Page 69; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. NO. 0.00011;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMRVR 12  
 Db 3 CFQWQRNMRVR 14  
 RESULT 9  
 AAY78050  
 ID AAY78050 standard; Peptide; 14 AA.  
 XX  
 AC AAY78050;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:50.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX  
 DR WPI; 2000-147388/13.  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 15; Page 75; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. NO. 0.00011;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMRVR 12  
 Db 3 CFQWQRNMRVR 14  
 RESULT 10  
 AAY78051  
 ID AAY78051 standard; Peptide; 14 AA.  
 XX  
 AC AAY78051;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human lactoferrin derived peptide SEQ ID NO:51.  
 XX  
 KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 18; Page 75; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 XX SQ Sequence 14 AA;  
 Query Match 92.9%; Score 65; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 0.00011;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNRAVR 12  
 DB 3 CFQWQRNRAVR 14  
 RESULT 11  
 AAR98554  
 ID AAR98554 standard; Peptide; 15 AA.  
 AC AAR98554;  
 XX  
 DT 12-NOV-1996 (first entry)  
 XX Peptide for anti-ulcer agent.  
 XX anti-ulcer agent; low toxicity; stable; heat-resistant.  
 XX Synthetic.  
 XX JP08143468-A.  
 XX 04-JUN-1996.  
 XX 17-NOV-1994; 94JP-0283869.  
 XX 17-NOV-1994; 94JP-0283869.  
 XX (MORG) MORINAGA MILK IND CO LTD.  
 XX WPI; 1996-318857/32.  
 XX Anti-ulcer agent contg. peptide - has low toxicity, is  
 PT heat-resistant and water-soluble  
 XX Claim 1; Page 11; 11pp; Japanese.

XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low  
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be  
 CC administered orally and be produced in large amounts.  
 XX SQ Sequence 15 AA;  
 Query Match 92.9%; Score 65; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00012;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQRNRAVR 12  
 DB 2 CFQWQRNRAVR 13  
 RESULT 12  
 AAY78035  
 ID AAY78035 standard; Peptide; 15 AA.  
 AC AAY78035;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX Human lactoferrin derived peptide SEQ ID NO:35.  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO2000001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 69; 102pp; English.  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00012;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRAVR 12  
 DB 4 CFQWQRMRAVR 15

RESULT 13  
 AAY78062  
 ID AAY78062 standard; Peptide; 15 AA.  
 AC AAY78062;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:62.  
 DE Human, lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS WO200001730-A1.  
 XX 13-JAN-2000.  
 PD 06-JUL-1999; 99WO-SE01230.  
 PF 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PT Claim 15; Page 81; 102pp; English.  
 PS AAY78001 to AAY78100 represent peptides having sequences based on human  
 XX lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 15 AA;  
 SQ Query Match 92.9%; Score 65; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00012;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMRAVR 12  
 DB 4 CFQWQRMRAVR 15

RESULT 15  
 AAY78031  
 ID AAY78031 standard; Peptide; 16 AA.  
 XX AC AAY78031;

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XX 25-APR-2000 (first entry)
XX
XX DE Human lactoferrin derived peptide SEQ ID NO:31.
XX
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO200001730-A1.
XX
XX PD 13-JAN-2000.
XX
XX PF 06-JUL-1999; 99WO-SE01230.
XX
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX
XX PA (ASCI-) A+ SCI INVEST AB.
XX
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX DR WPI; 2000-147388/13.
XX
XX PT New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food.
XX
XX PS Claim 11; Page 68; 102pp; English.
XX
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
XX through the circulation. A medicinal product of the peptide or fragment
XX can be used for treating and/or prevention of infections (such as
XX urinary tract infections, colitis, and Candida infection on a mucosal
XX membrane), inflammations and/or tumors. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also
XX fungicidal and bactericidal and may also be used as preservatives.
XX Even though native human lactoferrin have been shown to have desired
XX anti-inflammatory anti-infections and anti-tumoural properties they
XX cannot be used clinically on a broad basis because of high production
XX costs. Therefore, provision of peptides based on lactoferrin would
XX enable them to be used for the same purposes as lactoferrin at lower
XX cost.
XX
XX SQ Sequence 16 AA;
XX
XX Query Match 92.9%; Score 65; DB 21; Length 16;
XX Best Local Similarity 91.7%; Pred. No. 0.00013;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CFQWQRNRAVR 12
XX |||||
XX Db 5 CFQWQRNRAVR 16

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Search completed: February 21, 2003, 07:37:13  
Job time : 29.35 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-77

Perfect score: 70

Sequence: 1 CFQWRNRAVR 12

Scoring table: BLOSUM62

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	18	1	US-08-204-487-3
2	65	92.9	18	2	US-08-485-948-8
3	65	92.9	18	2	US-08-628-380-8
4	65	92.9	18	2	US-08-475-055-8
5	65	92.9	20	1	US-07-755-161A-3
6	65	92.9	20	1	US-07-891-174-3
7	65	92.9	20	1	US-08-204-487-1
8	65	92.9	20	1	US-08-256-771-24
9	65	92.9	20	1	US-08-256-771-25
10	65	92.9	20	1	US-08-381-984-24
11	65	92.9	20	1	US-08-381-984-25
12	65	92.9	22	4	US-03-508-734-4
13	65	92.9	24	4	US-03-508-734-6
14	65	92.9	25	1	US-07-755-161A-10
15	65	92.9	25	1	US-07-891-174-10
16	65	92.9	25	1	US-08-204-487-7
17	65	92.9	29	4	US-09-508-734-8
18	65	92.9	36	1	US-07-755-161A-8
19	65	92.9	36	1	US-07-891-174-8
20	65	92.9	36	1	US-08-256-771-30
21	65	92.9	36	1	US-08-381-984-29
22	65	92.9	47	2	US-08-464-182A-6
23	65	92.9	47	2	US-08-406-271-6
24	65	92.9	50	2	US-08-693-274A-7
25	65	92.9	52	4	US-03-017-043A-3
26	65	92.9	53	2	US-08-464-182A-5
27	65	92.9	53	2	US-08-406-271-5

28	65	92.9	54	2	US-08-464-182A-2
29	65	92.9	54	2	US-08-406-271-2
30	65	92.9	594	3	US-08-724-586-2
31	65	92.9	594	4	US-09-421-632-2
32	65	92.9	694	4	US-09-932-190-2
33	65	92.9	705	2	US-08-655-640-2
34	65	92.9	708	2	US-08-655-640-4
35	65	92.9	711	1	US-08-145-681-2
36	65	92.9	711	1	US-08-250-308-2
37	65	92.9	711	1	US-08-154-019-4
38	65	92.9	711	1	US-08-461-333-4
39	65	92.9	711	1	US-08-453-703-2
40	65	92.9	711	2	US-08-456-106-2
41	65	92.9	711	3	US-08-464-167-4
42	65	92.9	711	3	US-09-158-313-4
43	65	92.9	711	3	US-08-456-108-2
44	65	92.9	711	4	US-08-476-798-4
45	65	92.9	711	4	US-09-263-577-2

## ALIGNMENTS

RESULT 1  
US-08-204-487-3  
; Sequence 3, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIAKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESS: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO. 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..18  
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 6.4e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRAVR 12  
| | | | | | | | | | | | | | | | | |  
Db 1 CFQWQNNRKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,948  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-485-948-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 6.4e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRAVR 12  
| | | | | | | | | | | | | | | | | |  
Db 1 CFQWQNNRKVR 12

OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 92.9%; Score 65; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 6.4e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRAVR 12  
| | | | | | | | | | | | | | | | | |  
Db 1 CFQWQNNRKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI, YONG MING  
; APPLICANT: VLASSARA, HELEN  
; APPLICANT: CERAMI, ANTHONY  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-628-380-8

Query Match 92.9%; Score 65; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 6.4e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRAVR 12  
| | | | | | | | | | | | | | | | | |  
Db 1 CFQWQNNRKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 92.9%; Score 65; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRNMRVR 12
Db 1 CFQWRNMRVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA: US/07/755,161A
APPLICATION NUMBER: 07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEFAX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 92.9%; Score 65; DB 1; Length 20;
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? INFORMATION FOR SEQ ID NO: 24:
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? SEQUENCE CHARACTERISTICS:
?   LENGTH: 20 amino acids
?   TYPE: amino acid
?   STRANDEDNESS: single
?   TOPOLOGY: linear
?   MOLECULE TYPE: peptide
?   FEATURE:
?     NAME/KEY:
?     LOCATION:
?   IDENTIFICATION METHOD:
?   OTHER INFORMATION: /note= "Cys residues are linked by
?     OTHER INFORMATION: disulfide bond"
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```

```

US-08-256-771-25

Query Match          92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 CFQWQRMKRAVR 12
      |||||
Db  2 CFQWQRMKRV 13

RESULT 10
US-08-361-984-24

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Sequence 24, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack  
CITY: 805 Fifteenth Street, N.W., #700  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

## INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

## NAME/KEY:

LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2  
OTHER INFORMATION: and 19 are bonded by disulfide linkage"

## FEATURE:

NAME/KEY:

LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as  
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof

US-08-381-984-24

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNRAVR 12

Db 2 CFQWQRNRAVR 13

## RESULT 11

US-08-381-984-25  
Sequence 25, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

## INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

## NAME/KEY:

LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as  
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof

## FEATURE:

NAME/KEY:

LOCATION:

## IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2  
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"

US-08-381-984-25

Query Match 92.9%; Score 65; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 7.2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNRAVR 12

Db 2 CFQWQRNRAVR 13

## RESULT 12

US-09-508-734-4  
Sequence 4, Application US/09508734  
Patent No. 6423509  
GENERAL INFORMATION:  
APPLICANT: Samyang Genex Corporation  
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
TITLE OF INVENTION: useful microorganism thereof  
FILE REFERENCE: PA/SYG/00139  
CURRENT APPLICATION NUMBER: US/09/508,734  
CURRENT FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: PCT/KR99/00373  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: KR1998-29351  
PRIOR FILING DATE: 1998-07-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: KopatentIn 1.71  
SEQ ID NO 4

Qy 1 CFQWQRNRAVR 12

Db 2 CFQWQRNRAVR 13

LENGTH: 22  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-508-734-4

Query Match 92.9%; Score 65; DB 4; Length 22;  
Best Local Similarity 91.7%; Pred. No. 7.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRVR 12  
DB 2 CFQWQNNRKR 13

## RESULT 13

US-09-508-734-6

Sequence 6, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: PCT/KR99/00373

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 6

LENGTH: 24

TYPE: PRT

ORGANISM: Homo sapiens

US-09-508-734-6

Query Match 92.9%; Score 65; DB 4; Length 24;  
Best Local Similarity 91.7%; Pred. No. 8.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRVR 12  
DB 3 CFQWQNNRKR 14

## RESULT 14

US-07-755-161A-10

Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an

TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500KB

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/755.161A

FILING DATE: 19910905

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLSCULE TYPE:

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY: modified site

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 21"

FEATURE:

NAME/KEY: modified site

LOCATION: 21

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 92.9%; Score 65; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRVR 12

DB 4 CFQWQNNRKR 15

RESULT 15  
US-07-891-174-10  
; Sequence 10, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; MOLECULE TYPE: linear  
; TOPOLOGY: linear  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 4  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 21"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 21

; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 4"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-10  
Query Match 92.9%; Score 65; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CFQWRNMEAVR 12  
Db 4 CFQWRNMEAVR 15  
Search completed: February 21, 2003, 07:50:34  
Job time : 8.7 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107b-77  
Perfect score: 70  
Sequence: 1 CFQWQNMRAVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	92.9	15	9	US-09-798-869-2
2	65	92.9	25	9	US-09-798-869-20
3	65	92.9	694	9	US-10-023-096-2
4	57	81.4	15	9	US-09-798-869-6
5	48	68.6	15	9	US-09-798-869-3
6	48	68.6	25	9	US-09-798-869-23
7	40	57.1	15	9	US-09-798-869-7
8	39	55.7	15	9	US-09-798-869-4
9	39	55.7	25	9	US-09-798-869-22
10	38	54.3	338	9	US-09-798-295A-119
11	38	54.3	338	9	US-09-798-697-119
12	38	54.3	338	9	US-09-798-192A-119
13	38	54.3	338	9	US-09-999-832A-119
14	38	54.3	338	9	US-09-978-189-119
15	38	54.3	553	9	US-09-796-753-14
16	38	54.3	553	10	US-09-981-649A-6
17	38	54.3	553	10	US-09-981-649A-24
18	38	54.3	554	10	US-09-981-649A-30
19	38	54.3	554	10	US-09-981-649A-32

20	38	54.3	559	10	US-09-981-649A-28	Sequence 28, Appl
21	37	52.9	21	10	US-09-864-761-47985	Sequence 47985, A
22	37	52.9	333	9	US-09-796-753-26	Sequence 26, Appl
23	36	51.4	15	9	US-09-798-869-8	Sequence 8, Appl
24	36	51.4	15	9	US-09-798-869-29	Sequence 29, Appl
25	36	51.4	15	9	US-09-798-869-30	Sequence 30, Appl
26	36	51.4	46	10	US-09-864-761-48879	Sequence 48879, A
27	36	51.4	351	10	US-09-853-625B-16	Sequence 16, Appl
28	36	51.4	2273	10	US-09-995-542-12	Sequence 12, Appl
29	36	51.4	2310	10	US-09-995-542-10	Sequence 10, Appl
30	35	50.0	607	9	US-09-881-579-10	Sequence 10, Appl
31	35	50.0	688	9	US-09-881-579-15	Sequence 15, Appl
32	35	50.0	846	9	US-10-051-409-4	Sequence 4, Appl
33	34	48.6	40	10	US-09-864-761-46393	Sequence 46393, A
34	34	48.6	95	10	US-09-764-864-1031	Sequence 1031, Ap
35	34	48.6	209	10	US-09-904-536-8	Sequence 8, Appl
36	34	48.6	209	10	US-09-904-536-9	Sequence 9, Appl
37	34	48.6	209	10	US-09-904-536-11	Sequence 11, Appl
38	34	48.6	209	10	US-09-904-536-12	Sequence 12, Appl
39	34	48.6	209	10	US-09-904-536-13	Sequence 13, Appl
40	34	48.6	209	10	US-09-904-536-14	Sequence 14, Appl
41	34	48.6	209	10	US-09-904-536-15	Sequence 15, Appl
42	34	48.6	209	10	US-09-904-536-16	Sequence 16, Appl
43	34	48.6	209	10	US-09-904-536-17	Sequence 17, Appl
44	34	48.6	209	10	US-09-904-536-18	Sequence 18, Appl
45	34	48.6	212	10	US-09-904-536-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-09-798-869-2  
; Sequence 2, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINER (RNSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9819938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 92.9%; Score 65; DB 9; Length 15;  
Best Local Similarity 91.7%; Pred. No. 4e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNMRAVR 12  
DB 3 CFQWQNMRAVR 14

RESULT 2  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINER (RNSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match          92.9%; Score 65; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12
   |||||
Db 3 CFQWQRNMRKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Krugel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human.
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,566
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-10-023-096-2

; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match          92.9%; Score 65; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12
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Db 22 CFQWQRNMRKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
US-09-798-869-6

Query Match          81.4%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00089;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12
   |||||
Db 3 CFQWQRNMRKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match          68.6%; Score 48; DB 9; Length 15;
Best Local Similarity 77.8%; Pred. No. 0.029;
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Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 9  
|:|:|:|:|  
Db 3 CYQWQRMNR 11

RESULT 6  
US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 68.6%; Score 48; DB 9; Length 25;  
Best Local Similarity 77.8%; Pred. No. 0.047;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 9  
|:|:|:|:|  
Db 3 CYQWQRMNR 11

RESULT 7  
US-09-798-869-7  
; Sequence 7, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-7

Query Match 57.1%; Score 40; DB 9; Length 15;  
Best Local Similarity 66.7%; Pred. No. 0.65;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 9  
|:|:|:|:|  
Db 3 CYQWQRMNR 11

RESULT 8  
US-09-798-869-4  
; Sequence 4, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;  
Best Local Similarity 54.5%; Pred. No. 0.96;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 11  
|:|:|:|:|  
Db 3 CLRQWQMEKV 13

RESULT 9  
US-09-798-869-22  
; Sequence 22, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;  
Best Local Similarity 54.5%; Pred. No. 1.6;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQRMNR 11  
|:|:|:|:|  
Db 3 CLRQWQMEKV 13



## RESULT 10

US-09-978-295A-119  
; Sequence 119, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Pacini, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
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; PRIOR APPLICATION NUMBER: 60/077641  
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; PRIOR FILING DATE: 1998-03-11  
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; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
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; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
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; PRIOR FILING DATE: 1998-03-27  
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; PRIOR FILING DATE: 1998-03-30  
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; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
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; PRIOR APPLICATION NUMBER: 60/081195  
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; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
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; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
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; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496

1	PRIOR FILING DATE: 1998-04-29	60/083499
2	PRIOR APPLICATION NUMBER: 60/083499	
3	PRIOR FILING DATE: 1998-04-29	60/083545
4	PRIOR APPLICATION NUMBER: 60/083545	
5	PRIOR FILING DATE: 1998-04-29	60/083554
6	PRIOR APPLICATION NUMBER: 60/083554	
7	PRIOR FILING DATE: 1998-04-29	60/083558
8	PRIOR APPLICATION NUMBER: 60/083558	
9	PRIOR FILING DATE: 1998-04-29	60/083559
10	PRIOR APPLICATION NUMBER: 60/083559	
11	PRIOR FILING DATE: 1998-04-29	60/083500
12	PRIOR APPLICATION NUMBER: 60/083500	
13	PRIOR FILING DATE: 1998-04-29	60/083742
14	PRIOR APPLICATION NUMBER: 60/083742	
15	PRIOR FILING DATE: 1998-04-30	60/083436
16	PRIOR APPLICATION NUMBER: 60/083436	
17	PRIOR FILING DATE: 1998-05-05	60/084414
18	PRIOR APPLICATION NUMBER: 60/084414	
19	PRIOR FILING DATE: 1998-05-06	60/084441
20	PRIOR APPLICATION NUMBER: 60/084441	
21	PRIOR FILING DATE: 1998-05-06	60/084637
22	PRIOR APPLICATION NUMBER: 60/084637	
23	PRIOR FILING DATE: 1998-05-07	60/084639
24	PRIOR APPLICATION NUMBER: 60/084639	
25	PRIOR FILING DATE: 1998-05-07	60/084640
26	PRIOR APPLICATION NUMBER: 60/084640	
27	PRIOR FILING DATE: 1998-05-07	60/084598
28	PRIOR APPLICATION NUMBER: 60/084598	
29	PRIOR FILING DATE: 1998-05-07	60/084600
30	PRIOR APPLICATION NUMBER: 60/084600	
31	PRIOR FILING DATE: 1998-05-07	60/084627
32	PRIOR APPLICATION NUMBER: 60/084627	
33	PRIOR FILING DATE: 1998-05-07	60/084643
34	PRIOR APPLICATION NUMBER: 60/084643	
35	PRIOR FILING DATE: 1998-05-07	60/085339
36	PRIOR APPLICATION NUMBER: 60/085339	
37	PRIOR FILING DATE: 1998-05-13	60/085338
38	PRIOR APPLICATION NUMBER: 60/085338	
39	PRIOR FILING DATE: 1998-05-13	60/085323
40	PRIOR APPLICATION NUMBER: 60/085323	
41	PRIOR FILING DATE: 1998-05-13	60/085582
42	PRIOR APPLICATION NUMBER: 60/085582	
43	PRIOR FILING DATE: 1998-05-15	60/085700
44	PRIOR APPLICATION NUMBER: 60/085700	
45	PRIOR FILING DATE: 1998-05-15	60/085689
46	PRIOR APPLICATION NUMBER: 60/085689	
47	PRIOR FILING DATE: 1998-05-15	60/085579
48	PRIOR APPLICATION NUMBER: 60/085579	
49	PRIOR FILING DATE: 1998-05-15	60/085580
50	PRIOR APPLICATION NUMBER: 60/085580	
51	PRIOR FILING DATE: 1998-05-15	60/085573
52	PRIOR APPLICATION NUMBER: 60/085573	
53	PRIOR FILING DATE: 1998-05-15	60/085704
54	PRIOR APPLICATION NUMBER: 60/085704	
55	PRIOR FILING DATE: 1998-05-15	60/085697
56	PRIOR APPLICATION NUMBER: 60/085697	

Query Match 54.3%; Score 38; DB 9; Length 338;

Best Local Similarity 45.5%; Pred. No. 27;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY	1	CFQWQRMRAV	11
		: : : :	
Db	50	CYGWRRNSKGV	60

RESULT 11

US-09-978-697-119  
; Sequence 119, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.

; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
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; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
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; PRIOR APPLICATION NUMBER: 60/080327  
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; PRIOR APPLICATION NUMBER: 60/081229  
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; PRIOR APPLICATION NUMBER: 60/081955  
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; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
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; PRIOR APPLICATION NUMBER: 60/082700  
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; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
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; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
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; PRIOR FILING DATE: 1998-04-30  
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; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
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; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-5-07  
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score 38; DB 9; Length 338;

Best Local Similarity 45.5%; Pred. No. 27;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRNMRAV 11  
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Db 50 CYGWRNSKGV 60

## RESULT 12

US-09-978-192A-119  
; Sequence 119, Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang

Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Hillan, Kenneth J.  
Kljarin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Shelton, David L.  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score
Best Local Similarity 45.5%; Pred
Matches 5; Conservative 3; M: M:

QY 1 CQWQNRNAV 11
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DB 50 CYGWRNSKGV 60

RESULT 13
US-09-999-832A-119
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/ Publication No. US20020192706A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Bolstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerrisen, Wary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christophe
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.

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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score 38; DB 9; Length 338;  
Best Local Similarity 45.5%; Pred. No. 27;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOWQRMRAV 11  
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Db 50 CYGWRNRSGV 60

RESULT 14  
US-09-978-189-119  
; Sequence 119, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.3%; Score 38; DB 9; Length 338;  
Best Local Similarity 45.5%; Pred. No. 27;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMRAV 11  
|:|:|:|:  
Db 50 CYGWRNSKGV 60

## RESULT 15

US-09-796-753-14  
; Sequence 14, Application US/09796753  
; Publication No. US20030027998A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-227-999  
; CURRENT APPLICATION NUMBER: US/09/796,753  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/183,175  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 09/223,094  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/223,546  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/224,246  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/259,388  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/122,458  
; PRIOR FILING DATE: 1999-03-01  
; PRIOR APPLICATION NUMBER: 09/312,359  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/336,536  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 09/342,687  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 09/345,464  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: 09/365,164  
; PRIOR FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: 09/399,723  
; PRIOR FILING DATE: 1999-09-20  
; PRIOR APPLICATION NUMBER: 09/409,634

; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 09/471,179  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 09/474,071  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/474,072  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/514,010  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 09/516,745  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 09/572,002  
; PRIOR FILING DATE: 2000-05-14  
; PRIOR APPLICATION NUMBER: 09/597,993  
; PRIOR FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 09/599,596  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 09/630,334  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: 09/606,565  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/606,317  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/665,666  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 09/677,751  
; PRIOR FILING DATE: 2000-09-30  
; NUMBER OF SEQ ID NOS: 162  
; SEQ ID NO 14  
; LENGTH: 553  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-796-753-14

Query Match 54.3%; Score 38; DB 9; Length 553;  
Best Local Similarity 45.5%; Pred. No. 42;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRMRAV 11  
|:|:|:|:  
Db 50 CYGWRNSKGV 60

Search completed: February 21, 2003, 08:08:06  
Job time : 11.55 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107B-77

Perfect score: 70

Sequence: 1 CFQQRNRAVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TFHUL	lactotransferrin p
2	48	68.6	708	2 JC2323	lactoferrin - goat
3	45	64.3	33	2 S52107	lactoferrin - sheep
4	44	62.9	4568	2 T08030	dynamin beta heavy
5	42	60.0	932	2 T28820	hypothetical prote
6	39	55.7	205	2 E90094	26S proteasome SU
7	39	55.7	357	2 G97449	glutamine synthetase
8	39	55.7	707	1 A28438	lactoferrin precursor
9	38	54.3	515	2 T00510	probable cytochrome
10	38	54.3	543	2 T00513	cytochrome P450 ho
11	38	54.3	558	2 T17324	hypothetical prote
12	37	52.9	222	2 H70978	hypothetical prote
13	37	52.9	298	2 AD2346	hypothetical prote
14	37	52.9	357	2 T01607	probable triacylg
15	37	52.9	568	1 A55377	CPE-binding protei
16	37	52.9	681	2 T19429	hypothetical prote
17	37	52.9	758	1 A49343	calpain (EC 3.4.22
18	37	52.9	2671	1 A49873	inositol 1,4,5-tri
19	36	51.4	144	1 F46335	trans-regulatory s
20	36	51.4	289	2 G86403	33.3K hypothetical
21	36	51.4	290	2 C97414	hypothetical prote
22	36	51.4	344	2 C95884	probable oxidoredu
23	36	51.4	351	2 S20078	NOV protein - chic
24	36	51.4	511	2 AB0858	hypothetical prote
25	36	51.4	560	2 T29586	hypothetical prote
26	36	51.4	594	2 C84325	hypothetical prote
27	36	51.4	614	2 S42526	finger protein unk
28	36	51.4	820	2 G82168	trimethylamine-N-o
29	36	51.4	846	2 S52418	GTP-binding regula

## ALIGNMENTS

### RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence\_revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74;

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A>Status: preliminary; translated from GE/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AA860324.1; PID:G467237

R:Rev, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, P.R.

Nucleic Acids Res. 18, 5288, 1990

A>Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Feng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A>Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <REN>

A:Cross-references: GB:S2659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A>Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Molecule type: mRNA

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Residues: 20-31 <STI>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

RNA la protein - b  
sag polyprotein -  
hypothetical prote  
pyridoxamine 5'-ph  
pyridoxamine 5'-ph  
probable pyridoxam  
signal peptidase I  
hypothetical prote  
hypothetical prote  
hypothetical prote  
threonine synthase  
histidyl-tRNA synt  
conserved hypothet  
probable cytochrom  
cytochrome P450-li

R:Rado, T.A.; Wei, X.; Benz Jr., E.J.  
 Blood 70, 989-993, 1987  
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA  
 A:Reference number: S07160; MUID:88001031; PMID:3477300  
 A:Accession: S07160  
 A:Molecule type: mRNA  
 A:Residues: 436-487, 'A', 489-711 <RAD>  
 A:Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855  
 R:Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.  
 Cancer Res. 51, 3037-3043, 1991  
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes  
 A:Reference number: A61169; MUID:91235214; PMID:1674448  
 A:Accession: A61169  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 3-701, 'SWKPVN' <PAN>  
 A:Experimental source: normal breast tissue  
 R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, F.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984  
 A>Title: Human lactotransferrin: amino acid sequence and structural comparisons with other  
 A:Reference number: A31000; MUID:85076667; PMID:6510420  
 A:Accession: A31000  
 A:Molecule type: protein  
 A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4  
 A>Note: this is the final paper in a series  
 R:Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.  
 Eur. J. Biochem. 241, 303-308, 1996  
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affinity  
 A:Reference number: S74119; MUID:97054624; PMID:8898921  
 A:Accession: S74119  
 A:Molecule type: protein  
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>  
 A:Experimental source: neutrophil granulocytes  
 C:Genetics:  
 A:Gene: GDB:LTFF  
 A:Cross-references: GDB:119368; OMIM:150210  
 A:Map position: 3q21-3q23  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein; iron binding; milk  
 F:1-19/Domain: signal sequence Hstatus predicted <SIG>  
 F:20-711/Product: lactotransferrin Hstatus experimental <MAT>  
 F:21-356/Domain: transferrin repeat homology <TRH2>  
 F:360-699/Domain: transferrin repeat homology <TRH2>  
 F:29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-637, 595-609/Disulfide bonds: #status  
 F:157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:368-400, 378-391, 425-706, 647-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 92.9%; Score 65; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.0012; Mismatches 1; Indels 0; Gaps 0;  
 Matches 11; Conservative 0

QY 1 CFQWQRMRAVR 12  
 |||||  
 DB 39 CFQWQRMRAVR 50

RESULT 2  
 JC2323  
 lactoferrin - goat  
 C:Species: Capra aegagrus hircus (domestic goat)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C:Accession: JC2323  
 R:Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.  
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994  
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus  
 A:Reference number: JC2323; MUID:94380047; PMID:8093048  
 A:Accession: JC2323  
 A:Molecule type: mRNA  
 A:Residues: 1-708 <LEP>  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein  
 F:359-696/Domain: transferrin repeat homology <TRH2>  
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.6%; Score 48; DB 2; Length 708;  
 Best Local Similarity 77.8%; Pred. No. 1.2; Mismatches 1; Indels 0; Gaps 0;  
 Matches 7; Conservative 1

QY 1 CFQWQRMNR 9  
 |||||  
 DB 38 CYQWQRMNR 46

RESULT 3  
 S52107  
 lactoferrin - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 14-Jul-1995 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997  
 C:Accession: S52107  
 R:Qian, Z.Y.; Jolles, P.; Migliore-Samouri, D.; Fiat, A.M.  
 Biochim. Biophys. Acta 1243, 25-32, 1995  
 A>Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet  
 A:Reference number: S52107; MUID:95127729; PMID:7827104  
 A:Accession: S52107  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-33 <QIA>  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication

Query Match 64.3%; Score 45; DB 2; Length 33;  
 Best Local Similarity 66.7%; Pred. No. 0.2; Mismatches 2; Indels 0; Gaps 0;  
 Matches 6; Conservative 2

QY 1 CFQWQRMNR 9  
 |||||  
 DB 19 CYQWQRMNR 27

RESULT 4  
 T08030  
 dynin beta heavy chain - Chlamydomonas reinhardtii  
 C:Species: Chlamydomonas reinhardtii  
 C:Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 02-Feb-2001  
 C:Accession: T08030  
 R:Mitchell, D.R.; Brown, K.S.  
 J. Cell Sci. 107, 635-644, 1994  
 A>Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.  
 A:Reference number: Z16302; MUID:94274778; PMID:8006077  
 A:Accession: T08030  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-4568 <MIT>  
 A:Cross-references: EMBL:U02963; NID:G409965; PIDN:AAA19956.1; PID:G514215  
 A:Experimental source: strain 21gr  
 C:Genetics:  
 A:Gene: ODA4  
 A:Map position: IX  
 A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;  
 3334/3; 3686/3; 3882/3; 4240/3  
 C:Superfamily: dynein heavy chain, ciliary  
 C:Keywords: nucleotide binding; P-loop  
 F:1919-1936/Region: nucleotide-binding motif A (P-loop)  
 F:2202-2209/Region: nucleotide-binding motif A (P-loop)  
 F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 62.9%; Score 44; DB 2; Length 4568;  
 Best Local Similarity 50.0%; Pred. No. 40; Mismatches 3; Indels 0; Gaps 0;  
 Matches 6; Conservative 3

QY 1 CFQWQRMRAVR 12  
 |||||  
 DB 1852 CFQWQRMRAVR 1863

RESULT 5

## T28820

hypothetical protein F07C3.1 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C/Accession: T28820

R/Pavello, A.; Gattung, S.  
 submitted to the EMBL Data Library, March 1996  
 A/Description: The sequence of C. elegans cosmid F07C3.  
 A/Reference number: Z20528  
 A/Accession: T28820  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-932 <FAV>  
 A/Cross-references: EMBL:U50308; PIDN:AAK48001.1; GSPDB:GN00023; CESP:F07C3.1  
 A/Experimental source: strain Bristol N2; clone F07C3  
 C/Genetics:  
 A/Map position: 5  
 A/Gene: CESP:F07C3.1  
 A/Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599/3

Query Match 60.0%; Score 42; DB 2; Length 932;  
 Best Local Similarity 63.8%; Pred. No. 19;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQRMNRAVR 12  
 |||:|:|:  
 Db 579 FQWQSRRLVK 589

## RESULT 6

E90094  
 26S proteasome SU B5 [imported] - Guillardia theta nucleomorph  
 C/Species: nucleomorph Guillardia theta  
 A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
 C/Accession: E90094  
 R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif  
 Nature 410, 1091-1096, 2001  
 A/Title: The highly reduced genome of an enslaved algal nucleus.  
 A/Reference number: A99082; MUID:11323671; PMID:11323671  
 A/Accession: E90094  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-205 <DOU>  
 A/Cross-references: GB:AF165818; NID:gl3794510; PIDN:AAK39885.1; GSPDB:GN00150  
 C/Genetics:  
 A/Gene: prsB5  
 A/Map position: 1  
 A/Genome: nucleomorph  
 C/Keywords: nucleomorph

Query Match 55.7%; Score 39; DB 2; Length 205;  
 Best Local Similarity 45.5%; Pred. No. 14;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNRAVR 11  
 |||:|:|:  
 Db 63 CFFWERNLSSL 73

## RESULT 7

G97649  
 glutamine synthetase II (glutamate-ammonia ligase II) (gsII) [imported] - Agrobacterium  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
 C/Accession: G97649  
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A/Reference number: A97359; PMID:11743194  
 A/Accession: G97649  
 A/Status: preliminary

## A/Molecule type: DNA

A/Residues: 1-367 <KUR>  
 A/Cross-references: GB:AB007869; PIDN:AAK88152.1; PID:gl5157592; GSPDB:GN00169  
 C/Genetics:  
 A/Gene: AGR\_C\_4385  
 A/Map position: circular chromosome  
 C/Superfamily: glutamate-ammonia ligase

Query Match 55.7%; Score 39; DB 2; Length 367;  
 Best Local Similarity 50.0%; Pred. No. 25;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNRAVR 12  
 |||:|:|:  
 Db 2 CFFWQKPRQASR 13

## RESULT 8

A28438  
 lactoferrin precursor - mouse  
 N/Alternate names: lactotransferrin  
 C/Species: Mus musculus (house mouse)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: A28438; A41205  
 R/Pentecost, B.T.; Teng, C.T.  
 J. Biol. Chem. 262, 10134-10139, 1987  
 A/Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret  
 A/Reference number: A92596; MUID:87280033; PMID:3611056  
 A/Accession: A28438  
 A/Molecule type: mRNA  
 A/Residues: 3-707 <PEN>  
 A/Cross-references: EMBL:J03298  
 R/Liu, Y.; Teng, C.T.  
 J. Biol. Chem. 266, 21880-21885, 1991  
 A/Title: Characterization of estrogen-responsive mouse lactoferrin promoter.  
 A/Reference number: A41205; MUID:92042099; PMID:1939212  
 A/Accession: A41205  
 A/Molecule type: DNA  
 A/Residues: 1-15 <LIU>  
 A/Cross-references: GB:M74778  
 C/Superfamily: transferrin; transferrin repeat homology  
 C/Keywords: duplication; glycoprotein  
 F/1-19/Domain: signal sequence #status predicted <SIG>  
 F/20-707/Product: lactotransferrin #status predicted <MAT>  
 F/358-695/Domain: transferrin repeat homology <TRH2>  
 F/494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 707;  
 Best Local Similarity 54.5%; Pred. No. 48;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMNRAVR 11  
 |||:|:|:  
 Db 37 CFFWQKPRQASR 47

## RESULT 9

T00510  
 probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 23-Mar-2001  
 C/Accession: T00510; A84622  
 R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,  
 submitted to the EMBL Data Library, November 1997  
 A/Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.  
 A/Reference number: Z14164  
 A/Accession: T00510  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-515 <ROU>  
 A/Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642441  
 A/Experimental source: cultivar Columbia  
 R/Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 23-Mar-2001

C;Accession: T00513; F84621

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.

A;Reference number: Z14164

A;Accession: T00513

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-543 <ROU>

A;Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642444

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: P84621

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-543 <STO>

A;Cross-references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139

C;Genetics:

A;Gene: T20D16.18; At2g23190

A;Map position: 2

A;Introns: 211/3; 339/3

C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

F;Keywords: heme; iron; metalloprotein

F;341-500/Domain: cytochrome P450 homology <P45>

F;478/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 54.3%; Score 38; DB 2; Length 543;

Best Local Similarity 83.3%; Pred. No. 56;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6

DB 498 CFQWQR 474

RESULT 10

T00513

Cytochrome P450 homolog At2g23190 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 23-Mar-2001

C;Accession: T00513; F84621

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.

A;Reference number: Z14164

A;Accession: T00513

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-543 <ROU>

A;Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642444

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: P84621

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-543 <STO>

A;Cross-references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139

C;Genetics:

A;Gene: T20D16.18; At2g23190

A;Map position: 2

A;Introns: 211/3; 339/3

C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

F;Keywords: heme; iron; metalloprotein

F;341-500/Domain: cytochrome P450 homology <P45>

F;478/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 54.3%; Score 38; DB 2; Length 543;

Best Local Similarity 83.3%; Pred. No. 56;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6

DB 498 CFQWQR 503

RESULT 11

T17324

hypothetical protein DKFZp564P2063.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T17324

R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A;Reference number: Z18727

A;Accession: T17324

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-558 <DUE>

A;Cross-references: EMBL:AL117610

A;Experimental source: fetal brain; clone DKFZp564P2063

C;Genetics:

A;Note: DKFZp564P2063.1

Query Match 54.3%; Score 38; DB 2; Length 558;

Best Local Similarity 45.5%; Pred. No. 58;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNRAV 11

DB 55 CYGWRNRSGV 65

RESULT 12

H70978

hypothetical protein Rv3271c - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 15-Sep-2000

C;Accession: H70978

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtrooyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70978

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-222 <COL>

A;Cross-references: GB:Z92771; GB:AL123456; NID:g3242259; PIDN:CAB07084.1; PID:g306655;

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv3271c

C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv3271c

Query Match 52.9%; Score 37; DB 2; Length 222;

Best Local Similarity 60.0%; Pred. No. 35;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQRNRAVR 12

DB 24 EWQRNVRWAR 33

RESULT 13

AD2346

hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp.

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C;Accession: AD2346

R;kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AD2346

A;Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-298 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA076022.1; PID:g17133459; GSPDB:GN00179  
A:Experimental source: strain FCC 7120  
C:Genetics:  
A:Gene: alr4323

Query Match 52.9%; Score 37; DB 2; Length 298;  
Best Local Similarity 75.0%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CFQWQNR 9  
| | | | |  
Db 163 FHWQNR 170

## RESULT 14

T01607  
Probable triacylglycerol lipase At2g44810 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F16B22.30; hypothetical protein T13E15.18  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 02-Feb-2001  
C:Accession: T00412; T01607; A84883  
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc  
submitted to the EMBL Data Library, July 1997  
A:Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.  
A:Reference number: Z14146

A:Accession: T00412  
A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-357 <ROU>

A:Cross-references: EMBL:AC002388; NID:g3420042; PID:g2344903

A:Experimental source: cultivar Columbia

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, July 1998

A:Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.

A:Reference number: Z14284

A:Accession: T01607

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-357 <ROW>

A:Cross-references: EMBL:AC003672; NID:g3341671; PID:g3341700

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
cuse, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84883

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <STO>

A:Cross-references: GB:AE002093; NID:g2344903; PIDN:AAC31843.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g44810; T13E15.18; F16B22.30

A:Map position: 2

Query Match 52.9%; Score 37; DB 2; Length 357;  
Best Local Similarity 50.0%; Pred. No. 56;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNR 10  
| | | | |  
Db 130 CLEWENLRA 139

## RESULT 15

A55377

CPE-binding protein - African clawed frog

N:Alternate names: cytoplasmic polyadenylation element-binding protein

C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C:Accession: A55377  
R:Hake, L.E.; Richter, J.D.  
Cell 79, 617-627, 1994  
A:Title: CPB is a specificity factor that mediates cytoplasmic polyadenylation during X;  
A:Reference number: A55377; MUID:95042759; PMID:7954828  
A:Accession: A55377

A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA

A:Residues: 1-568 <HAK>

A:Cross-references: GB:U14169; NID:g987224; PIDN:AAA80483.1; PID:g624634

C:Superfamily: African clawed frog CPB-binding protein; ribonucleoprotein repeat homology;  
F:314-388/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 52.9%; Score 37; DB 1; Length 568;  
Best Local Similarity 41.7%; Pred. No. 88;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQNR 12  
| | | | |  
Db 542 CWHQHSMEILR 553

Search completed: February 21, 2003, 07:47:49  
Job time : 10.65 secs

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107B-77  
Perfect score: 70  
Sequence: 1 CFQWQNMRAVR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	92.9	711	1 TRFL_HUMAN	P02788 homo sapien
2	48	68.6	708	1 TRFL_CAMDR	Q9tum0 camelus dro
3	48	68.6	708	1 TRFL_CAPHI	Q29477 capra hircu
4	44	62.9	4568	1 DYHE_CHLRE	Q39565 chlamydomon
5	40	57.1	695	1 TRFL_HORSE	Q77811 equus cabal
6	39	55.7	707	1 TRFL_MOUSE	P08071 mus musculu
7	37	52.9	758	1 CAN_SCHMA	P27730 schistosoma
8	37	52.9	2671	1 IP3T_HUMAN	Q14573 homo sapien
9	36	51.4	144	1 REV_OMVVS	P16903 ovine lenti
10	36	51.4	292	1 NLA_DROME	Q9x218 drosophila
11	36	51.4	351	1 NOV_CHICK	P28686 gallus gall
12	36	51.4	322	1 SOA2_HUMAN	Q75908 homo sapien
13	36	51.4	525	1 SOA2_MOUSE	O88908 mus musculu
14	36	51.4	961	1 VIA_BMV	P03588 bromo mosai
15	36	51.4	2273	1 ABCR_HUMAN	P78363 homo sapien
16	35.5	50.7	441	1 GAG_CAEVC	P33458 caprine art
17	35	50.0	428	1 SYH_CHLAMU	Q9p119 chlamydia m
18	35	50.0	455	1 YKX1_CABEL	Q15910 caenorhabdi
19	35	50.0	502	1 C911_ARATH	Q9f965 arabidopsis
20	35	50.0	728	1 KDG1_ARATH	Q39017 arabidopsis
21	35	50.0	749	1 VP4_ROTGA	Q04916 rotavirus (
22	35	50.0	765	1 Y008_HUMAN	Q15398 homo sapien
23	35	50.0	857	1 EF2_CHICK	Q90705 gallus gall
24	35	50.0	857	1 EF2_CRIGR	P09445 cricetus
25	35	50.0	857	1 EF2_HUMAN	P13639 homo sapien
26	35	50.0	857	1 EF2_MESAU	P05086 mesocricetu
27	35	50.0	857	1 EF2_MOUSE	P58252 mus musculu
28	35	50.0	857	1 EF2_RAT	P05197 rattus norv
29	35	50.0	958	1 V1A_CCMV	P27752 cowpea chlo
30	35	50.0	966	1 V1A_BBMV	Q00020 broad bean
31	35	50.0	1203	1 SDG1_CABEL	P24349 caenorhabdi
32	34	48.6	235	1 FL3L_HUMAN	P49771 homo sapien
33	34	48.6	238	1 PELX_ERWCA	P16530 erwinia car

## RESULT 1

## TRFL\_HUMAN

ID TRFL\_HUMAN STANDARD; PRT; 711 AA.  
AC P02788; Q16780; Q16785; Q16789; O00756; Q9H1Z3; Q96KZ4;  
AC Q96KZ5;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Lactoferrin precursor (lactoferrin) [Contains: Lactoferrin A;  
Lactoferrin B; Lactoferrin C].  
GN LTF OR LF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90384839; PubMed=2402455;  
RA Rev M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;  
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";  
RL Nucleic Acids Res. 18:5288-5288(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cho Y.Y.;  
RL Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Conneely O.M.;  
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Liang Q., Jimenez-Flores R., Richardson T.;  
RL "Molecular cloning and sequence analysis of human lactoferrin.";  
RN Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Wei X., Han J., Rado T.A.;  
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA  
sequences.";  
RN Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Cheng H., Chen X., Huan L.;  
RL "cDNA cloning and sequence analysis of human lactoferrin.";  
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]

## ALIGNMENTS

34	34	48.6	246	1	Y495_SVNY3
35	34	48.6	306	1	BUB2_YEAST
36	34	48.6	316	1	NORC_CHLTR
37	34	48.6	318	1	VG17_BPMD2
38	34	48.6	325	1	VG17_BPMLS
39	34	48.6	334	1	CATL_MOUSE
40	34	48.6	334	1	CATL_RAT
41	34	48.6	360	1	HIS8_LACIA
42	34	48.6	374	1	PEL2_ERWCA
43	34	48.6	401	1	O88A_DROME
44	34	48.6	487	1	VGLI_HCMVA
45	34	48.6	566	1	YJ19_SVNY3

Q55185 synechocyst  
P26448 saccharomyc  
O84281 chlamydia t  
O64210 mycobacteri  
Q05223 mycobacteri  
P06797 mus musculu  
P07154 rattus norv  
Q02135 lactococcus  
P11431 erwinia car  
Q9vfn2 drosophila  
P16778 human cytom  
P73121 synechocyst

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE-Mammary Gland;  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Oden J.E.;  
RT "Nucleotide sequence of human lactoferrin cDNA.";  
RL Nucleic Acids Res. 18:4013-4013(1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
RX Legrand D., Spik G., Montreuil J., Jolles P.;  
RA "Human lactoferrin: amino acid sequence and structural  
RT comparisons with other transferrins.";  
RL Eur. J. Biochem. 145:659-666(1984).  
RN [10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
RA Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
RT alignment of the cyanogen bromide fragments and characterization of  
RT N- and C-terminal domains.";  
RL Biochim. Biophys. Acta 670:243-254(1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,  
RA Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
RT lactotransferrin.";  
RL FEBS Lett. 142:1107-110(1982).  
RN [12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
RT expression of mRNA during normal and leukemic myelopoiesis.";  
RL Blood 70:989-993(1987).  
RN [13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RA Sagripanti J.L.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2585506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
RT and refinement at 2.8-A resolution.";  
RL J. Mol. Biol. 209:711-734(1989).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
RT resolution.";  
RL Acta Crystallogr. D 51:629-646(1995).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
RA Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
RT binding properties and crystal structure of the histidine-  
RT 253-->methionine mutant.";  
RL Biochemistry 36:341-346(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in *Aspergillus*  
RL *awamori*.";  
RX Acta Crystallogr. D 55:403-407(1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
RL and analysis of ligand-induced conformational change.";  
RX Acta Crystallogr. D 54:1319-1335(1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of oploid antagonist peptides derived  
RT from human lactoferrin.";  
RL Agric. Biol. Chem. 54:1803-1810(1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,  
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejmancik J.F., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RL Mol. Vision 4:31-32(1998).  
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
CC OF AN ANION, USUALLY BICARBONATE.  
CC -!- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST  
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC -----  
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CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X53961; CAA37914.1; -;  
DR EMBL; U07643; AAB60324.1; -;  
DR EMBL; M93150; AAA36159.1; -;  
DR EMBL; M83202; AAA59511.1; -;  
DR EMBL; M83205; AAA58656.1; -;  
DR EMBL; M18642; AAA86665.1; -;  
DR EMBL; AF332168; AAC48753.1; -;  
DR EMBL; BC015822; AAH15822.1; -;  
DR EMBL; BC015823; AAH15823.1; -;  
DR EMBL; M73700; AAA59479.1; -;  
DR EMBL; X52941; CAA37116.1; -;  
DR EMBL; U95626; AAB57795.1; -;  
DR PIR; S11228; TFHUL.  
DR PDB; 1LCP; 31-AUG-94.  
DR PDB; 1LCT; 31-OCT-93.  
DR PDB; 1LFG; 31-JUL-94.  
DR PDB; 1LFH; 31-OCT-93.  
DR PDB; 1LFT; 31-OCT-93.  
DR PDB; 1LGB; 31-AUG-94.  
DR PDB; 1LGC; 31-AUG-94.  
DR PDB; 1BKA; 08-NOV-96.  
DR PDB; 1DSN; 08-VAR-96.  
DR PDB; 1HSE; 12-MAR-97.  
DR PDB; 1VFD; 21-APR-97.

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Query Match          92.9%; Score 65; DB 1; Length 711;
Best Local Similarity 91.7%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRVR 12
DB 39 CFQWQRNMRKVR 50

RESULT 2
TRFL CAMDR          STANDARD;          PRT; 708 AA.
AC Q2TUMG; Q2MZS5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Somali; TISSUE=Lactating mammary gland;
RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhon Z.;
RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
RL Int. Dairy J. 9:481-486(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; AJ131674; CAB53387.1; -
DR EMBL; AF165879; AAP82241.1; -
DR HSP: O77811; 131X
DR InterPro; IPR011156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SMC0094; TR FER; 2.
DR PROSITE; PS00205; TRANSFERRIN 1; 2.
DR PROSITE; PS00206; TRANSFERRIN 2; 2.
DR PROSITE; PS00207; TRANSFERRIN 3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.

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FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT BINDING 140 140 ANION (BY SIMILARITY).
FT BINDING 482 482 ANION (BY SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 261 261 F -> S (IN REF. 2).
FT CONFLICT 304 304 G -> A (IN REF. 2).
FT CONFLICT 330 330 S -> P (IN REF. 2).
FT CONFLICT 492 494 LLS -> PLP (IN REF. 2).
FT CONFLICT 506 506 L -> F (IN REF. 2).
FT CONFLICT 609 609 A -> P (IN REF. 2).
FT CONFLICT 642 642 R -> Q (IN REF. 2).
SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match          68.6%; Score 48; DB 1; Length 708;
Best Local Similarity 66.7%; Pred. No. 0.41;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNMRVR 12
DB 38 CAQWQRMRKVR 49

RESULT 3
TRFL CAPHI          STANDARD;          PRT; 708 AA.
ID TRFL CAPHI
AC Q29477; Q29479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Lee T.; Yu S.; Kim S.; Lee K.; Yu D.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=94380047; PubMed=8093048;
RA le Provost F.; Nocart M.; Guerin G.; Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RL relevant locus to bovine U12 syntenic group.";
RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.

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DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).  
 GN LTF.  
 OS Equus caballus (Horse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "cDNA sequence of mare lactoferrin";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RC TISSUE=Milk;  
 RX MEDLINE=9296631; PubMed=10366507;  
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution";  
 RL J. Mol. Biol. 289:303-317(1999).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION. USUALLY BICARBONATE.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
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 DR EMBL; AJ010930; CRA09407.1; -.  
 DR PDB; 1BX; 02-DEC-98.  
 DR PDB; 1B7U; 02-FEB-99.  
 DR PDB; 1B7Z; 02-FEB-99.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 1.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 FT Signal; 3D-structure.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 6  
 FT CHAIN 7 695 LACTOTRANSFERRIN.  
 FT REPEAT 7 350 1.  
 FT REPEAT 351 695 2.  
 FT DISULFID 15 51  
 FT DISULFID 25 42  
 FT DISULFID 121 204  
 FT DISULFID 163 179  
 FT DISULFID 166 189  
 FT DISULFID 176 187  
 FT DISULFID 237 251  
 FT DISULFID 354 386  
 FT DISULFID 364 377  
 FT DISULFID 411 690  
 FT DISULFID 431 653  
 FT DISULFID 463 538  
 FT DISULFID 487 681  
 FT DISULFID 497 511  
 FT DISULFID 508 521  
 FT DISULFID 579 593  
 FT DISULFID 631 636  
 FT METAL 66 66 IRON 1 (BY SIMILARITY).

FT METAL 98 98 IRON 1 (BY SIMILARITY).  
 FT METAL 198 198 IRON 1 (BY SIMILARITY).  
 FT METAL 259 259 IRON 1 (BY SIMILARITY).  
 FT METAL 401 401 IRON 2 (BY SIMILARITY).  
 FT METAL 439 439 IRON 2 (BY SIMILARITY).  
 FT METAL 532 532 IRON 2 (BY SIMILARITY).  
 FT METAL 601 601 IRON 2 (BY SIMILARITY).  
 FT BINDING 127 127 ANION (BY SIMILARITY).  
 FT BINDING 469 469 ANION (BY SIMILARITY).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 57.1%; Score 40; DB 1; Length 695;

Best Local Similarity 58.3%; Pred. No. 11;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWORNRAVR 12

Db 25 CAKFQNMKKVR 36

# RESULT 6

## TRFL MOUSE

ID TRFL\_MOUSE STANDARD; PRT; 707 AA.

AC P08071; P70690; Q61799; Q922P2;

DT 01-AUG-1988 (Rel. 08, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Lactotransferrin precursor (Lactoferrin).

GN LTF.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RX MEDLINE=87280033; PubMed=3611056;

RA Pentecost B.T., Teng C.T.;

RT "Lactotransferrin is the major estrogen inducible protein of mouse

uterine secretions";

RL J. Biol. Chem. 262:10134-10139(1987).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RA Morilishi K.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 1-14 FROM N.A.

RX MEDLINE=92042099; PubMed=1939212;

RA Liu Y., Teng C.T.;

RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";

RL J. Biol. Chem. 266:21880-21885(1991).

CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUALLY BICARBONATE.

CC -!- SUBUNIT: MONOMER.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC EMBL; J03298; AAA40525.1; -;  
DR EMBL; D88510; BAA13633.1; -;  
DR EMBL; BC006904; AAA06904.1; -;  
DR EMBL; M74778; AAA39427.1; -;  
DR PIR; A28438; A28438;  
DR HSP; P02788; 1CB6;  
DR MGD; MGI:96837; Lcf;  
DR InterPro; IPR001156; Transferrin.  
DR Pfam; PF00405; transferrin; 2;  
DR PRINTS; PR00422; TRANSFERRIN.  
DR SMART; SMO0094; TR\_FER; 2;  
DR PROSITE; PS00205; TRANSFERRIN\_1; 1;  
DR PROSITE; PS00206; TRANSFERRIN\_2; 2;  
DR PROSITE; PS00207; TRANSFERRIN\_3; 2;  
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
Signal.  
FT SIGNAL 1 19 BY SIMILARITY.  
FT CHAIN 20 707 LACTOTRANSFERRIN.  
FT REPEAT 20 357 1.  
FT REPEAT 357 707 2.  
FT DISULFID 27 63 BY SIMILARITY.  
FT DISULFID 37 54 BY SIMILARITY.  
FT DISULFID 133 216 BY SIMILARITY.  
FT DISULFID 175 191 BY SIMILARITY.  
FT DISULFID 188 199 BY SIMILARITY.  
FT DISULFID 249 263 BY SIMILARITY.  
FT DISULFID 366 398 BY SIMILARITY.  
FT DISULFID 376 389 BY SIMILARITY.  
FT DISULFID 423 702 BY SIMILARITY.  
FT DISULFID 443 665 BY SIMILARITY.  
FT DISULFID 475 550 BY SIMILARITY.  
FT DISULFID 499 693 BY SIMILARITY.  
FT DISULFID 509 523 BY SIMILARITY.  
FT DISULFID 520 533 BY SIMILARITY.  
FT DISULFID 591 605 BY SIMILARITY.  
FT DISULFID 643 648 BY SIMILARITY.  
FT METAL 78 78 IRON 1 (BY SIMILARITY).  
FT METAL 110 110 IRON 1 (BY SIMILARITY).  
FT METAL 210 210 IRON 1 (BY SIMILARITY).  
FT METAL 271 271 IRON 1 (BY SIMILARITY).  
FT METAL 413 413 IRON 2 (BY SIMILARITY).  
FT METAL 451 451 IRON 2 (BY SIMILARITY).  
FT METAL 544 544 IRON 2 (BY SIMILARITY).  
FT METAL 613 613 IRON 2 (BY SIMILARITY).  
FT BINDING 139 139 ANION (POTENTIAL).  
FT BINDING 481 481 ANION (POTENTIAL).  
FT CARBOHYD 118 118 N-LINKED (GLCNAC. ...) (POTENTIAL).  
FT CARBOHYD 494 494 MR -> IQG (IN REF. 1).  
FT CONFLICT 1 2 R -> Q (IN REF. 2).  
FT CONFLICT 25 25 M -> L (IN REF. 2).  
FT CONFLICT 82 82 S -> T (IN REF. 2).  
FT CONFLICT 359 359 A -> D (IN REF. 1).  
FT CONFLICT 382 382 E -> G (IN REF. 2).  
FT CONFLICT 449 449 L -> V (IN REF. 1).  
FT CONFLICT 629 629  
SQ SEQUENCE 707 AA; 77865 MW; F26AE03404C19A8 CRC64;  
Query Match 55.7%; Score 39; DB 1; length 707;  
Best Local Similarity 54.5%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CFQQRNRAV 11  
Db 37 CLRQWENRKY 47  
RESULT 7  
CAN\_SCHWA STANDARD; PRT; 758 AA.  
ID CAN\_SCHWA  
AC P27730;  
DR 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Calpain (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP).  
OS Schistosoma mansoni (Blood fluke)  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6183;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=92131071; PubMed=1775175;  
RA Karcz S.R., Podesta R.B., Siddiqui A.A., Dekaban G.A., Strejan G.H.,  
RA Clarke M.W.;  
RT "Molecular cloning and sequence analysis of a calcium-activated  
RT neutral protease (calpain) from Schistosoma mansoni.";  
RL Mol. Biochem. Parasitol. 49:333-336(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Puerto Rican;  
RX MEDLINE=91332027; PubMed=1869543;  
RA Andresen K., Tom T.D., Strand M.;  
RT "Characterization of cDNA clones encoding a novel calcium-activated  
RT neutral proteinase from Schistosoma mansoni.";  
RL J. Biol. Chem. 266:15085-15090(1991).  
CC -|- FUNCTION: CALPAINS ARE CALCIUM-ACTIVATED NON-LYSOSOMAL THIO-  
CC PROTEASES.  
CC -|- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa or  
CC Arg-|-Xaa with Leu or Val as the P2 residue.  
CC -|- ENZYME REGULATION: IS ACTIVATED BY FREE CYTOSOLIC CALCIUM.  
CC -|- DEVELOPMENTAL STAGE: IN SPOROCYSTS AND ADULT WORMS.  
CC -|- MISCELLANEOUS: THIS PROTEIN BINDS CALCIUM.  
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.  
CC -|- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.  
CC -|- CAUTION: POSSESSES AN ADDITIONAL EF-HAND REGION LOCATED BETWEEN  
CC DOMAINS II AND III.  
-----  
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-----  
EMBL; M74233; AAA29857.1; -;  
EMBL; M67499; AAA29858.1; -;  
PIR; A39343; A39343.  
HSP; Q07009; IDFO.  
MEROPS; C02.UFW; -;  
InterPro; IPR002048; EF-hand.  
InterPro; IPR001300; Protease C2.  
InterPro; IPR00169; SHprot\_acsite.  
Pfam; PF00036; ehand; 3.  
Pfam; PF00648; Peptidase C2; 1.  
Pfam; PF01067; Calpain III; 1.  
PRINTS; PR00704; CALPAIN.  
SMART; SMO0230; Cyspc; 1.  
PROSITE; PS00018; EF HAND; FALSE NEG.  
PROSITE; PS00139; THIOL PROTEASE CYS; 1.  
PROSITE; PS00639; THIOL PROTEASE HIS; FALSE NEG.  
PROSITE; PS00640; THIOL PROTEASE ASN; FALSE NEG.  
Hydrolase; Thiol protease; Calcium-binding.  
DOMAIN 74 262 THIOL PROTEASE DOMAIN I.  
DOMAIN 263 412 THIOL PROTEASE DOMAIN II.  
DOMAIN 413 562 DOMAIN III, C2-LIKE DOMAIN.  
DOMAIN 563 582 LINKER.  
DOMAIN 583 757 DOMAIN IV.  
CA\_BIND 641 652 EF-HAND 1 (PROBABLE).  
CA\_BIND 671 682 EF-HAND 2 (PROBABLE).  
DOMAIN 707 718 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).  
DOMAIN 737 748 ANCESTRAL CALCIUM SITE 4 (POTENTIAL).  
ACT\_SITE 154 154 BY SIMILARITY.  
ACT\_SITE 313 313 BY SIMILARITY.  
ACT\_SITE 337 337 BY SIMILARITY.

FT CONFLICT 128 128 H -> L (IN REF. 2).  
 FT CONFLICT 214 214 R -> L (IN REF. 2).  
 FT CONFLICT 385 387 VTC -> CYL (IN REF. 2).  
 FT CONFLICT 441 441 S -> N (IN REF. 2).  
 FT CONFLICT 755 755 S -> R (IN REF. 2).  
 FT CONFLICT 757 757 Y -> D (IN REF. 2).  
 SQ SEQUENCE 758 AA; 86863 MW; 9F5E0C98B62AF19 CRC64;  
  
 Query Match 52.9%; Score 37; DB 1; Length 758;  
 Best Local Similarity 75.0%; Pred. No. 41;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 3 QWQNRMEA 10  
 DB 421 QWQNRVNA 428  
  
 RESULT 8  
 ID IP3T\_HUMAN STANDARD; PRT; 2671 AA.  
 AC Q14573; Q14649;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-trisphosphate receptor) (Type 3 Insp3 receptor) (IP3 receptor isoform 3) (insp3R3).  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamamoto-Hino M., Sugiyama T., Hikiti K., Mattei M.G., Hasegawa K., Sekine S., Sakurada K., Miyawaki A., Furuchi T., Hasegawa M., Mikoshiba K.; PubMed=8081734;  
 RA "Cloning and characterization of human type 2 and type 3 inositol 1,4,5-trisphosphate receptors.";  
 RL Recept. Channels 2:9-22(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=94117432; PubMed=8288584;  
 RA Maranto A.R.;  
 RA "Primary structure, ligand binding, and localization of the human type 3 inositol 1,4,5-trisphosphate receptor expressed in intestinal epithelium.";  
 RL J. Biol. Chem. 269:1222-1230(1994).  
 CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY). INTERACTS WITH TRPC1, TRPC3 AND TRPC4.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN INTESTINAL CRYPT AND VILLUS EPITHELIAL CELLS.  
 CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.  
 CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.  
 CC -----  
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 CC -----  
 EMBL; D26351; BAA05385.1; -

DR EMBL; U01062; AAC50064.1; -.  
 DR Genew; HGNC:6182; ITPR3.  
 DR MIN; 147267;  
 DR InterPro; IPR000699; Ca-rel\_channel.  
 DR InterPro; IPR001682; Ca/Na\_pore.  
 DR InterPro; IPR000493; Insp3\_receptor.  
 DR InterPro; IPR000636; M+channel\_mlg.  
 DR InterPro; IPR003608; MIR.  
 DR Pfam; PF00520; ion\_trans; 1.  
 DR Pfam; PF01365; RYDE\_ITPR; 2.  
 DR Pfam; PF02835; MIR; 4.  
 DR PRINTS; PR00779; INSP3RECEPTR.  
 DR SMART; SM00472; MIR; 4.  
 KW Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1 2202  
 FT TRANSMEM 2203 2223  
 FT DOMAIN 2224 2235  
 FT TRANSMEM 2236 2256  
 FT DOMAIN 2257 2264  
 FT TRANSMEM 2265 2285  
 FT DOMAIN 2286 2325  
 FT TRANSMEM 2326 2346  
 FT DOMAIN 2347 2368  
 FT TRANSMEM 2369 2389  
 FT DOMAIN 2390 2496  
 FT TRANSMEM 2497 2517  
 FT DOMAIN 2518 2671  
 FT MOD\_RES 2583 2583  
 FT CONFLICT 524 524 A -> V (IN REF. 2).  
 FT CONFLICT 562 562 H -> Y (IN REF. 2).  
 FT CONFLICT 989 989 H -> Y (IN REF. 2).  
 FT CONFLICT 1143 1143 A -> T (IN REF. 2).  
 FT CONFLICT 1391 1391 L -> V (IN REF. 2).  
 FT CONFLICT 1496 1497 TI -> PV (IN REF. 2).  
 FT CONFLICT 1674 1674 L -> V (IN REF. 2).  
 FT CONFLICT 2436 2436 V -> L (IN REF. 2).  
 SQ SEQUENCE 2671 AA; 304036 MW; 69F618CF27B681D7 CRC64;  
  
 Query Match 52.9%; Score 37; DB 1; Length 2671;  
 Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 3 QWQNRMEA 11  
 DB 2183 QWQNRVRS 2191  
  
 RESULT 9  
 ID REV\_OMVVS STANDARD; PRT; 144 AA.  
 AC P16903;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE REV protein (Anti-repression transactivator protein) (ART/TRS).  
 GN REV.  
 OS Ovine lentivirus (strain SA-OMV).  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90223989; PubMed=2158181;  
 RA Querat G., Audoly G., Sonigo P., Vigne R.;  
 RT Nucleotide sequence analysis of SA-OMV, a visna-related ovine lentivirus: phylogenetic history of lentiviruses.";  
 RL Virology 175:434-447(1990).  
 CC -----  
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 CC -----  
 EMBL; D26351; BAA05385.1; -

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CC -----  
 DR EMBL: M31646; AAA66816.1; -  
 DR PIR: F46335; F46335.  
 DR HIV: M3419; REV50MVSACG.  
 KW Transcription regulation; Trans-acting factor; Activator;  
 Nuclear protein.  
 SQ SEQUENCE 144 AA; 16546 MW; 3B7B34E7F0611F2E CRC64;

Query Match 51.4%; Score 36; DB 1; Length 144;  
 Best Local Similarity 66.7%; Pred. No. 11;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWORNRA 10  
 ||| | : :  
 Db 81 FQWLRLRA 89

## RESULT 10

ID NL4\_DROME STANDARD; PRT; 292 AA.  
 AC Q9XZL8; Q9V391.  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Nebula protein.  
 GN NL4 OR CG6072.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McCormick A.V., Goldberg M.L.;  
 RT "Gene required for elongation of meiosis I spindle in Drosophila females";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Branton R.C., Rogers Y.-H.C., Siatz J.R.G., Champagne M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA Allred J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Beres P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster";  
 RT Science 287:2185-2195(2000).  
 RL Science 287:2185-2195(2000).  
 CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.  
 CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.

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DR EMBL: AF147700; AAD33987.1; -  
 DR EMBL: AE003712; AAF55285.1; -  
 DR FlyBase; FBgn0026629; nla.  
 SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

Query Match 51.4%; Score 36; DB 1; Length 292;  
 Best Local Similarity 54.5%; Pred. No. 23;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FQWORNRAVR 12  
 ||| | : :  
 Db 150 FQWLRSFRLR 160

## RESULT 11

ID NOV\_CHICK STANDARD; PRT; 351 AA.  
 AC P28686;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE NOV protein precursor (Nephroblastoma overexpressed gene protein).  
 GN NOV.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Brown leghorn;  
 RX MEDLINE=92107157; PubMed=1309586;  
 RA Joliet V., Martinerie C., Dambrine G., Plassiat G., Brisac M.,  
 RA Crochet J., Perbal B.;  
 RT "Proviral rearrangements and overexpression of a new cellular gene  
 RT (nov) in myeloblastosis-associated virus type 1-induced  
 RT nephroblastomas";  
 RL Mol. Cell. Biol. 12:10-21(1992).  
 CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL  
 CC GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH  
 CC TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION  
 CC OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) IS SUFFICIENT  
 CC TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.  
 CC -!- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN  
 CC MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN AND  
 CC SPLEEN, IN ADULT CHICKEN.  
 CC -!- DEVELOPMENTAL STAGE: MAV1-INDUCED NEPHROBLASTOMAS EXPRESS A HIGH  
 CC LEVEL OF NOV GENE WHOSE TRANSCRIPTION IS NORMALLY ARRESTED IN  
 CC ADULT KIDNEY.  
 CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING  
 CC PROTEIN FAMILY. CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 VMFC DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.

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CC -----  
 DR EMBL; X59284; CAA14975.1; -;  
 DR PIR; S20078; S20078.  
 DR InterPro; IPR000359; Cys knot.  
 DR InterPro; IPR000867; Ins1\_gro\_fac\_pr.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR001007; VWFC.  
 DR Pfam; PF00007; Cys\_knot; 1.  
 DR Pfam; PF00090; tsp\_1; 1.  
 DR Pfam; PF00093; vwc\_1.  
 DR Pfam; PF00219; IGFBP; 1.  
 DR SMART; SM00041; CT; 1.  
 DR SMART; SM00121; IB; 1.  
 DR SMART; SM00209; TSP1; 1.  
 DR SMART; SM00214; VWC; 1.  
 DR PROSITE; PS00222; IGF BINDING; 1.  
 DR PROSITE; PS01185; CTCK\_1; 1.  
 DR PROSITE; PS01225; CTCK\_2; 1.  
 DR PROSITE; PS01208; VWFC; 1.  
 KW Proto-oncogene; Growth factor binding; Signal.  
 FT SIGNAL 25 24  
 FT CHAIN 1 351  
 FT DOMAIN 104 170  
 FT DOMAIN 258 332  
 FT DISULFID 258 295  
 FT DISULFID 275 309  
 FT DISULFID 286 325  
 FT DISULFID 289 327  
 FT DISULFID 294 331  
 FT CARBOHYD 274 274  
 SQ SEQUENCE 351 AA; 38268 MW; 1ECB3FA3058C6797 CRC64;

Query Match 51.4%; Score 36; DB 1; Length 351;  
 Best Local Similarity 50.0%; Pred. No. 27;  
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRNRAVR 12  
 DB 258 CIQTKSKNAVR 269

RESULT 12  
 SOA2 HUMAN  
 ID \_SOA2 HUMAN STANDARD; PRT; 522 AA.  
 AC 075908; Q9UNR2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sterol O-acyltransferase 2 (EC 2.3.1.26) [Cholesterol acyltransferase  
 DE 2) (Acyl coenzyme A:cholesterol acyltransferase 2) (ACAT-2).  
 GN SOAT2 OR ACAT2 OR ACAT2.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95434592; PubMed=9756920;  
 RA Oelkers P., Behari A., Cromley D., Billheimer J.T., Sturley S.L.;  
 RT "Characterization of two human genes encoding acyl coenzyme  
 RT A:cholesterol acyltransferase-related enzymes.";  
 RL J. Biol. Chem. 273:26765-26771(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Intestine;  
 RC MEDLINE=20428724; PubMed=10846185;  
 RX

RA Chang C.C.Y., Sakashita N., Ornvold K., Lee O., Chang E.T., Dong R.,  
 RA Lin S., Lee C.-Y.G., Strom S.C., Kashyap R., Fung J.J.,  
 RA Farsee R.V. Jr., Patriceau J.-P., Delhon A., Chang T.-Y.;  
 RT "Immunological quantitation and localization of ACAT-1 and ACAT-2 in  
 RT human liver and small intestine.";  
 RL J. Biol. Chem. 275:28083-28092(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21225021; PubMed=11325614;  
 RA Katsuren K., Tamura T., Arashiro R., Takata K., Matsuura T.,  
 RA Nishikawa N., Ohta T.;  
 RT "Structure of the human acyl-CoA:cholesterol acyltransferase-2  
 RT (ACAT-2) gene and its relation to dyslipidemia.";  
 RL Biochim. Biophys. Acta 1531:230-240(2001).  
 CC -!- FUNCTION: PLAYS A ROLE IN LIPOPROTEIN ASSEMBLY AND DIETARY  
 CC CHOLESTEROL ABSORPTION. IN ADDITION TO ITS ACYLTRANSFERASE  
 CC ACTIVITY, IT MAY ACT AS A LIGASE. MAY PROVIDE CHOLESTERYL ESTERS  
 CC FOR LIPOPROTEIN SECRETION FROM HEPATOCYTES AND INTESTINAL MUCOSA.  
 CC -!- CATALYTIC ACTIVITY: Acyl-CoA + cholesterol = CoA + cholesterol  
 CC ester.  
 CC -!- SUBUNIT: MAY FORM HOMO- OR HETERODIMERS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum.  
 CC -!- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.  
 CC  
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CC -----  
 DR EMBL; AF059203; AAC63998.1; -;  
 DR EMBL; AF099031; AAC78335.2; -;  
 DR EMBL; AF331516; AAK18275.1; -;  
 DR EMBL; AF331502; AAK18275.1; JOINED.  
 DR EMBL; AF331503; AAK18275.1; JOINED.  
 DR EMBL; AF331504; AAK18275.1; JOINED.  
 DR EMBL; AF331505; AAK18275.1; JOINED.  
 DR EMBL; AF331506; AAK18275.1; JOINED.  
 DR EMBL; AF331507; AAK18275.1; JOINED.  
 DR EMBL; AF331508; AAK18275.1; JOINED.  
 DR EMBL; AF331509; AAK18275.1; JOINED.  
 DR EMBL; AF331510; AAK18275.1; JOINED.  
 DR EMBL; AF331511; AAK18275.1; JOINED.  
 DR EMBL; AF331512; AAK18275.1; JOINED.  
 DR EMBL; AF331513; AAK18275.1; JOINED.  
 DR EMBL; AF331514; AAK18275.1; JOINED.  
 DR EMBL; AF331515; AAK18275.1; JOINED.  
 DR Genew; HGNC:11178; SOAT2.  
 DR MIM; 601311; -;  
 DR InterPro; IPR002688; ACAT.  
 DR Pfam; PF01800; ACAT; 1.  
 KW Transferase; Acyltransferase; Transmembrane; Endoplasmic reticulum;  
 KW Cholesterol metabolism.  
 FT TRANSMEM 124 144  
 FT TRANSMEM 155 175  
 FT TRANSMEM 200 220  
 FT TRANSMEM 262 282  
 FT TRANSMEM 304 324  
 FT TRANSMEM 344 366  
 FT TRANSMEM 437 457  
 FT TRANSMEM 472 492  
 FT TRANSMEM 524 554  
 FT CONFLICT 254 254 T -> I (IN REF. 2).  
 SQ SEQUENCE 522 AA; 59896 MW; BEAC2DB569FE729 CRC64;

Query Match 51.4%; Score 36; DB 1; Length 522;  
 Best Local Similarity 60.0%; Pred. No. 42;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWRNRAVR 12  
 ||| :||| :|||

```

Db 40 QWTRHMEAVK 49

RESULT 13
SOR2_MOUSE
ID SOA2_MOUSE STANDARD; PRT; 525 AA.
AC O88908;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sterol O-acyltransferase 2 (EC 2.3.1.26) (Cholesterol acyltransferase 2) (ACAT-2).
GN SOA2 OR ACAT2 OR ACAT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=98434591; PubMed=9756919;
RA Cases S., Novak S., Zheng Y.-W., Myers H.M., Lear S.R., Sande E.,
RA Welch C.B., Luis A.J., Spencer T.A., Krause B.R., Erickson S.K.,
RA Parsee R.V., Jr.;
RT "ACAT-2, a second mammalian acyl-CoA:cholesterol acyltransferase. Its
RT cloning, expression, and characterization."
RL J. Biol. Chem. 273:26755-26764(1998).
CC -1- FUNCTION: PLAYS A ROLE IN LIPOPROTEIN ASSEMBLY AND DIETARY
CC CHOLESTEROL ABSORPTION. IN ADDITION TO ITS ACYLTRANSFERASE
CC ACTIVITY, IT MAY ACT AS A LIGASE. MAY PROVIDE CHOLESTERYL ESTERS
CC FOR LIPOPROTEIN SECRETION FROM HEPATOCYTES AND INTESTINAL MUCOSA.
CC -1- CATALYTIC ACTIVITY: Acyl-CoA + cholesterol = CoA + cholesterol
CC ester.
CC -1- SUBUNIT: MAY FORM HOMO- OR HETERODIMERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC -1- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
CC
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CC
CC EMBL: AF078751; AAC64057.1; -.
CC MGD; MGI:1332226; Soat2.
CC InterPro: IPR002688; ACAT.
CC Pfam: PF01800; ACAT; 1.
CC Transferase; Acyltransferase; Transmembrane; Endoplasmic reticulum;
CC Cholesterol metabolism.
CC TRANSMEM 123 143 POTENTIAL.
CC TRANSMEM 154 174 POTENTIAL.
CC TRANSMEM 197 217 POTENTIAL.
CC TRANSMEM 265 285 POTENTIAL.
CC TRANSMEM 307 327 POTENTIAL.
CC TRANSMEM 350 370 POTENTIAL.
CC TRANSMEM 440 460 POTENTIAL.
CC TRANSMEM 475 495 POTENTIAL.
CC SEQUENCE 525 AA; 60823 MW; 01CD5E206B5C397 CRC64;
Query Match 51.4%; Score 36; DB 1; Length 525;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 3 QWTRHMEAVR 12
| | | | |
Db 39 QWTRHMEAVK 48

RESULT 14
VIA_BMV
Db 40 QWTRHMEAVK 49

VIA_BMV STANDARD; PRT; 961 AA.
P03588;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1A protein [includes: Helicase; Methyltransferase].
OS Brome mosaic virus (BMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Bromovirus.
OX NCBI_TaxID=12302;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=84114904; PubMed=6594215;
RA Ahlquist P., Dasgupta R., Kaesberg P.;
RT "Nucleotide sequence of the brome mosaic virus genome and its
RT implications for viral replication."
RL J. Mol. Biol. 172:369-383(1984).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CC CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN. THE
CC METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
CC CAPPING.
CC -1- SIMILARITY: TO 1A PROTEIN FROM CMV, CMV, PSV AND TAV.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: X02380; CAA36228.1; -.
CC F01; A04196; P1EVA.
CC InterPro: IPR002588; Vmethyltransf.
CC InterPro: IPR000606; Viral_helicase1.
CC Pfam: PF01443; Viral_helicase1; 1.
CC Pfam: PF01660; Vmethyltransf; 1.
CC Helicase; ATP-binding; Transferase; Methyltransferase.
CC NP_BIND 685 692 ATP (POTENTIAL)
CC SEQUENCE 961 AA; 109209 MW; 4F315CE2E2F4EFC CRC64;
Query Match 51.4%; Score 36; DB 1; Length 961;
Best Local Similarity 46.7%; Pred. No. 80;
Matches 7; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
Qy 1 CF-----QWQNRNAV 11
| | | | |
Db 346 CFKESKEWTENMKAV 360

RESULT 15
ACBR_HUMAN
ID ACBR_HUMAN STANDARD; PRT; 2273 AA.
AC P78363; O60438; O60915; O15112;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Retinal-specific ATP-binding cassette transporter (RIM ABC
DE transporter) (RIM protein) (RMP) (Stargardt disease protein).
GN ABCA4 OR ABCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. VARIANTS STGD, AND VARIANTS HIS-846 AND GLN-943.
RX MEDLINE=97207641; PubMed=9054934;
RA Allikmets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
RA Chidambaram A., Gerrard B., Baird L., Stauffer D., Pfeiffer A.,
RA Rattner A., Smallwood P.M., Li Y., Anderson K.L., Lewis R.A.,
RA Nathans J., Leppert M., Dean M., Lupski J.R.;
RT "A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is
RT mutated in recessive Stargardt macular dystrophy."

```

- RL Nat. Genet. 15:236-246(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97345663; PubMed=92020155;  
RA Aarlan S.M., Travis G.H.;  
RT "The photoreceptor rim protein is an ABC transporter encoded by the  
RT gene for recessive Stargardt's disease (ABCR).";  
RL FEBS Lett. 409:247-252(1997).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.  
RX MEDLINE=98163759; PubMed=9503029;  
RA Garber S., Rozet J.-M., van de Pol T.J.R., Hoyng C.B., Munnich A.,  
RA Blankenagel A., Kaplan J., Cremers F.P.M.;  
RT "Complete exon-intron structure of the retina-specific ATP binding  
RT transporter gene (ABCR) allows the identification of novel mutations  
RT underlying Stargardt disease.";  
RL Genomics 48:139-142(1998).  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANTS STGD.  
RX MEDLINE=98141123; PubMed=9490294;  
RA Nasonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,  
RA Weber B.H.F.;  
RT "Mapping of the rod photoreceptor ABC transporter (ABCR) to 1p21-p22.1  
RT and identification of novel mutations in Stargardt's disease.";  
RL Hum. Genet. 102:21-26(1998).  
RN [5]  
RP CHARACTERIZATION.  
RX MEDLINE=99175213; PubMed=10075733;  
RA Sun H., Molday R.S., Nathans J.;  
RT "Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR,  
RT the photoreceptor-specific ATP-binding cassette transporter  
RT responsible for Stargardt disease.";  
RL J. Biol. Chem. 274:8269-8281(1999).  
RN [6]  
RP DISEASE.  
RX MEDLINE=98133912; PubMed=9465990;  
RA Cremers F.P.M., van de Pol D.J.R., van Driel M.A., den Hollander A.I.,  
RA van Haren F.J.J., Knops N.V.A.M., Tijmes N., Bergen A.A.B.,  
RA Rohrschneider K., Blankenagel A., Pinckers A.J.L.G., Deutman A.F.,  
RA Hoyng C.B.;  
RT "Autosomal recessive retinitis pigmentosa and cone-rod dystrophy  
RT caused by splice site mutations in the Stargardt's disease gene  
RT ABCR.";  
RL Hum. Mol. Genet. 7:355-362(1998).  
RN [7]  
RP VARIANTS ARMD2, AND VARIANTS.  
RX MEDLINE=97442530; PubMed=9295268;  
RA Allikmets R., Shroyer N.F., Singh N., Seddon J.M., Lewis R.A.,  
RA Bernstein P.S., Peiffer A., Zabitskie N.A., Li Y., Hutchinson A.,  
RA Dean M., Lupske J.R., Leppert M.;  
RT "Mutation of the Stargardt disease gene (ABCR) in age-related macular  
RT degeneration.";  
RL Science 277:1805-1807(1997).  
RN [8]  
RP VARIANTS STGD W-18; C-212; H-636; M-1019; V-1038; C-1108; W-1640;  
RP S-1977 AND H-2107, AND VARIANTS FFM P-11; P-541; V-1038; E-1091;  
RP C-1508; F-1970 AND R-1971.  
RX MEDLINE=98454319; PubMed=9781034;  
RA Rozet J.-M., Gerber S., Souied E., Perrault I., Chatelain S., Ghazi I.,  
RA Leowski C., Dufier J.-L., Munnich A., Kaplan J.;  
RT "Spectrum of ABCR gene mutations in autosomal recessive macular  
RT dystrophies";  
RL Eur. J. Hum. Genet. 6:291-295(1998).  
RN [9]  
RP VARIANTS STGD.  
RX MEDLINE=99138655; PubMed=9973280;  
RA Lewis R.A., Shroyer N.F., Singh N., Allikmets R., Hutchinson A.,  
RA Li Y., Lupske J.R., Leppert M., Dean M.;  
RT "Genotype/phenotype analysis of a photoreceptor-specific ATP-binding  
RT cassette transporter gene, ABCR, in Stargardt disease.";  
RL Am. J. Hum. Genet. 64:422-434(1999).  
RN [10]  
RP VARIANTS STGD, AND VARIANTS.  
RX MEDLINE=99192348; PubMed=10090887;  
RA Maugeri A., van Driel M.A., van de Pol D.J.R., Klevering B.J.,  
RA van Haren F.J.J., Tijmes N., Bergen A.A.B., Rohrschneider K.,  
RA Blankenagel A., Pinckers A.J.L.G., Dahl N., Brunner H.G.,  
RA Deutman A.F., Hoyng C.B., Cremers F.P.M.;  
RT "The 2586G->C mutation in the ABCR gene is a mild frequent founder  
RT mutation in the western European population and allows the  
RT classification of ABCR Mutations in patients with Stargardt disease.";  
RL Am. J. Hum. Genet. 64:1024-1035(1999).  
RN [11]  
RP VARIANTS STGD TYR-54, AND VARIANT ALA-863.  
RX MEDLINE=2007755; PubMed=10612508;  
RA Zhang K., Garibaldi D.C., Kniazeva M., Albini T., Chiang M.F.,  
RA Kerrigan M., Sunness J.S., Han M., Allikmets R.;  
RT "A novel mutation in the ABCR gene in four patients with autosomal  
RT recessive Stargardt disease.";  
RL Am. J. Ophthalmol. 128:720-724(1999).  
RN [12]  
RP VARIANTS STGD V-60; R-206; N-300; P-541; A-849; P-974; V-1038; C-1108;  
RP L-1408; R-1486; D-1652; P-1729; E-1961; W-2038; M-2077; H-2107; R-2128  
RP AND Y-2150.  
RX MEDLINE=99221420; PubMed=10206579;  
RA Fishman G.A., Stone E.M., Grover S., Derlacki D.J., Kaines H.L.,  
RA Hockey R.;  
RT "Variation of clinical expression in patients with Stargardt dystrophy  
RT and sequence variations in the ABCR gene.";  
RL Arch. Ophthalmol. 117:504-510(1999).  
RN [13]  
RP VARIANTS GLU-1961 AND ASN-2177.  
RX MEDLINE=20349288; PubMed=10880298;  
RA Allikmets R., Tamur J., Hutchinson A., Lewis R.A., Shroyer N.F.,  
RA Dalakishvili K., Lupske J.R., Steiner K., Paulschoff D., Holz F.G.,  
RA Weber B.H.F., Dean M., Atkinson A., Gail M.H., Bernstein P.S.,  
RA Singh N., Peiffer A., Zabitskie N.A., Leppert M., Seddon J.M.,  
RA Zhang K., Sunness J.S., Udar N.S., Velchits S., Silva-Garcia R.,  
RA Small K.W., Simionelli F., Testa F., D'Urso M., Brancato R.,  
RA Rinaldi E., Ingavst J.J.M., ten Brink J.B., de Jong P.T.V.M.,  
RA Kaplan J., Maugeri A., van Driel M.A., Hoyng C.B., Cremers F.P.M.,  
RA Paloma E., Cocco R., Balcells S., Gonzalez-Duarte A., Kermani S.,  
RA Stanga P., Bhattacharya S.S., Bird A.C.;  
RT "Further evidence for an association of ABCR alleles with age-related  
RT macular degeneration.";  
RL Am. J. Hum. Genet. 67:487-491(2000).  
RN [14]  
RP VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247;  
RP V-328; K-471; P-541; Q-572; R-607; K-635; C-653; Y-764; R-765; A-901;  
RP I-959; K-1036; V-1038; P-1063; D-1087; C-1097; C-1108; L-1380; K-1399;  
RP P-1430; V-1440; H-1443; L-1486; Y-1488; M-1537; P-1689; L-1705;  
RP T-1733; R-1748; P-1763; K-1885; H-1898; E-1961; R-1975; S-1977; G-2077  
RP W-2077 AND V-2241, AND VARIANTS Q-152; H-212; R-423; I-552; R-914;  
RP Q-943; T-1562; I-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND  
RP V-2216.  
RX MEDLINE=20442027; PubMed=10958763;  
RA Rivera A., White K., Stoehr H., Steiner K., Hemmrich N., Grimm T.,  
RA Jurkiles B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,  
RA Weber B.H.F.;  
RT "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene  
RT in Stargardt disease and age-related macular degeneration.";  
RL Am. J. Hum. Genet. 67:800-813(2000).  
RN [15]  
RP VARIANTS CORD3 GLU-65; CYS-212; PRO-541; ALA-863; GLY-863 DEL;  
RP VAL-1038; LYS-1122; TYR-1490 AND ASP-1598.  
RX MEDLINE=20442040; PubMed=10958761;  
RA Maugeri A., Klevering B.J., Rohrschneider K., Blankenagel A.,  
RA Brunner H.G., Deutman A.F., Hoyng C.B., Cremers F.P.M.;  
RT "Mutations in the ABCA4 (ABCR) gene are the major cause of autosomal  
RT recessive cone-rod dystrophy.";  
RL Am. J. Hum. Genet. 67:960-966(2000).  
RN [16]  
RP VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780  
RP AND HIS-1898, AND VARIANT GLN-943.  
RX MEDLINE=20208356; PubMed=10746567;



RA Shroyer N.F., Lewis R.A., Lupeki J.R.;  
 RT "Complex inheritance of ABCR mutations in Stargardt disease: linkage  
 RT disequilibrium, complex alleles, and pseudodominance."  
 RL Hum. Genet. 106:244-248(2000).  
 RN [17]  
 RN VARIANTS STGD.  
 RP MEDLINE=20098082; PubMed=10634594;  
 RA Papaioannou M., Ocaka L., Bessant D., Lois N., Bird A.C., Payne A.,  
 RA Bhattacharya S.S.;  
 RT "An analysis of ABCR mutations in British patients with recessive  
 RT retinal dystrophies."  
 RL Invest. Ophthalmol. Vis. Sci. 41:16-19(2000).  
 RN [18]  
 RP VARIANTS STGD C-212; D-767; I-897; V-1038; K-1087; K-1399; Q-1640 AND  
 RP E-1961, AND VARIANT HIS-212.  
 RX MEDLINE=20174852; PubMed=10711710;  
 RA Simonelli F., Testa F., de Crecchio G., Rinaldi E., Hutchinson A.,  
 RA Atkinson A., Dean M., D'Urso M., Allikmets R.;  
 RT "New ABCR mutations and clinical phenotype in Italian patients with  
 RT Stargardt disease."  
 RL Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).  
 RN [19]  
 RP CHARACTERIZATION OF VARIANTS, AND MUTAGENESIS OF GLY-966; LYS-969;  
 RP GLY-1975 AND LYS-1978.  
 RX MEDLINE=20472331; PubMed=11017087;  
 RA Sun H., Smallwood P.M., Nathans J.;  
 RT "Biochemical defects in ABCR protein variants associated with human  
 RT retinopathies."  
 RL Nat. Genet. 26:242-246(2000).  
 RN [20]  
 RP VARIANT STGD ASN-972, AND VARIANTS GLN-943; ILE-1868 AND LEU-1948.  
 RX MEDLINE=21478761; PubMed=11594993;  
 RA Eksandh L., Ekstroem U., Abrahamson M., Bauer B., Andreasson S.;

Query Match 51.4%; Score 36; DB 1; Length 2273;  
 Best local similarity 60.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQNNMRA 10  
 Db 779 CFQWQNNMRA 788

Search completed: February 21, 2003, 07:27:52  
 Job time : 5.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107B-77

Perfect score: 70

Sequence: 1 CFQWQNRWRAV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:\*  
1: sp\_archea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	85.7	711	4 Q8TCD2	Q8Tcd2 homo sapien
2	56	80.0	38	4 Q9UCY5	Q9ucy5 homo sapien
3	45	84.3	33	6 Q9TR80	Q9tr80 ovis aries
4	42	60.0	932	5 Q19153	Q19153 caenorhabdi
5	41	58.6	148	10 Q9XHP1	Q9xhp1 sesamum ind
6	41	58.6	279	16 Q8XSE2	Q8xse2 ralstonia s
7	40	57.1	306	4 Q8TAX2	Q8tax2 homo sapien
8	40	57.1	466	4 Q9NUS2	Q9nus2 homo sapien
9	40	57.1	531	10 Q9LTD4	Q9ltd4 arabidopsis
10	40	57.1	864	5 Q62582	Q62582 encephalito
11	40	57.1	864	5 Q8SRG3	Q8srg3 encephalito
12	40	57.1	864	5 Q8SQ16	Q8sq16 encephalito
13	39.5	56.4	395	12 Q92283	Q92283 molluscum c
14	39	55.7	205	8 Q98R22	Q98rr2 guillardia
15	39	55.7	274	4 Q96M21	Q96m21 homo sapien
16	39	55.7	367	16 Q8UCR7	Q8ucr7 agrobacteri

17	39	55.7	372	10 Q81653	Q81653 hemerocalli
18	39	55.7	488	10 Q8S934	Q8s934 diospyros k
19	39	55.7	726	5 Q9BNX0	Q9bnx0 unidentified
20	39	55.7	727	5 Q9BNW0	Q9bnw0 peripatus s
21	39	55.7	728	5 Q9BNW7	Q9bnw7 scolopendra
22	39	55.7	844	5 Q9BME7	Q9bme7 aedes aegypt
23	39	55.7	844	5 Q9SP39	Q9sp39 aedes aegypt
24	39	55.7	844	5 Q8T4S0	Q8t4s0 aedes aegypt
25	39	55.7	844	5 Q8T4R9	Q8t4r9 aedes aegypt
26	38	54.3	105	10 Q9XPD5	Q9xpd5 oryza sativ
27	38	54.3	143	9 Q8ZXA7	Q8zxa7 bacterioph
28	38	54.3	341	11 Q8R2A4	Q8r2a4 mus musculu
29	38	54.3	356	16 Q9AK86	Q9ak86 streptomyce
30	38	54.3	515	10 Q22185	Q22185 arabidopsis
31	38	54.3	543	10 Q22188	Q22188 arabidopsis
32	38	54.3	544	10 Q949E1	Q949e1 oryza sativ
33	38	54.3	553	4 Q9NZL7	Q9nzl7 homo sapien
34	38	54.3	554	4 Q9NY67	Q9ny67 homo sapien
35	38	54.3	558	4 Q9UFK6	Q9ufk6 homo sapien
36	38	54.3	1130	4 Q9H1V5	Q9h1v5 homo sapien
37	38	54.3	1778	5 Q9NE65	Q9ne65 leishmania
38	38	54.3	2186	5 Q9N906	Q9n906 trypanosoma
39	37	52.9	222	16 P96876	P96876 mycobacteri
40	37	52.9	298	16 Q8YP77	Q8yp77 anabaena sp
41	37	52.9	332	10 Q8SAG4	Q8sag4 oryza sativ
42	37	52.9	357	10 Q22170	Q22170 arabidopsis
43	37	52.9	415	5 Q9U4M9	Q9u4m9 leishmania
44	37	52.9	447	10 Q948R1	Q948r1 arabidopsis
45	37	52.9	469	9 Q98115	Q98115 bacterioph

#### ALIGNMENTS

#### RESULT 1

Q8TCD2 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.  
AC Q8TCD2;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Lactotransferrin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022347; AAH22347.1; -- 1B9C7EE097C45FAF CRC64;  
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 85.7%; Score 60; DB 4; Length 711;  
Best Local Similarity 90.9%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRWRAV 11  
DB 39 CFQWQNRWRAV 49

#### RESULT 2

Q9UCY5 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.  
AC Q9UCY5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Lactoferrin homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=96081613; PubMed=8551695;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSSP; P02788; 1BKA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDBB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNNRAVR 12
Db 21 FQWQNNRAVR 31

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSSP; O77698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;
Best Local Similarity 66.7%; Pred. No. 0.25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNR 9
Db 19 CYQWQNNR 27

RESULT 4
Q19153 PRELIMINARY; PRT; 932 AA.
AC Q19153;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 105.1 kDa protein.
GN F07C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match 60.0%; Score 42; DB 5; Length 932;
Best Local Similarity 63.6%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNNRAVR 12
Db 579 FQWQNNRAVR 589

RESULT 5
Q9XHP1 PRELIMINARY; PRT; 148 AA.
AC Q9XHP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=TAINAN 1;
RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RT storage proteins in sesame.";
RL J. Agric. Food Chem. 47:4932-4938(1999).
DR EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000617; Napin.
DR InterPro; IPR001768; Try/alpha_inhtr.
DR Pfam; PF00234; try_alpha_aml; 1.
DR PRINTS; PR00496; NAPIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 58.6%; Score 41; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNR 9
Db 54 CMQWQNNR 62

RESULT 6
Q8XSE2 PRELIMINARY; PRT; 279 AA.
ID Q8XSE2
AC Q8XSE2;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=96081613; PubMed=8551695;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSSP; P02788; 1BKA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDBB CRC64;

Query Match 80.0%; Score 56; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQNNRAVR 12
Db 21 FQWQNNRAVR 31

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSSP; O77698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 64.3%; Score 45; DB 6; Length 33;
Best Local Similarity 66.7%; Pred. No. 0.25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNR 9
Db 19 CYQWQNNR 27

RESULT 4
Q19153 PRELIMINARY; PRT; 932 AA.
AC Q19153;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 105.1 kDa protein.
GN F07C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match 60.0%; Score 42; DB 5; Length 932;
Best Local Similarity 63.6%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNNRAVR 12
Db 579 FQWQNNRAVR 589

RESULT 5
Q9XHP1 PRELIMINARY; PRT; 148 AA.
AC Q9XHP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=TAINAN 1;
RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RT storage proteins in sesame.";
RL J. Agric. Food Chem. 47:4932-4938(1999).
DR EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000617; Napin.
DR InterPro; IPR001768; Try/alpha_inhtr.
DR Pfam; PF00234; try_alpha_aml; 1.
DR PRINTS; PR00496; NAPIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 58.6%; Score 41; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNR 9
Db 54 CMQWQNNR 62

RESULT 6
Q8XSE2 PRELIMINARY; PRT; 279 AA.
ID Q8XSE2
AC Q8XSE2;

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DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Purative ICC protein homolog.  
 GN ICC OR RSP0534 OR RS00414.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OG Plasmid megaplasmid.  
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
 OC Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GM11000;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,  
 RA Gapin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;  
 RL "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
 RL Nature 415:497-502(2002).  
 DR EMBL: AL646079; CADI7685.1; -  
 DR InterPro: IPR004843; M-PPase.  
 DR InterPro: IPR004844; S/T\_phosphatase.  
 DR Pfam: PF00149; Metallophos; 1.  
 KW Plasmid; Complete proteome.  
 SQ SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 58.6%; Score 41; DB 16; Length 279;  
 Best Local Similarity 41.7%; Pred. No. 13;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CFQWQNNRAVR 12  
 |||||:  
 Db 244 CFQWEKGTAK 255

RESULT 7  
 ID Q8TAX2 PRELIMINARY; PRT; 306 AA.  
 AC Q8TAX2;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Similar to hypothetical protein FLJ11175.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PANCREAS;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC025708; AAH25708.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;

Query Match 57.1%; Score 40; DB 4; Length 306;  
 Best Local Similarity 50.0%; Pred. No. 21;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNRA 10  
 |||||:  
 Db 269 CFQWESTLRS 278

RESULT 8  
 ID Q9NUS2 PRELIMINARY; PRT; 466 AA.  
 AC Q9NUS2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE CDNA FJ111175 fis. clone PIACB1007375, weakly similar to phorbol  
 ester/diacylglycerol-binding protein UNC-13.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Isozaki T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi N., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Yamanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,  
 RA Ninomiya K., Iwavanagi T.;  
 RL "NEO human cDNA sequencing project.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK002037; BAA92048.1; -  
 DR HSSP: P21707; 1BYN.  
 DR InterPro: IPR000008; C2.  
 DR InterPro: IPR000504; RNA\_rec\_mct.  
 DR Pfam: PF00168; C2; 1.  
 DR PRINTS: PRO0360; C2DOMAIN.  
 DR SMART: SM00239; C2; 1.  
 DR PROSITE: PS00499; C2\_DOMAIN\_1; UNKNOWN\_1.  
 DR PROSITE: PS00004; C2\_DOMAIN\_2; 1.  
 DR PROSITE: PS00030; RNP\_RNP\_1; UNKNOWN\_1.  
 SQ SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;

Query Match 57.1%; Score 40; DB 4; Length 466;  
 Best Local Similarity 50.0%; Pred. No. 33;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNRA 10  
 |||||:  
 Db 269 CFQWESTLRS 278

RESULT 9  
 ID Q9LTD4 PRELIMINARY; PRT; 531 AA.  
 AC Q9LTD4;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Similarity to unknown protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsia.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT clones.";  
 RT DNA Res. 7:131-135(2000).  
 RL EMBL: AB025608; BAA95727.1; -  
 SQ SEQUENCE 531 AA; 60377 MW; C229982FFFB175E CRC64;

Query Match 57.1%; Score 40; DB 10; Length 531;  
 Best Local Similarity 60.0%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNMRA 10

Db 518 CFQWQSCRA 527

RESULT 10

062582 ID O62582 PRELIMINARY; PRT; 864 AA.  
AC O62582;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Aminopectidase (EC 3.4.11.7).  
OS Encephalitozoon cuniculi.  
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.  
OX NCBI\_TaxID=6035;  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=20468003; PubMed=11013707;  
RA Duffieux F., Peyret P., Roe B.A., Vivares C.P.;  
RT "First report on the systematic sequencing of the small genome of  
RT Encephalitozoon cuniculi (Microsporida, Protozoa) : gene organization of  
RT a 4.3 kbp region on chromosome I.";  
RL Microb. Comp. Genomics 3:1-11(1998).  
DR EMBL; AJ005644; CRA06646.1; -.  
DR InterPro; IPR000130; Ala.peptase.  
DR InterPro; IPR000130; Zn.MTpeptase.  
DR Pfam; PF01433; Peptidase M1; 1.  
DR PRINTS; PR00756; ALADPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
DR Aminopectidase; Hydrolase.  
SQ SEQUENCE 864 AA; 97387 MW; 6617AE5B6472F703 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 864;

Best Local Similarity 60.0%; Pred. No. 64;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQNMRAVR 12

Db 842 QWRMRMGIR 851

RESULT 11

Q8SRG3 ID Q8SRG3 PRELIMINARY; PRT; 864 AA.  
AC Q8SRG3;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Glutamyl aminopeptidase.  
GN ECU08.0070.  
OS Encephalitozoon cuniculi.  
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.  
OX NCBI\_TaxID=6035;  
[1]  
RN SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RA Genoscope;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RX MEDLINE=21576510; PubMed=11719806;  
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,  
RA Prensler G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
RA Weissbach J., Vivares C.P.;  
RT "Genome sequence and gene compaction of the eukaryote parasite  
RT Encephalitozoon cuniculi";  
RL Nature 414:450-453(2001).  
DR EMBL; AL590448; CAD26312.1; -.

Query Match 57.1%; Score 40; DB 5; Length 864;

Best Local Similarity 60.0%; Pred. No. 64;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQNMRAVR 12

Db 842 QWRMRMGIR 851

RESULT 11

Q8SRG3 ID Q8SRG3 PRELIMINARY; PRT; 864 AA.  
AC Q8SRG3;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Glutamyl aminopeptidase.  
GN ECU08.0070.  
OS Encephalitozoon cuniculi.  
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.  
OX NCBI\_TaxID=6035;  
[1]  
RN SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RA Genoscope;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RX MEDLINE=21576510; PubMed=11719806;  
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,  
RA Prensler G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
RA Weissbach J., Vivares C.P.;  
RT "Genome sequence and gene compaction of the eukaryote parasite  
RT Encephalitozoon cuniculi";  
RL Nature 414:450-453(2001).  
DR EMBL; AL590448; CAD26312.1; -.

SQ SEQUENCE 864 AA; 97521 MW; EF65005145C57CF5 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 864;

Best Local Similarity 60.0%; Pred. No. 64;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQNMRAVR 12

Db 842 QWRMRMGIR 851

RESULT 12

Q8SQI6 ID Q8SQI6 PRELIMINARY; PRT; 864 AA.  
AC Q8SQI6;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Glutamyl aminopeptidase.  
GN ECU01.0140 OR ECU01.1470.  
OS Encephalitozoon cuniculi.  
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.  
OX NCBI\_TaxID=6035;  
[1]  
RN SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RA Genoscope;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RX MEDLINE=21576510; PubMed=11719806;  
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,  
RA Prensler G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
RA Weissbach J., Vivares C.P.;  
RT "Genome sequence and gene compaction of the eukaryote parasite  
RT Encephalitozoon cuniculi";  
RL Nature 414:450-453(2001).  
DR EMBL; AL391737; CAD24886.1; -.  
DR EMBL; AL391737; CAD25018.1; -.  
SQ SEQUENCE 864 AA; 97364 MW; 44DD93320CC5B153 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 864;

Best Local Similarity 60.0%; Pred. No. 64;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQNMRAVR 12

Db 842 QWRMRMGIR 851

RESULT 13

O92283 ID O92283 PRELIMINARY; PRT; 395 AA.  
AC O92283;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE MC080R.  
OS Molluscum contagiosum virus subtype 2 (MCVII).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OX Molluscipoxvirus.  
OX NCBI\_TaxID=10281;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=99011469; PubMed=9792850;  
RA Senkevich T.G., Moss B.;  
RT "Domain structure, intracellular trafficking, and beta2-microglobulin  
RT binding of a major histocompatibility complex class I homolog encoded  
RT by molluscum contagiosum virus.";  
RL Virology 250:397-407(1998).  
DR EMBL; AF085225; AAC72821.1; -.

DR InterPro; IPR003597; Ig ci.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR Pfam; PF00050; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGC1; 1.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN 1.  
 SQ SEQUENCE 395 AA; 43312 MW; D98B574419AC0AD CRC64;

Query Match 56.4%; Score 39.5; DB 12; Length 395;  
 Best Local Similarity 63.6%; Pred. No. 34;  
 Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 CFQWQRNRAV 10  
 |||||:|:|:  
 DB 224 CFQWLERHLRA 234

## RESULT 14

Q98RR2 ID Q98RR2 PRELIMINARY; PRT; 205 AA.  
 AC Q98RR2:  
 DT 01-OCT-2001 (TrEMBLrel. 19, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE 268 proteasome SU B5.  
 GN PRS5.  
 OS Guillardia theta (Cryptomonas phi).  
 OG Nucleomorph.  
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.  
 OX NCBI\_TaxID=55523;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21223349; PubMed=11333671;  
 RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,  
 Wu X., Reith M., Cavalier-Smith T., Maier U.G.;  
 RT "The highly reduced genome of an enslaved algal nucleus."  
 RL Nature 410:1091-1096(2001).  
 DR EMBL; AF165818; AAK39885.1; -  
 DR InterPro; IPR000243; Proteasome\_B.  
 DR InterPro; IPR001353; Proteasome.  
 DR Pfam; PF00227; proteasome; 1.  
 DR PRINTS; PR00141; PROTEASOME.  
 KW Proteasome.  
 SQ SEQUENCE 205 AA; 22691 MW; D30F5289CBC85049 CRC64;

Query Match 55.7%; Score 39; DB 8; Length 205;  
 Best Local Similarity 45.8%; Pred. No. 21;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNRAV 11  
 |||||:|:|:  
 DB 63 CFFWERNLSSL 73

## RESULT 15

Q96M21 ID Q96M21 PRELIMINARY; PRT; 274 AA.  
 AC Q96M21:  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE CDNA FLJ32891. fis, clone TESTI2004929.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,  
 Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,

RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
 RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,  
 RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AK057453; BAB71493.1; -  
 SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

Query Match 55.7%; Score 39; DB 4; Length 274;  
 Best Local Similarity 50.0%; Pred. No. 29;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNRAV 12  
 |||||:|:|:  
 DB 66 CFQWRNGVRYLR 77

Search completed: February 21, 2003, 07:44:31  
 Job time : 21.8 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107B-78  
Perfect score: 71  
Sequence: 1 CFQWRNMRXR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
1: /SID82/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID82/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID82/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SID82/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SID82/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SID82/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SID82/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SID82/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SID82/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SID82/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SID82/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SID82/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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15: /SID82/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
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18: /SID82/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SID82/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SID82/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	12	21	AAV78078 Human lactoferrin
2	67	94.4	12	21	AAV78038 Human lactoferrin
3	67	94.4	12	21	AAV78046 Human lactoferrin
4	67	94.4	12	21	AAV78047 Human lactoferrin
5	67	94.4	13	21	AAV78037 Human lactoferrin
6	67	94.4	13	21	AAV78048 Human lactoferrin
7	67	94.4	13	21	AAV78049 Human lactoferrin
8	67	94.4	14	21	AAV78036 Human lactoferrin
9	67	94.4	14	21	AAV78050 Human lactoferrin
10	67	94.4	14	21	AAV78051 Human lactoferrin

11	67	94.4	15	17	AAV98554 Peptide for anti-u
12	67	94.4	15	21	AAV78035 Human lactoferrin
13	67	94.4	15	21	AAV78062 Human lactoferrin
14	67	94.4	15	21	AAV78063 Human lactoferrin
15	67	94.4	16	21	AAV78031 Human lactoferrin
16	67	94.4	16	21	AAV78064 Human lactoferrin
17	67	94.4	16	21	AAV78065 Human lactoferrin
18	67	94.4	17	21	AAV78034 Human lactoferrin
19	67	94.4	17	21	AAV78066 Human lactoferrin
20	67	94.4	17	21	AAV78067 Human lactoferrin
21	67	94.4	18	15	AAV69352 Human lactoferrin
22	67	94.4	18	17	AAV13397 Advanced glycosyla
23	67	94.4	18	21	AAV78033 Human lactoferrin
24	67	94.4	19	21	AAV68867 Amino acid sequenc
25	67	94.4	19	21	AAV78032 Human lactoferrin
26	67	94.4	20	13	AAV21810 Anti microbial pep
27	67	94.4	20	14	AAV48441 Lactoferrin-relate
28	67	94.4	20	15	AAV48530 Lactoferrin derive
29	67	94.4	20	15	AAV48531 Lactoferrin derive
30	67	94.4	20	15	AAV57461 Lactoferrin derive
31	67	94.4	20	15	AAV57462 Lactoferrin derive
32	67	94.4	20	16	AAV84698 Bovine lactoferrin
33	67	94.4	20	16	AAV84699 Bovine lactoferrin
34	67	94.4	20	16	AAV80263 Anti-parasitic lac
35	67	94.4	20	16	AAV80264 Anti-parasitic lac
36	67	94.4	20	17	AAV98553 Peptide for anti-u
37	67	94.4	20	17	AAV91852 Lactoferrin-derive
38	67	94.4	20	17	AAV03045 Lactoferrin-derive
39	67	94.4	20	17	AAV90607 Lactoferrin-derive
40	67	94.4	20	17	AAV87621 Lactoferrin-derive
41	67	94.4	20	17	AAV87622 Lactoferrin-derive
42	67	94.4	20	18	AAV26150 Lactoferrin deriva
43	67	94.4	20	18	AAV14036 Anti-parasitic pep
44	67	94.4	20	19	AAV70310 Thrombus formation
45	67	94.4	20	19	AAV53224 Lactoferrin hydrol

## ALIGNMENTS

## RESULT 1

AAV78078	ID	AAV78078 standard; Peptide; 12 AA.
XX	AC	AAV78078;
XX	DT	25-APR-2000 (first entry)
XX	DE	Human lactoferrin derived peptide SEQ ID NO:78.
XX	KW	Human; lactoferrin; modification; infection; inflammation; tumour;
XX	KW	food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX	KW	urinary tract infection; colitis; Candida infection; fungicidal;
XX	KW	bactericidal; preservative.
OS		Homo sapiens.
OS		Synthetic.
XX		WO200001730-A1.
XX		13-JAN-2000.
XX		06-JUL-1999; 99WO-SE01230.
XX		06-JUL-1998; 98SE-0002441.
XX		17-JUL-1998; 98SE-0002562.
XX		29-DEC-1998; 98SE-0004614.
XX		(ASCI-) A+ SCI INVEST AB.
PI		Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
DR		WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 22; Page 35; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.  
XX  
XX SQ Sequence 12 AA;  
SQ Query Match 100.0%; Score 71; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CFQWQRNKRKAR 12  
DB 1 CFQWQRNKRKAR 12  
RESULT 2  
AAY78038  
ID AAY78038 standard; Peptide; 12 AA.  
XX  
XX AAY78038;  
XX  
XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:38.  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.  
XX Homo sapiens.  
XX Synthetic.  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX  
XX PF 06-JUL-1999; 99WO-SE01230.  
XX  
XX PR 06-JUL-1998; 98SE-0002441.  
XX PR 17-JUL-1998; 98SE-0002562.  
XX PR 29-DEC-1998; 98SE-0004614.  
XX  
XX PA (ASCI-) A+ SCI INVEST AB.  
XX  
XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
XX inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 12; Page 70; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.  
XX  
XX SQ Sequence 12 AA;  
SQ Query Match 94.4%; Score 67; DB 21; Length 12;  
Best Local Similarity 91.7%; Pred. No. 6.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQRNKRKAR 12  
DB 1 CFQWQRNKRKAR 12  
RESULT 3  
AAY78046  
ID AAY78046 standard; Peptide; 12 AA.  
XX  
XX AAY78046;  
XX  
XX 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:46.  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.  
XX Homo sapiens.  
XX Synthetic.  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX  
XX PF 06-JUL-1999; 99WO-SE01230.  
XX  
XX PR 06-JUL-1998; 98SE-0002441.  
XX PR 17-JUL-1998; 98SE-0002562.  
XX PR 29-DEC-1998; 98SE-0004614.  
XX  
XX PA (ASCI-) A+ SCI INVEST AB.  
XX  
XX PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
XX inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 15; Page 35; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also



CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

SQ Sequence 12 AA;  
 Query Match 94.4%; Score 67; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 6.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKAR 12  
 |||||  
 DB 1 CFQWQRNMRKVR 12

RESULT 4  
 ID AAY78047  
 ID AAY78047 standard; Peptide; 12 AA.

AC AAY78047;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

OS WO200001730-A1.

XX 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;  
 Query Match 94.4%; Score 67; DB 21; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 6.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKAR 12  
 |||||  
 DB 1 CFQWQRNMRKVR 12

RESULT 5  
 ID AAY78037  
 ID AAY78037 standard; Peptide; 13 AA.

AC AAY78037;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.  
 OS Synthetic.

OS WO200001730-A1.

XX 13-JAN-2000.

PD 06-JUL-1999; 99WO-SE01230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.  
 XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 13 AA;

Query Match 94.4%; Score 67; DB 21; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 6.8e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12  
 |||||  
 Db 2 CFQWQNNRKVR 13

## RESULT 6

AAV78048  
 ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

AC AAY78048;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:48.

DE Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

XX lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

XX Query Match 94.4%; Score 67; DB 21; Length 13;

XX Best Local Similarity 91.7%; Pred. No. 6.8e-05;

XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12

Db 2 CFQWQNNRKVR 13

RESULT 7

AAV78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;

AC AAY78049;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:49.

DE Human; lactoferrin; modification; infection; inflammation; tumour;

KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

KW urinary tract infection; colitis; Candida infection; fungicidal;

KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

XX lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 13 AA;

XX Query Match 94.4%; Score 67; DB 21; Length 13;

XX Best Local Similarity 91.7%; Pred. No. 6.8e-05;

XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12

Db 2 CFQWQNNRKVR 13

RESULT 8

AAV78036

ID AAY78036 standard; Peptide; 14 AA.

XX AAY78036;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:36.

XX

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-S01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 12; Page 69; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 94.4%; Score 67; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKVR 12  
 Db 3 CFQWQNRKVR 14  
 RESULT 9  
 AAY78050  
 ID AAY78050 standard; Peptide; 14 AA.  
 AC AAY78050;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:50.  
 DE  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-S01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 PA (ASCI-) A+ SCI INVEST AB.  
 XX  
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 15; Page 75; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 94.4%; Score 67; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKVR 12  
 Db 3 CFQWQNRKVR 14  
 RESULT 10  
 AAY78051  
 ID AAY78051 standard; Peptide; 14 AA.  
 AC AAY78051;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:51.  
 DE  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 XX urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 XX 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-S01230.  
 PF

XX PR 06-JUL-1998; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.  
 XX PA (ASCI-) A+ SCI INVEST AB.  
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX PT New peptides used for treatment and prevention of infections,  
 XX PT inflammations and tumors and for use in infant formula food -  
 XX PS Claim 18; Page 75; 102pp; English.  
 XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX SQ Sequence 14 AA;  
 Query Match 94.4%; Score 67; DB 21; Length 14;  
 Best Local Similarity 91.7%; Pred. No. 7.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKAR 12  
 DB 3 CFQWQNRKVR 14  
 RESULT 11  
 AAR98554  
 ID AAR98554 standard; Peptide; 15 AA.  
 XX AC AAR98554;  
 XX DT 12-NOV-1996 (first entry)  
 XX DE Peptide for anti-ulcer agent.  
 XX KW anti-ulcer agent; low toxicity; stable; heat-resistant.  
 XX OS Synthetic.  
 XX PN JP08143468-A.  
 XX PD 04-JUN-1996.  
 XX PF 17-NOV-1994; 94JP-0283869.  
 XX PR 17-NOV-1994; 94JP-0283869.  
 XX PA (MORG) MORINAGA MILK IND CO LTD.  
 XX DR WPI; 1996-318857/32.  
 XX PT Anti-ulcer agent contg. peptide - has low toxicity, is  
 XX PT heat-resistant and water-soluble  
 XX PS Claim 1; Page 11; 11pp; Japanese.

XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low  
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be  
 CC administered orally and be produced in large amounts.  
 XX SQ Sequence 15 AA;  
 Query Match 94.4%; Score 67; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 7.8e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKAR 12  
 DB 2 CFQWQNRKVR 13  
 RESULT 12  
 AAY78035  
 ID AAY78035 standard; Peptide; 15 AA.  
 XX AC AAY78035;  
 XX DT 25-APR-2000 (first entry)  
 XX DE Human lactoferrin derived peptide SEQ ID NO:35.  
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200001730-A1.  
 XX PD 13-JAN-2000.  
 XX PF 06-JUL-1999; 99WO-SE01230.  
 XX PR 06-JUL-1999; 98SE-0002441.  
 XX PR 17-JUL-1998; 98SE-0002562.  
 XX PR 29-DEC-1998; 98SE-0004614.  
 XX PA (ASCI-) A+ SCI INVEST AB.  
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 XX WPI; 2000-147388/13.  
 XX PT New peptides used for treatment and prevention of infections,  
 XX PT inflammations and tumors and for use in infant formula food -  
 XX PS Claim 12; Page 69; 102pp; English.  
 XX CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX SQ Sequence 15 AA;

Query Match 94.4%; Score 67; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 7.8e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12  
 DB 4 CFQWQNNRKVR 15

## RESULT 13

AAV78062  
 ID AAV78062 standard; Peptide; 15 AA.

XX AAV78062;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:62.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCII-) A+ SCI INVEST AB.

XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PS Claim 15; Page 81; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 15 AA;

Query Match 94.4%; Score 67; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 7.8e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12  
 DB 4 CFQWQNNRKVR 15

## RESULT 14

AAV78063  
 ID AAV78063 standard; Peptide; 15 AA.

XX AAV78063;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:63.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCII-) A+ SCI INVEST AB.

XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 PS Claim 18; Page 81; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 15 AA;

Query Match 94.4%; Score 67; DB 21; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 7.8e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNRKAR 12  
 DB 4 CFQWQNNRKVR 15

## RESULT 15

AAV78031  
 ID AAV78031 standard; Peptide; 16 AA.

XX AAV78031;

XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:31.  
 XX  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WC200001730-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX  
 PR 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX  
 XX (ASCII-) A+ SCI INVEST AB.  
 PA  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI  
 XX WPI; 2000-147388/13.  
 DR  
 XX  
 PT New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 PS Claim 11; Page 68; 102pp; English.  
 XX  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 94.4%; Score 67; DB 21; Length 16;  
 Best Local Similarity 91.7%; Pred. No. 8.3e-05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CFQWQNNRKR 12  
 DB 5 CFQWQNNRKR 16

Search completed: February 21, 2003, 07:37:13  
 Job time : 28.35 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:59 ; Search time 8.65 Seconds  
(without alignments)  
40.818 Million cell updates/sec

Title: US-09-743-107B-78  
Perfect score: 71  
Sequence: 1 CFQWQNNKXAR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
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5: /cgn2\_6/prodata/1/iaa/6C\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/6D\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	94.4	18	1	US-08-204-487-3
2	67	94.4	18	2	US-08-485-948-8
3	67	94.4	18	2	US-08-628-380-8
4	67	94.4	18	2	US-08-475-055-8
5	67	94.4	20	1	US-07-755-161A-3
6	67	94.4	20	1	US-07-891-174-3
7	67	94.4	20	1	US-08-204-487-1
8	67	94.4	20	1	US-08-256-771-24
9	67	94.4	20	1	US-08-256-771-25
10	67	94.4	20	1	US-08-381-984-24
11	67	94.4	20	1	US-08-381-984-25
12	67	94.4	22	4	US-09-508-734-4
13	67	94.4	24	4	US-09-508-734-6
14	67	94.4	25	1	US-07-755-161A-10
15	67	94.4	25	1	US-07-891-174-10
16	67	94.4	25	1	US-08-204-487-7
17	67	94.4	29	4	US-09-508-734-8
18	67	94.4	36	1	US-07-755-161A-8
19	67	94.4	36	1	US-07-891-174-8
20	67	94.4	36	1	US-08-256-771-30
21	67	94.4	36	1	US-08-381-984-29
22	67	94.4	47	2	US-08-464-182A-6
23	67	94.4	47	2	US-08-406-271-6
24	67	94.4	50	2	US-08-693-274A-7
25	67	94.4	52	4	US-09-017-043A-3
26	67	94.4	53	2	US-08-464-182A-5
27	67	94.4	53	2	US-08-406-271-5

28. 67 94.4 54 2 US-08-464-182A-2 Sequence 2, Appli  
29. 67 94.4 54 2 US-08-406-271-2 Sequence 2, Appli  
30. 67 94.4 694 3 US-08-724-586-2 Sequence 2, Appli  
31. 67 94.4 694 4 US-09-421-632-2 Sequence 2, Appli  
32. 67 94.4 694 4 US-09-932-190-2 Sequence 2, Appli  
33. 67 94.4 705 2 US-08-655-640-2 Sequence 2, Appli  
34. 67 94.4 708 2 US-08-655-640-4 Sequence 4, Appli  
35. 67 94.4 711 1 US-08-154-019-4 Sequence 4, Appli  
36. 67 94.4 711 1 US-08-461-333-4 Sequence 4, Appli  
37. 67 94.4 711 3 US-08-464-167-4 Sequence 4, Appli  
38. 67 94.4 711 3 US-09-158-313-4 Sequence 4, Appli  
39. 67 94.4 711 4 US-08-476-798-4 Sequence 4, Appli  
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43. 64 90.1 711 2 US-08-456-106-2 Sequence 2, Appli  
44. 64 90.1 711 3 US-08-456-108-2 Sequence 2, Appli  
45. 64 90.1 711 4 US-09-265-577-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-204-487-3  
; Sequence 3, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOIKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: TANAKA, SHUN'ICHI  
; APPLICANT: DOSAKO, TOSHIHIRO  
; APPLICANT: KAWASAKI, TOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: RJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..18  
; OTHER INFORMATION: /note= "HUMAN LACTOPERRIN PEPTIDE"

/ OTHER INFORMATION: (20-37)"  
US-08-204-487-3

Query Match 94.4%; Score 67; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 1.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNRKAR 12  
||| ||||| |||  
Db 1 CFQWQRNRKVR 12

## RESULT 2

US-08-485-948-8  
; Sequence 8, Application US/08485948  
; Patent No. 5855882  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,948  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,217  
; FILING DATE: JUNE 7, 1995  
; APPLICATION NUMBER: 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-485-948-8

Query Match 94.4%; Score 67; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 1.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNRKAR 12  
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Db 1 CFQWQRNRKVR 12

## RESULT 3

US-08-628-380-8  
; Sequence 8, Application US/08628380  
; Patent No. 5891341  
; GENERAL INFORMATION:  
; APPLICANT: LI YONG MING  
; APPLICANT: VLASSARA, HELEN  
; APPLICANT: CERAMI, ANTHONY  
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/628,380  
; FILING DATE: April 4, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/418,642  
; FILING DATE: APRIL 7, 1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: LF-C1, 8-25  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-628-380-8

Query Match 94.4%; Score 67; DB 2; Length 18;  
Best Local Similarity 91.7%; Pred. No. 1.9e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNRKAR 12  
||| ||||| |||  
Db 1 CFQWQRNRKVR 12

## RESULT 4

US-08-475-055-8  
; Sequence 8, Application US/08475055  
; Patent No. 5962245  
; GENERAL INFORMATION:  
; APPLICANT: YONG MING LI  
; APPLICANT: HELEN VLASSARA  
; APPLICANT: ANTHONY CERAMI  
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE  
; NUMBER OF SEQUENCES: 9



```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475.055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/419,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-C1, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;;
US-08-475-055-8
Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. NO. 1.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFWQWRNMRKAR 12
Db 1 CFWQWRNMRKVR 12

RESULT 5
US-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
;
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
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;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755,161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
;;
US-07-755-161A-3
Query Match 94.4%; Score 67; DB 1; Length 20;
```

Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNRKAR 12  
| | | | | | | | | |  
Db 2 CFQWRNRKVR 13

RESULT 6  
US-07-891-174-3  
; Sequence 3, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLER:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site

; LOCATION: 2  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 19"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 19  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 2"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
; US-07-891-174-3

Query Match 94.4%; Score 67; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRNRKAR 12  
| | | | | | | | | |  
Db 2 CFQWRNRKVR 13

RESULT 7  
US-08-204-487-1  
; Sequence 1, Application US/08204487  
; Patent No. 5565425  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, NAOKI  
; APPLICANT: NAKASHIMA, HIDEKI  
; APPLICANT: MOSUCHI, WATARU  
; APPLICANT: TANAKA, SHIGEKI  
; APPLICANT: DOSAKO, SHUN'ICHI  
; APPLICANT: KAWASAKI, YOSHIHIRO  
; APPLICANT: UCHIDA, TOSHIAKI  
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESS: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/204,487  
; APPLICATION NUMBER: US/08/204,487  
; FILING DATE: 02-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, PAULA A.  
; REGISTRATION NUMBER: 32,503  
; REFERENCE/DOCKET NUMBER: FJN-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..20  
; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE  
; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"  
US-08-204-487-1

Query Match 94.4%; Score 67; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKAR 12  
| | | | | | | | | |  
Db 2 CFQWQRMNRKVR 13

## RESULT 8

US-08-256-771-24  
; Sequence 24, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,771  
; FILING DATE: July 22, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER:

FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:

TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY:

LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "Cys residues are linked by  
; OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 94.4%; Score 67; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKAR 12  
| | | | | | | | | |  
Db 2 CFQWQRMNRKVR 13

## RESULT 9

US-08-256-771-25  
; Sequence 25, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,771  
; FILING DATE: July 22, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:

FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:

TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:

NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "Cys residues are protected to  
; OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25

Query Match 94.4%; Score 67; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKAR 12  
| | | | | | | | | |  
Db 2 CFQWQRMNRKVR 13

## RESULT 10

US-08-381-984-24

Sequence 24, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "cysteine residues at positions 2  
OTHER INFORMATION: and 19 are bonded by disulfide linkage"  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "the specified peptide as well as  
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
US-08-381-984-24  
Query Match 94.4%; Score 67; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQRMNRKAR 12  
DB 2 CFQWQRMNRKVR 13  
RESULT 11  
US-08-381-984-25  
Sequence 25, Application US/08381984  
Patent No. 5804555  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: ANTIOXIDANT  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "the specified peptide as well as  
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
US-08-381-984-25  
Query Match 94.4%; Score 67; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQRMNRKAR 12  
DB 2 CFQWQRMNRKVR 13  
RESULT 12  
US-09-508-734-4  
Sequence 4, Application US/09508734  
Patent No. 6423509  
GENERAL INFORMATION:  
APPLICANT: Samyang Genex Corporation  
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
TITLE OF INVENTION: useful microorganism thereof  
FILE REFERENCE: PA/SYG/00139  
CURRENT APPLICATION NUMBER: US/09/508,734  
CURRENT FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: PCT/KR99/00373  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: KR1998-29351  
PRIOR FILING DATE: 1998-07-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Kopatentin 1.71  
SEQ ID NO 4

STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,984  
FILING DATE: April 11, 1995  
CLASSIFICATION: 252  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note= "the specified peptide as well as  
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"  
US-08-381-984-25  
Query Match 94.4%; Score 67; DB 1; Length 20;  
Best Local Similarity 91.7%; Pred. No. 2.1e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQRMNRKAR 12  
DB 2 CFQWQRMNRKVR 13  
RESULT 12  
US-09-508-734-4  
Sequence 4, Application US/09508734  
Patent No. 6423509  
GENERAL INFORMATION:  
APPLICANT: Samyang Genex Corporation  
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
TITLE OF INVENTION: useful microorganism thereof  
FILE REFERENCE: PA/SYG/00139  
CURRENT APPLICATION NUMBER: US/09/508,734  
CURRENT FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: PCT/KR99/00373  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: KR1998-29351  
PRIOR FILING DATE: 1998-07-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Kopatentin 1.71  
SEQ ID NO 4

LENGTH: 22  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-508-734-4

Query Match 94.4%; Score 67; DB 4; Length 22;  
Best Local Similarity 91.7%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMKVR 12  
|||  
DB 2 CFQWQRNMKVR 13  
|||

## RESULT 13

US-09-508-734-6  
Sequence 6, Application US/09508734  
Patent No. 6423509

## GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation  
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and  
FILE REFERENCE: PA/SYG/00139  
CURRENT APPLICATION NUMBER: US/09/508,734  
CURRENT FILING DATE: 2000-06-01  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: PCT/KR99/00373  
PRIOR FILING DATE: 1998-07-13  
PRIOR APPLICATION NUMBER: KR1998-29351  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: KopatentIn 1.71  
SEQ ID NO 6  
LENGTH: 24  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-508-734-6

Query Match 94.4%; Score 67; DB 4; Length 24;  
Best Local Similarity 91.7%; Pred. No. 2.5e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMKVR 12  
|||  
DB 3 CFQWQRNMKVR 14  
|||

## RESULT 14

US-07-755-161A-10  
Sequence 10, Application US/07755161A  
Patent No. 5304633

## GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptides and an  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/755,161A  
FILING DATE: 19910905  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:

ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:

POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:

FEATURE:  
NAME/KEY: modified site

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of  
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 21"

FEATURE:

NAME/KEY: modified site

LOCATION: 21

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
OTHER INFORMATION: thiol group of Cys residue at location 4"

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10

Query Match 94.4%; Score 67; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 2.6e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRNMKVR 12

|||

DB 4 CFQWQRNMKVR 15

|||

## RESULT 15

US-07-891-174-10  
; Sequence 10, Application US/07891174  
; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 4  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 21"  
; FEATURE:  
; NAME/KEY: modified site  
; LOCATION: 21

IDENTIFICATION METHOD:  
; OTHER INFORMATION: /note= "thiol group of  
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with  
; OTHER INFORMATION: thiol group of Cys residue at location 4"  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-891-174-10  
Query Match 94.4%; Score 67; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 2.6e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CFQWQNRNRKAR 12  
DB 4 CFQWQNRNRKVR 15  
Search completed: February 21, 2003, 07:50:35  
Job time : 9.7 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:51:54 ; Search time 10.5 Seconds  
(without alignments)  
35.508 Million cell updates/sec

Title: US-09-743-107b-78

Perfect score: 71

Sequence: 1 CFQWRNMRKAR 12

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_FUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_FUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_FUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_FUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_FUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_FUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_FUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	94.4	15	9	US-09-798-869-2
2	67	94.4	25	9	US-09-798-869-20
3	67	94.4	694	9	US-10-023-096-2
4	59	83.1	15	9	US-09-798-869-6
5	53	74.6	15	9	US-09-798-869-3
6	53	74.6	25	9	US-09-798-869-23
7	45	63.4	15	9	US-09-798-869-7
8	41	57.7	15	9	US-09-798-869-4
9	41	57.7	15	9	US-09-798-869-29
10	41	57.7	15	9	US-09-798-869-30
11	41	57.7	25	9	US-09-798-869-22
12	38	53.5	15	9	US-09-798-869-8
13	37	52.1	21	10	US-09-864-761-47985
14	37	52.1	489	9	US-09-888-320-2
15	36	50.7	209	10	US-09-904-536-8
16	36	50.7	209	10	US-09-904-536-9
17	36	50.7	209	10	US-09-904-536-11
18	36	50.7	209	10	US-09-904-536-12
19	36	50.7	209	10	US-09-904-536-13

20	36	50.7	209	10	US-09-904-536-14	Sequence 14, Appl
21	36	50.7	209	10	US-09-904-536-15	Sequence 15, Appl
22	36	50.7	209	10	US-09-904-536-16	Sequence 16, Appl
23	36	50.7	209	10	US-09-904-536-17	Sequence 17, Appl
24	36	50.7	209	10	US-09-904-536-18	Sequence 18, Appl
25	36	50.7	212	10	US-09-904-536-10	Sequence 10, Appl
26	36	50.7	235	9	US-10-095-449-6	Sequence 6, Appl
27	36	50.7	235	10	US-09-448-378-1	Sequence 1, Appl
28	36	50.7	235	10	US-09-983-806-6	Sequence 6, Appl
29	36	50.7	235	10	US-09-904-536-1	Sequence 1, Appl
30	36	50.7	607	9	US-09-881-579-10	Sequence 10, Appl
31	36	50.7	688	9	US-09-881-579-15	Sequence 15, Appl
32	35	49.3	97	9	US-09-738-626-5597	Sequence 5597, Ap
33	35	49.3	738	9	US-10-173-123-13	Sequence 13, Appl
34	35	49.3	745	9	US-10-173-123-11	Sequence 11, Appl
35	35	49.3	846	9	US-10-051-409-4	Sequence 4, Appl
36	34	47.9	15	9	US-09-798-869-5	Sequence 5, Appl
37	34	47.9	40	10	US-09-864-761-46393	Sequence 46393, A
38	34	47.9	95	10	US-09-764-864-1031	Sequence 1031, Ap
39	34	47.9	119	10	US-09-205-858-244	Sequence 244, App
40	34	47.9	239	10	US-09-864-761-37353	Sequence 37353, A
41	34	47.9	338	9	US-09-978-295A-119	Sequence 119, App
42	34	47.9	338	9	US-09-978-697-119	Sequence 119, App
43	34	47.9	338	9	US-09-978-192A-119	Sequence 119, App
44	34	47.9	338	9	US-09-999-832A-119	Sequence 119, App
45	34	47.9	338	9	US-09-978-189-119	Sequence 119, App

#### ALIGNMENTS

RESULT 1  
US-09-798-869-2  
; Sequence 2, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798, 869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-798-869-2

Query Match 94.4%; Score 67; DB 9; Length 15;  
Best Local Similarity 91.7%; Pred. No. 2.4e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRNMRKAR 12  
|||  
DB 3 CFQWRNMRKVR 14

RESULT 2  
US-09-798-869-20  
; Sequence 20, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON

```
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match      94.4%; Score 67; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CFQWQNNMKR 12
      |||||
Db      3 CFQWQNNMKR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/PS8185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2
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Query Match      94.4%; Score 67; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.00087;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CFQWQNNMKR 12
      |||||
Db      22 CFQWQNNMKR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match      83.1%; Score 59; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00052;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CFQWQNNMKR 12
      |||||
Db      3 CFQWQNNMKR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match      74.6%; Score 53; DB 9; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0052;
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Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10  
|:|:|:|:|:|  
Db 3 CYQWQRMNRK 12

RESULT 6  
US-09-798-869-23  
; Sequence 23, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: CAPRINE  
US-09-798-869-23

Query Match 74.6%; Score 53; DB 9; Length 25;  
Best Local Similarity 80.0%; Pred. No. 0.0084;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10  
|:|:|:|:|:|  
Db 3 CYQWQRMNRK 12

RESULT 7  
US-09-798-869-7  
; Sequence 7, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens  
; OTHER INFORMATION: sequence)  
US-09-798-869-7

Query Match 63.4%; Score 45; DB 9; Length 15;  
Best Local Similarity 70.0%; Pred. No. 0.11;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10  
|:|:|:|:|:|  
Db 3 CYQWQRMNRK 12

RESULT 8  
US-09-798-869-4  
; Sequence 4, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-4

Query Match 57.7%; Score 41; DB 9; Length 15;  
Best Local Similarity 60.0%; Pred. No. 0.53;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10  
|:|:|:|:|:|  
Db 3 CLRWQNMNRK 12

RESULT 9  
US-09-798-869-29  
; Sequence 29, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT APPLICATION NUMBER: US/09/798,869  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-29

Query Match 57.7%; Score 41; DB 9; Length 15;  
Best Local Similarity 60.0%; Pred. No. 0.53;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMNRK 10  
|:|:|:|:|:|  
Db 3 CFRWQRMNRK 12

## RESULT 10

US-09-798-869-30  
; Sequence 30, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: BOVINE  
US-09-798-869-30

Query Match 57.7%; Score 41; DB 9; Length 25;  
Best Local Similarity 60.0%; Pred. No. 0.53;  
Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

Qy 1 CFQWQNRK 10  
| : ||| : ||  
Db 3 CFQWQNRK 12

## RESULT 11

US-09-798-869-22  
; Sequence 22, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: MURINE  
US-09-798-869-22

Query Match 57.7%; Score 41; DB 9; Length 25;  
Best Local Similarity 60.0%; Pred. No. 0.85;  
Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

Qy 1 CFQWQNRK 10  
| : ||| : ||  
Db 3 CLRWQNRK 12

## RESULT 12

US-09-798-869-8  
; Sequence 8, Application US/09798869  
; Publication No. US20030022821A1  
; GENERAL INFORMATION:

; APPLICANT: JOHN SIGURD SVENDSEN  
; APPLICANT: (YSTEIN REKDAL  
; APPLICANT: BALDUR SVEINBJ (RNSSON  
; APPLICANT: LARS VORLAND  
; TITLE OF INVENTION: BIOACTIVE PEPTIDES  
; FILE REFERENCE: A34049-PCT-USA-A  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB99/02851  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: GB9818938.4  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine  
; OTHER INFORMATION: sequence)  
; OTHER INFORMATION: sequence)  
US-09-798-869-8

Query Match 53.5%; Score 38; DB 9; Length 15;  
Best Local Similarity 60.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQNRK 10  
| : ||| : ||  
Db 3 CLRWQNRK 12

## RESULT 13

US-09-864-761-47985  
; Sequence 47985, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wenheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aesomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 47985  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL096701.14  
; OTHER INFORMATION: EXPRESSED IN LUNG SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6  
; OTHER INFORMATION: EST\_HUMAN HIT: AW294800.1, EVALUE 1.00e-06  
US-09-864-761-47985

Query Match 52.1%; Score 37; DB 10; Length 21;  
Best Local Similarity 83.3%; Pred. No. 3.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWQR 6  
|||:  
Db 16 CFQWRR 21

## RESULT 14

US-09-888-320-2  
; Sequence 2, Application US/09888320  
; Publication No. US20030013090A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry III, Clifton E.  
; APPLICANT: DeBarber, Andrea E.  
; APPLICANT: Mdull, Khisimuzi  
; APPLICANT: Bekker, Linda-Gail  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis  
; FILE REFERENCE: 015280-4131000US  
; CURRENT APPLICATION NUMBER: US/09/888,320  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/214,187  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854C, EthA)  
US-09-888-320-2

Query Match 52.1%; Score 37; DB 9; Length 489;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQRNRK 10  
|||:  
Db 253 CQWPRRKRK 262

## RESULT 15

US-09-904-536-8  
; Sequence 8, Application US/09904536  
; Patent No. US20020111475A1  
; GENERAL INFORMATION:

; APPLICANT: Graddis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/904,536  
; PRIOR FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-536-8

Query Match 50.7%; Score 36; DB 10; Length 209;  
Best Local Similarity 50.0%; Pred. No. 42;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQRNRK 10  
|||:  
Db 178 CLHWQETRRR 187

Search completed: February 21, 2003, 08:08:06  
Job time : 10.55 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 9.6 Seconds  
(without alignments)  
120.168 Million cell updates/sec

Title: US-09-743-107b-78

Perfect score: 71

Sequence: 1 CFQQRNMRKAR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.\*

1: Pirl.\*

2: Pirl.\*

3: Pirl.\*

4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	711	1 TFHUL	lactotransferrin p
2	53	74.6	708	2 JC2323	lactoferrin - goat
3	50	70.4	33	2 S52107	lactoferrin - shee
4	43	60.6	298	2 AD2346	hypothetical prote
5	42	59.2	4568	2 T08030	dynein beta heavy
6	41	57.7	222	2 H70978	hypothetical prote
7	41	57.7	275	2 T22597	hypothetical prote
8	41	57.7	707	1 A28438	lactoferrin precu
9	40	56.3	584	2 C94325	hypothetical prote
10	39	54.9	742	2 T25415	hypothetical prote
11	39	54.9	1693	2 AC3240	helicase, SNF2 fam
12	38	53.5	205	2 E30094	26S proteasome SU
13	38	53.5	275	1 JCL113	interleukin-2 rece
14	38	53.5	275	1 S07442	interleukin-2 rece
15	38	53.5	397	2 T35361	hypothetical prote
16	38	53.5	464	2 A12343	hypothetical prote
17	38	53.5	511	2 AB0858	probable cytochrom
18	38	53.5	515	2 T00510	cytochrome P450 ho
19	38	53.5	425	2 H44185	cell division prot
20	37.5	52.8	425	2 H44185	potassium channel p
21	37	52.1	135	2 JC5272	interleukin-2 rece
22	37	52.1	272	1 UHHU2	apolipoprotein B-1
23	37	52.1	274	2 B60950	cell cycle arrest
24	37	52.1	306	1 A39654	hypothetical prote
25	37	52.1	361	2 T29571	glutamine syntheta
26	37	52.1	367	2 G97649	anthranilate synth
27	37	52.1	487	2 A82835	probable monooxyge
28	37	52.1	489	2 C70655	hypothetical sh3-c
29	37	52.1	501	2 T39801	hypothetical sh3-c

## RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence\_revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:X53961; NID:G467236; PIDN:AAB60324.1; PID:G467237

R/Rey, M.M.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1989-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

R; Mitchell, D.R.; Brown,

J. Cell Sci. 107, 635-644, 1994  
 A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.  
 A:Reference number: Z16302; MUID:94274778; PMID:806077  
 A:Accession: T08030  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-4568 <MIT>  
 A:Cross-references: EMBL:U02963; NID:9409965; PIDN:AAA19956.1; PID:g514215  
 A:Experimental source: strain 21gr  
 C:Genetics:  
 A:Gene: ODA4  
 A:Map position: IX  
 A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3  
 C:Superfamily: dynein heavy chain, ciliary  
 C:Keywords: nucleotide binding; P-loop  
 F:1919-1926/Region: nucleotide-binding motif A (P-loop)  
 F:2202-2209/Region: nucleotide-binding motif A (P-loop)  
 F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 59.2%; Score 42; DB 2; Length 4568;  
 Best Local Similarity 66.7%; Pred. No. 96;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRK 9  
 |||||:  
 Db 1852 CFQWQSQLR 1860

RESULT 6  
 H70978  
 Hypothetical protein RV3271c - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 15-Sep-2000  
 C:Accession: H70978  
 C:Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9634230  
 A:Accession: H70978  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-222 <COL>  
 A:Cross-references: GB:Z92771; GB:AL123456; NID:g3242259; PIDN:CAB07084.1; PID:e306655;  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: RV3271c  
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV3271c

Query Match 57.7%; Score 41; DB 2; Length 222;  
 Best Local Similarity 70.0%; Pred. No. 7.3;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWQNRK 12  
 :|||:  
 Db 24 EWQNRVWAR 33

RESULT 7  
 T22597  
 Hypothetical protein F53H4.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
 C:Accession: T22597  
 R:Dobson, R.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19587  
 A:Accession: T22597  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A:Residues: 1-275 <WIL>  
 A:Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4  
 A:Experimental source: clone F53H4  
 C:Genetics:  
 A:Gene: CESP:F53H4.4  
 A:Map position: X  
 A:Introns: 67/1; 153/1  
 C:Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 57.7%; Score 41; DB 2; Length 275;  
 Best Local Similarity 63.6%; Pred. No. 9;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWQNRK 12  
 |||||:  
 Db 262 FQWQNRK 272

RESULT 8  
 A28438  
 lactoferrin precursor - mouse  
 N:Alternate names: lactotransferrin  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A28438; A1205  
 R:Pentecost, B.T.; Teng, C.T.  
 J. Biol. Chem. 262, 10134-10139, 1987  
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre  
 A:Reference number: A92596; MUID:87280033; PMID:3611056  
 A:Accession: A28438  
 A:Molecule type: mRNA  
 A:Residues: 3-707 <PEN>  
 A:Cross-references: EMBL:J03298  
 R:Li, Y.; Teng, C.T.  
 J. Biol. Chem. 266, 21880-21885, 1991  
 A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.  
 A:Reference number: A41205; MUID:92042099; PMID:1939212  
 A:Accession: A41205  
 A:Molecule type: DNA  
 A:Residues: 1-15 <LIU>  
 A:Cross-references: GB:M74778  
 C:Superfamily: transferrin; transferrin repeat homology  
 C:Keywords: duplication; glycoprotein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-707/Product: lactotransferrin #status predicted <MAT>  
 F:358-595/Domain: transferrin repeat homology <TRH2>  
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.7%; Score 41; DB 1; Length 707;  
 Best Local Similarity 60.0%; Pred. No. 23;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQNRK 10  
 :|||:  
 Db 37 CLRQWNRK 46

RESULT 9  
 C84325  
 Hypothetical protein Vngl732c [imported] - Halobacterium sp. NRC-1  
 C:Species: Halobacterium sp. NRC-1  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: C84325  
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
 Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
 A:Title: Genome sequence of Halobacterium species NRC-1.  
 A:Reference number: A84160; MUID:20504483; PMID:11016950  
 A:Accession: C84325  
 A:Status: preliminary  
 A:Molecule type: DNA

A;Residues: 1-584 <STO>  
 A;Cross-references: GB:AE0044337; NID:G10581192; PIDN:AA619967.1; GSPDB:GN00138  
 C;Genetics:  
 A;Gene: VNG1732C

Query Match 56.3%; Score 40; DB 2; Length 584;  
 Best Local Similarity 41.7%; Pred. No. 29;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKAR 12  
 |||:|:|:  
 Db 445 CFTWRKMERK 456

RESULT 10  
 T25415  
 Hypothetical protein T28D6.5 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
 C;Accession: T25415  
 R;Wilkinson, J.  
 submitted to the EMBL Data Library, October 1996  
 A;Reference number: Z20031  
 A;Accession: T25415  
 A;Status: Preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-742 <WIL>  
 A;Cross-references: EMBL:Z81134; PIDN:CAB03450.1; GSPDB:GN00021; CESP:T28D6.5  
 A;Experimental source: clone T28D6  
 C;Genetics:  
 A;Gene: CESP:T28D6.5  
 A;Map position: 3  
 A;Introns: 9/3; 36/3; 112/3; 258/3; 319/3; 468/2; 586/1; 638/3; 671/1  
 C;Superfamily: Caenorhabditis elegans hypothetical protein T28D6.5

Query Match 54.9%; Score 39; DB 2; Length 742;  
 Best Local Similarity 50.8%; Pred. No. 54;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CFQWQNRKAR 12  
 |||:|:|:  
 Db 193 CFRVWRKSKAK 204

RESULT 11  
 AC3240  
 Helicase, SNF2 family [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C;Accession: AC3240  
 R;Wood, D.W.; Sebval, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A;Reference number: AB2577; PMID:11743193  
 A;Accession: AC3240  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1693 <KUP>  
 A;Cross-references: GB:AE008690; PIDN:AAL46337.1; PID:G17744125; GSPDB:GN00189  
 A;Experimental source: strain C58 (Dupont)  
 C;Genetics:  
 A;Gene: Atu6101  
 A;Genome: plasmid

Query Match 54.9%; Score 39; DB 2; Length 1693;  
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 WQNRKAR 12

Db 1429 WONNERKAR 1437  
 |||:|:|:

RESULT 12  
 E90094  
 26S proteasome SU B5 [imported] - Guillardia theta nucleomorph  
 C;Species: nucleomorph Guillardia theta  
 A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
 C;Accession: E90094  
 R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re;  
 Nature 410, 1091-1096, 2001  
 A;Title: The highly reduced genome of an enslaved algal nucleus.  
 A;Reference number: A99082; MUID:11323671; PMID:11323671  
 A;Accession: E90094  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-205 <DOU>  
 A;Cross-references: GB:AF165818; NID:G13794510; PIDN:AAK39885.1; GSPDB:GN00150  
 C;Genetics:  
 A;Gene: pr8B5  
 A;Map position: 1  
 A;Genome: nucleomorph  
 C;Keywords: nucleomorph

Query Match 53.5%; Score 38; DB 2; Length 205;  
 Best Local Similarity 62.5%; Pred. No. 23;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNRNM 8  
 |||:|:|:  
 Db 63 CFFWERNL 70

RESULT 13  
 JC1113  
 Interleukin-2 receptor alpha chain precursor - sheep  
 N;Alternate names: CD25  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 11-Sep-1998 #sequence\_revision 11-Sep-1998 #text\_change 22-Jun-1999  
 C;Accession: JC1113; S18899; S18910  
 R;Bujdosó, R.; Sargan, D.; Williamson, M.; McConnell, I.  
 Gene 113, 283-284, 1992  
 A;Title: Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD  
 A;Reference number: JC1113; MUID:92241682; PMID:1572550  
 A;Accession: JC1113  
 A;Molecule type: mRNA  
 A;Residues: 1-275 <BU>  
 A;Cross-references: EMBL:X60149; NID:G1287; PIDN:CAA42723.1; PID:G1288  
 R;Verhagen, A.A.  
 submitted to the EMBL Data Library, December 1991  
 A;Description: Molecular cloning, expression and characterisation of the ovine IL-2R al  
 A;Reference number: S18899  
 A;Accession: S18899  
 A;Status: Preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-165, 'S', 167-275 <VER>  
 A;Cross-references: EMBL:Z11560; NID:G1275; PIDN:CAA77652.1; PID:G1276  
 C;Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chain  
 C;Function:  
 A;Description: receptor for interleukin-2  
 A;Pathway: Interleukin-2 stimulated growth and differentiation of T cells, B cells, NK c  
 C;Superfamily: Interleukin-2 receptor alpha chain; complement factor H repeat homology  
 C;Keywords: cytokine receptor; duplication; glycoprotein; T-cell proliferation; transmem  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-275/Product: interleukin-2 receptor alpha chain #status predicted <NAT>  
 F;22-243/Domain: extracellular #status predicted <EXT>  
 F;24-77/Domain: complement factor H repeat homology <PH1>  
 F;123-184/Domain: complement factor H repeat homology <PH2>  
 F;244-264/Domain: transmembrane #status predicted <TMW>  
 F;265-275/Domain: intracellular #status predicted <INT>  
 F;24-64, 51-77, 123-168, 152-184/Disulfide bonds: #status predicted

F;80/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.5%; Score 38; DB 1; Length 275;  
Best Local Similarity 50.0%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQNRKAR 12  
| | | | |  
Db 261 CLTWQRWKKNR 272

## RESULT 14

S07442  
Interleukin-2 receptor alpha chain precursor - bovine  
N:Alternate names: CD25  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 11-Sep-1998 #sequence\_revision 11-Sep-1998 #text\_change 22-Jun-1999  
C:Accession: S07442  
R:Weinberg, A.D.; Shaw, J.; Paetkau, V.; Bleackley, R.C.; Magnuson, N.S.; Reeves, R.; Ma  
Immunology 63, 603-610, 1988  
A:Title: Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).  
A:Reference number: S07442; MUID:88212503; PMID:2835311  
A:Accession: S07442  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-275 <WEI>  
A:Cross-references: EMBL:M20818; NID:G163208; PIDN:AAA51414.1; PID:G163209  
C:Function: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains  
A:Description: receptor for interleukin-2  
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK c  
C:Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology  
C:Keywords: cytokine receptor; duplication; glycoprotein; T-cell proliferation; transmem  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-275/Product: interleukin-2 receptor alpha chain #status predicted <MAT>  
F:22-243/Domain: extracellular #status predicted <EXT>  
F:24-77/Domain: complement factor H repeat homology <PH1>  
F:123-184/Domain: complement factor H repeat homology <PH2>  
F:244-284/Domain: transmembrane #status predicted <TM>  
F:265-275/Domain: intracellular #status predicted <INT>  
F:24-64,51-77,123-168,152-184/Disulfide bonds: #status predicted  
F:80,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.5%; Score 38; DB 1; Length 275;  
Best Local Similarity 50.0%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFQWQNRKAR 12  
| | | | |  
Db 261 CLTWQRWKKNR 272

## RESULT 15

T35361  
Hypothetical protein SC66T3.04 - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
C:Accession: T35361  
R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, June 1999  
A:Reference number: Z21576  
A:Accession: T35361  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-397 <MUR>  
A:Cross-references: EMBL:AL079348; PIDN:CAB45460.1; GSPDB:GN00070; SCOEDB:SC66T3.04  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC66T3.04

Query Match 53.5%; Score 38; DB 2; Length 397;  
Best Local Similarity 75.0%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WQNNMEKA 11  
| | | | |  
Db 206 WRRNIRKA 213

Search completed: February 21, 2003, 07:47:50  
Job time: 10.65 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 4.6 Seconds  
(without alignments)  
108.199 Million cell updates/sec

Title: US-09-743-107B-78

Perfect score: 71

Sequence: 1 CFQQRNRKAR 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	711	1 TRFL_HUMAN	P02788 homo sapien
2	53	74.6	708	1 TRFL_CAPHI	Q29477 capra hircu
3	50	70.4	708	1 TRFL_CAMDR	Q9tun0 camelus dro
4	42	59.2	695	1 TRFL_HORSE	Q77811 equus caball
5	42	59.2	4568	1 DYHE_CHLRE	Q39565 chlamydomon
6	41	57.7	707	1 TRFL_MOUSE	P08071 mus musculu
7	38	53.5	146	1 RPOB_LIBAF	P41187 liberibacte
8	38	53.5	275	1 IL2A_BOVIN	P12342 bos taurus
9	38	53.5	275	1 IL2A_SHEEP	P26898 ovis aries
10	37.5	52.8	425	1 FTSA_HAFIN	P45068 haemophilus
11	37	52.1	272	1 IL2A_HUMAN	P01589 homo sapien
12	37	52.1	222	1 NLA_DROME	Q9x218 drosophila
13	37	52.1	306	1 BUB2_YEAST	P26448 saccharomyc
14	37	52.1	455	1 YKYL_CABEL	Q19910 caenorhabdi
15	37	52.1	1293	1 XPC_DROME	Q24595 drosophila
16	36	50.7	62	1 RL32_AQUAE	Q67187 aquifex aeo
17	36	50.7	214	1 VIF_SIVS4	P12505 simian immu
18	36	50.7	235	1 FL3I_HUMAN	P49771 homo sapien
19	36	50.7	267	1 IL2A_RAT	P26897 rattus norv
20	36	50.7	268	1 IL2A_CANFA	O62802 canis fami
21	36	50.7	275	1 IL2A_FELCA	P41690 felis silve
22	36	50.7	2483	1 COA2_HUMAN	O00763 homo sapien
23	35	49.3	85	1 PMRD_SALTY	P37589 salmonella
24	35	49.3	159	1 YICN_ECOLI	P31439 escherichia
25	35	49.3	428	1 SYH_CHLMU	Q9PJ19 chlamydia m
26	35	49.3	502	1 C91I_ARATH	Q9f965 arabidopsis
27	35	49.3	663	1 PD1I_HUMAN	Q9ulc6 homo sapien
28	35	49.3	728	1 KDG1_ARATH	Q39017 arabidopsis
29	35	49.3	765	1 Y008_HUMAN	Q15398 homo sapien
30	35	49.3	1179	1 ATX1_ARATH	Q91t02 arabidopsis
31	35	49.3	1213	1 T2D2_DROME	Q24325 drosophila
32	35	49.3	2671	1 IF3T_HUMAN	Q14573 homo sapien
33	35	49.3	3680	1 DMD_CANFA	O97592 canis fami

## RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrroxin A;			
DE	Lactoferrroxin B; Lactoferrroxin C].			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely C.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RL	sequences.";			
RN	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Straussberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

## ALIGNMENTS

34	34	47.9	155	1	Y481_SINY3	Q55827 synechocyst
35	34	47.9	211	1	LOLB_VIBCH	P57070 vibrio chol
36	34	47.9	215	1	VIF_HV2SB	P12452 human immun
37	34	47.9	215	1	VIF_HV2ST	P20878 human immun
38	34	47.9	246	1	Y495_SINY3	Q55185 synechocyst
39	34	47.9	316	1	NQRC_CHLTR	O84281 chlamydia t
40	34	47.9	369	1	SP11_MYXVL	P12393 myxoma viru
41	34	47.9	401	1	O88A_DROME	Q9vfn2 drosophila
42	34	47.9	410	1	SECY_CYACA	P46249 cyanidium c
43	34	47.9	538	1	RO60_HUMAN	P10155 homo sapien
44	34	47.9	538	1	RO60_MOUSE	O08848 mus musculu
45	34	47.9	538	1	RO60_XENLA	P42700 xenopus lae

RP SEQUENCE OF 3-711 FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=90326549; PubMed=2374734;  
RA Powell M.J., Ouden J.E.;  
RT "Nucleotide sequence of human lactoferrin cDNA.";  
RL Nucleic Acids Res. 18:4013-4013(1990).  
RN [9]  
RP SEQUENCE OF 20-711.  
RX MEDLINE=85076667; PubMed=6510420;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,  
RT Legrand D., Spik G., Montreuil J., Jolles P.;  
RT "Human lactotransferrin: amino acid sequence and structural  
RL comparisons with other transferrins.";  
RN Eur. J. Biochem. 145:659-666(1984).  
RN [10]  
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.  
RX MEDLINE=82046817; PubMed=6794640;  
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,  
RT Jolles P.;  
RT "The present state of the human lactotransferrin sequence. Study and  
RL alignment of the cyanogen bromide fragments and characterization of  
RN N- and C-terminal domains.";  
RX Biochim. Biophys. Acta 670:243-254(1981).  
RN [11]  
RP SEQUENCE OF 609-711.  
RX MEDLINE=82262043; PubMed=7049727;  
RA Metz-Boutigue M.-H., Jolles J., Mazurier J.,  
RT Jolles P.;  
RT "An 88 amino acid long C-terminal sequence of human  
RL lactotransferrin.";  
RN FEBS Lett. 142:107-110(1982).  
RN [12]  
RP SEQUENCE OF 436-711 FROM N.A.  
RX MEDLINE=88001031; PubMed=3477300;  
RA Rado T.A., Wei X., Benz E.J. Jr.;  
RT "Isolation of lactoferrin cDNA from a human myeloid library and  
RL expression of mRNA during normal and leukemic myelopoiesis.";  
RN Blood 70:989-993(1987).  
RN [13]  
RP SEQUENCE OF 237-711 FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RX Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
RX Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desliva U.,  
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RA Sagripanti J.L.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.  
RX MEDLINE=90064528; PubMed=2585506;  
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;  
RT "Structure of human lactoferrin: crystallographic structure analysis  
RL and refinement at 2.8-A resolution.";  
RN J. Mol. Biol. 209:711-734(1989).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RA Haridas M., Anderson B.F., Baker E.N.;  
RT "Structure of human diferric lactoferrin refined at 2.2-A  
RL resolution.";  
RN Acta Crystallogr. D 51:629-646(1995).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.  
RX MEDLINE=97156796; PubMed=9003186;  
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,  
RA Baker E.N.;  
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron  
RL binding properties and crystal structure of the histidine-  
RN 253-->methionine mutant.";  
RX Biochemistry 36:341-346(1997).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=99190892; PubMed=10089347;  
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;  
RT "Structure of recombinant human lactoferrin expressed in Aspergillus  
RL awamori.";  
RN Acta Crystallogr. D 55:403-407(1999).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=99192677; PubMed=10089508;  
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;  
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement  
RL and analysis of ligand-induced conformational change.";  
RN Acta Crystallogr. D 54:1319-1335(1998).  
RN [19]  
RP CHARACTERIZATION OF LACTOFERROXINS.  
RX MEDLINE=91166929; PubMed=1369293;  
RA Tani F., Iio K., Chiba H., Yoshikawa M.;  
RT "Isolation and characterization of opioid antagonist peptides derived  
RL from human lactoferrin.";  
RN Agric. Biol. Chem. 54:1803-1810(1990).  
RN [20]  
RP VARIANTS THR-30 AND ARG-48.  
RX PubMed=9873069;  
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,  
RA Qumsiyeh M.B., Lin P.-Y., Baati S., Reddy M.K., Kanai A., Hotta Y.,  
RA Sugar J., Kumaramanickavel G., Munier P., Schorderet D.F.,  
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,  
RA Hejtmancik J.F., Teng C.T.;  
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like  
RL corneal dystrophy): exclusion of linkage to lactoferrin gene.";  
RN Mol. Vision 4:31-32(1998).  
RN -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
CC OF AN ANION, USUALLY BICARBONATE.  
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST  
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE  
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE  
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X53961; CAA37914.1; -  
DR EMBL; U07643; BAB60324.1; -  
DR EMBL; M93150; AAA36159.1; -  
DR EMBL; M83202; AAA59511.1; -  
DR EMBL; M83205; AAA58656.1; -  
DR EMBL; M18642; AAA86665.1; -  
DR EMBL; AF332168; AAG48753.1; -  
DR EMBL; BC015822; AAH15822.1; -  
DR EMBL; BC015823; AAH15823.1; -  
DR EMBL; M73700; AAA59479.1; -  
DR EMBL; X52941; CAA37116.1; -  
DR EMBL; U95626; BAB57795.1; -  
DR PIR; S11228; TFHUL.  
DR PDB; 1LCF; 31-AUG-94.  
DR PDB; 1LCT; 31-OCT-93.  
DR PDB; 1LFG; 31-JUL-94.  
DR PDB; 1LFH; 31-OCT-93.  
DR PDB; 1LFI; 31-OCT-93.  
DR PDB; 1LGB; 31-AUG-94.  
DR PDB; 1LGC; 31-AUG-94.  
DR PDB; 1BKA; 08-NOV-96.  
DR PDB; 1DSN; 08-MAR-96.  
DR PDB; 1HSE; 12-MAR-97.  
DR PDB; 1VFD; 21-APR-97.

Query Match 94.4%; Score 67; DB 1; Length 711;  
 Best Local Similarity 91.7%; Pred. No. 0.00022;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 12  
 |||||  
 Db 39 CFQWQNRKVR 50

## RESULT 2

TRFL\_CAPHI STANDARD; PRT; 708 AA.  
 AC Q29477; Q29479;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactoferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;  
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA MEDLINE=9438004; PubMed=8093048;  
 RA le Provost F., Nocart M., Guerin G., Martin P.;  
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the  
 relevant locus to bovine U12 syteny group."  
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 OF AN ANION, USUALLY BICARBONATE.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 CC -----

DR EMBL; U53857; AAA97958.1; --  
 DR EMBL; X78902; CAA55517.1; --  
 DR HSP; O77698; ICE2  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 2.  
 DR PRINTS; PR00422; TRANSFERRIN.  
 DR SMART; SM00094; TR FER; 2.  
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.  
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.  
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.  
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 708  
 FT REPEAT 20 363  
 FT REPEAT 364 708  
 FT DISULFID 28 64  
 FT DISULFID 38 55  
 FT DISULFID 134 217  
 FT DISULFID 176 192

FT DISULFID 189  
 FT DISULFID 250  
 FT DISULFID 367  
 FT DISULFID 377  
 FT DISULFID 424  
 FT DISULFID 444  
 FT DISULFID 476  
 FT DISULFID 500  
 FT DISULFID 510  
 FT DISULFID 521  
 FT DISULFID 592  
 FT DISULFID 644  
 FT METAL 79  
 FT METAL 111  
 FT METAL 211  
 FT METAL 272  
 FT METAL 414  
 FT METAL 452  
 FT METAL 545  
 FT METAL 614  
 FT BINDING 140  
 FT BINDING 482  
 FT CARBOHYD 252  
 FT CARBOHYD 300  
 FT CARBOHYD 387  
 FT CARBOHYD 495  
 FT CARBOHYD 564  
 FT CONFLICT 56  
 FT CONFLICT 88  
 FT CONFLICT 124  
 FT CONFLICT 154  
 FT CONFLICT 304  
 FT CONFLICT 414  
 SQ SEQUENCE 708 AA; 77358 MW; P2EDA3C83539960D CRC64;

Query Match 74.6%; Score 53; DB 1; Length 708;

Best Local Similarity 80.0%; Pred. No. 0.066;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQNRKVR 10  
 |||||  
 Db 38 CFQWQNRKVR 47

## RESULT 3

TRFL\_CAMDR STANDARD; PRT; 708 AA.  
 ID TRFL\_CAMDR STANDARD; PRT; 708 AA.  
 AC Q9TUM0; Q9WZS5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Camelus dromedarius (Dromedary) (Arabian camel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;  
 RA Kapeller S.R., Ackermann M., Farah Z., Puhon Z.;  
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin";  
 RL Int. Dairy J. 9:481-486(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH  
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING  
 OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AJ131674; CAB53387.1; -;  
 CC EMBL; AF165879; AAF82241.1; -;  
 CC HSP; O77811; 1B1X.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SM00094; TR\_FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN 1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN 2; 2.  
 CC PROSITE; PS00207; TRANSFERRIN 3; 2.  
 CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19 BY SIMILARITY.  
 FT CHAIN 20 708 LACTOTRANSFERRIN.  
 FT REPEAT 20 363 1.  
 FT REPEAT 364 708 2.  
 FT DISULFID 28 64 BY SIMILARITY.  
 FT DISULFID 38 55 BY SIMILARITY.  
 FT DISULFID 134 217 BY SIMILARITY.  
 FT DISULFID 176 192 BY SIMILARITY.  
 FT DISULFID 189 200 BY SIMILARITY.  
 FT DISULFID 250 264 BY SIMILARITY.  
 FT DISULFID 367 399 BY SIMILARITY.  
 FT DISULFID 427 390 BY SIMILARITY.  
 FT DISULFID 424 703 BY SIMILARITY.  
 FT DISULFID 444 666 BY SIMILARITY.  
 FT DISULFID 476 551 BY SIMILARITY.  
 FT DISULFID 500 694 BY SIMILARITY.  
 FT DISULFID 510 524 BY SIMILARITY.  
 FT DISULFID 521 534 BY SIMILARITY.  
 FT DISULFID 592 606 BY SIMILARITY.  
 FT DISULFID 644 649 BY SIMILARITY.  
 FT METAL 79 79 IRON 1 (BY SIMILARITY).  
 FT METAL 111 111 IRON 1 (BY SIMILARITY).  
 FT METAL 211 211 IRON 1 (BY SIMILARITY).  
 FT METAL 272 272 IRON 1 (BY SIMILARITY).  
 FT METAL 414 414 IRON 2 (BY SIMILARITY).  
 FT METAL 452 452 IRON 2 (BY SIMILARITY).  
 FT METAL 545 545 IRON 2 (BY SIMILARITY).  
 FT METAL 614 614 IRON 2 (BY SIMILARITY).  
 FT BINDING 140 140 ANION (BY SIMILARITY).  
 FT BINDING 482 482 ANION (BY SIMILARITY).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 261 261 F -> S (IN REF. 2).  
 FT CONFLICT 304 304 G -> A (IN REF. 2).  
 FT CONFLICT 330 330 S -> P (IN REF. 2).  
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).  
 FT CONFLICT 506 506 L -> F (IN REF. 2).  
 FT CONFLICT 609 609 A -> P (IN REF. 2).  
 FT CONFLICT 609 609 R -> Q (IN REF. 2).  
 FT CONFLICT 642 642 R -> Q (IN REF. 2).  
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 70.4%; Score 50; DS 1; Length 708;  
 Best Local Similarity 66.7%; Pred. No. 0.22;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKXAR 12  
 DB 38 CAQWQRMKXAR 49

## RESULT 4

TRFL HORSE STANDARD; PRT; 695 AA.  
 ID TRFL HORSE  
 AC O77811;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).  
 GN LTF.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "cDNA sequence of mare lactoferrin";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RC TISSUE=Milk;  
 RX MEDLINE=9296631; PubMed=10366507;  
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;  
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution.";  
 RL J. Mol. Biol. 289:303-317(1999).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AJ010930; CAA09407.1; -;  
 CC PDB; 1B1X; 02-DEC-98.  
 CC PDB; 1B7U; 02-FEB-99.  
 CC PDB; 1B7Z; 02-FEB-99.  
 CC InterPro; IPR001156; Transferrin.  
 CC Pfam; PF00405; transferrin; 2.  
 CC PRINTS; PR00422; TRANSFERRIN.  
 CC SMART; SM00094; TR\_FER; 2.  
 CC PROSITE; PS00205; TRANSFERRIN 1; 2.  
 CC PROSITE; PS00206; TRANSFERRIN 2; 2.  
 CC PROSITE; PS00207; TRANSFERRIN 3; 1.  
 CC Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;  
 KW Signal; 3D-structure.  
 FT SIGNAL 1 1  
 FT CHAIN <1 6 LACTOTRANSFERRIN.  
 FT REPEAT 7 695 1.  
 FT REPEAT 351 695 2.  
 FT DISULFID 15 51  
 FT DISULFID 25 42  
 FT DISULFID 121 204  
 FT DISULFID 163 179  
 FT DISULFID 166 189  
 FT DISULFID 176 187  
 FT DISULFID 237 251  
 FT DISULFID 354 395  
 FT DISULFID 364 377  
 FT DISULFID 411 690  
 FT DISULFID 431 653

FT DISULFID 463 538  
 FT DISULFID 487 681  
 FT DISULFID 497 511  
 FT DISULFID 508 521  
 FT DISULFID 579 593  
 FT DISULFID 631 636  
 FT METAL 66 66  
 FT METAL 98 98  
 FT METAL 198 198  
 FT METAL 259 259  
 FT METAL 401 401  
 FT METAL 439 439  
 FT METAL 532 532  
 FT METAL 601 601  
 FT BINDING 127 127  
 FT BINDING 469 469  
 FT CARBOHYD 143 143  
 FT CARBOHYD 287 287  
 FT CARBOHYD 482 482  
 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 59.2%; Score 42; DB 1; Length 695;  
 Best Local Similarity 58.3%; Pred. No. 5.7;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRKXAR 12  
 DB 25 CAKFORNMKKVR 36

## RESULT 5

DIHB\_CHLRE  
 ID DYHB\_CHLRE STANDARD; PRT; 4568 AA.  
 AC Q39565;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Dynein beta chain, flagellar outer arm.  
 GN ODA4 OR ODA-4 OR SUP1.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=21gr;  
 RX MEDLINE=94274778; PubMed=8006077;  
 RA Mitchell D.R.; Brown K.S.;  
 RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes";  
 RL J. Cell Sci. 107:635-644(1994).  
 CC -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEIN HAS ATPASE ACTIVITY.  
 CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.  
 CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.

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EMBL; U02963; AAA19956.1;  
 InterPro; IPR004273; Dynein heavy.  
 Pfam; PF03028; Dynein heavy; 1.  
 Motor protein; Microtubules; Dynein; ATP-binding; Flagella;  
 Coiled coil.  
 KW DOMAIN 277 293 COILED COIL (POTENTIAL).  
 FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).

FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).  
 FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).  
 FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).  
 FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).  
 FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).  
 FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).  
 FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).  
 FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).  
 FT NP\_BIND 1919 1926 ATP (POTENTIAL).  
 FT NP\_BIND 2202 2209 ATP (POTENTIAL).  
 FT NP\_BIND 2530 2537 ATP (POTENTIAL).  
 FT NP\_BIND 2879 2886 ATP (POTENTIAL).  
 SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 59.2%; Score 42; DB 1; Length 4568;  
 Best Local Similarity 66.7%; Pred. No. 41;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRMR 9  
 DB 1852 CFQWQSQLR 1860

## RESULT 6

TRFL\_MOUSE  
 ID TRFL\_MOUSE STANDARD; PRT; 707 AA.  
 AC P08071; P70690; O61799; Q922P2;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lactotransferrin precursor (Lactoferrin).  
 GN LTF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RX MEDLINE=87280033; PubMed=3611056;  
 RA Pentecost B.T.; Teng C.T.;  
 RT "Lactotransferrin is the major estrogen inducible protein of mouse uterine secretions";  
 RL J. Biol. Chem. 262:10134-10139(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Moriishi K.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-14 FROM N.A.  
 RX MEDLINE=92042099; PubMed=1939212;  
 RA Liu Y.; Teng C.T.;  
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter";  
 RL J. Biol. Chem. 266:21880-21885(1991).  
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC -----
DR EMBL; J03298; AAA40525.1; -
DR EMBL; D88510; BAA13633.1; -
DR EMBL; BC006904; AAH08904.1; -
DR EMBL; M74778; AAA39427.1; -
DR DR PIR; A28438; A28438.
DR HSSP; P02788; 1CB6.
DR MGD; MGI:96837; Ltf.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PRO0422; TRANSFERRIN.
DR SMART; SW00094; TR FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 M -> L (IN REF. 2).
FT CONFLICT 359 359 S -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE03404C19A8 CRC64;
Query Match 57.7%; Score 41; DB 1; Length 707;
Best Local Similarity 60.0%; Pred. No. 8.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 CFQWQNRK 10  
DB 37 CLRQWNRK 46

RESULT 7  
RPOB LIBAF STANDARD; PRT; 146 AA.  
ID RPOB LIBAF  
AC P4187;  
DT 01-FEB-1995 (Rel. 31, Created)

```

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit) (Fragment).
GN RPOB.
OS Liberibacter africanus (Liberibacter africanus).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Candidatus Liberibacter.
OX NCBI_TaxID=34020;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nelspruit;
RA Planet P.; Jagoueix S.; Bove J.M.; Garnier M.;
RT "Detection and characterization of the African Citrus Greening
RT Liberibacter by amplification, cloning and sequencing of the rplKJL-
RT rpoBC operon.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION. DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC -----
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CC -----
DR EMBL; U09675; AAA1957.1; -
DR InterPro; IPR001572; RNA_pol_B.
DR Pfam; PF00562; RNA_pol_B_1.
DR PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
KW Transferase; Transcription; DNA-directed RNA polymerase.
FT NON TER 146 146
SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
Query Match 53.5%; Score 38; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 CFQWQNRK 10  
DB 10 CVQWSRGARK 19

RESULT 8  
IL2A\_BOVIN STANDARD; PRT; 275 AA.  
ID IL2A\_BOVIN  
AC P12342;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha  
DE subunit) (P55) (TAC antigen) (CD25).  
GN IL2RA.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88212503; PubMed=2835311;  
RA Weinberg A.D.; Shaw J.; Paetkau V.; Bleackley R.C.; Magnuson N.S.;  
RA Reeves R.; Magnuson J.A.;  
RT "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";

Immunology 63:603-610(1998).

RL [2]  
 RN SEQUENCE OF 1-21 FROM N.A.  
 RP MEDLINE=96116968; PubMed=8563178;  
 RA Yoo J., de Leon F.A., Stone R.T., Beattie C.W.;  
 RX "Cloning and chromosomal assignment of the bovine interleukin-2  
 RT receptor alpha (IL-2R alpha) gene.";  
 RL Mamm. Genome 6:751-753(1995).

CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.  
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE  
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA  
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE  
 CC WITH A GAMMA CHAIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

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DR EMBL; M20818; AA51414.1; -;  
 DR EMBL; U24226; AAC48487.1; -;  
 DR PIR; S07442; S07442.  
 DR HSP; P01589; IILM.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00084; sushi; 2.  
 DR SMART; SM00032; CCP; 2.  
 DR Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.  
 FT SIGNAL 1 21  
 FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 244 262 POTENTIAL.  
 FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 223 78 SUSHI 1.  
 FT DOMAIN 122 185 SUSHI 2.  
 FT DISULFID 24 64 BY SIMILARITY.  
 FT DISULFID 751 77 BY SIMILARITY.  
 FT DISULFID 123 168 BY SIMILARITY.  
 FT DISULFID 152 184 BY SIMILARITY.  
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 275;  
 Best Local Similarity 50.0%; Pred. No. 11;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKAR 12  
 Db 261 CLTWQRWKKR 272

RESULT 9  
 IL2A\_SHEEP STANDARD; PRT; 275 AA.  
 AC P26898;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha  
 DE subunit) (P55) (TAC antigen) (CD25).  
 GN IL2RA.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RA Verhagen A.A.;  
 RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92241682; PubMed=1572550;  
 RA Bujdosó R., Sargan D.R., Williams M.L., McConnell I.;  
 RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa  
 RL protein, CD25.";  
 RL Gene 113:283-284(1992).

CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.  
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE  
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA  
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE  
 CC WITH A GAMMA CHAIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

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DR EMBL; Z11560; CAA7652.1; -;  
 DR EMBL; X60149; CAA42723.1; -;  
 DR EMBL; A19167; CAA01447.1; -;  
 DR PIR; S18910; S18910.  
 DR PIR; S18899; S18899.  
 DR PIR; JC1113; JC1113.  
 DR HSP; P01589; IILM.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00084; sushi; 2.  
 DR SMART; SM00032; CCP; 2.  
 DR Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.  
 FT SIGNAL 1 21  
 FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 244 262 POTENTIAL.  
 FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 223 78 SUSHI 1.  
 FT DOMAIN 122 185 SUSHI 2.  
 FT DISULFID 24 64 BY SIMILARITY.  
 FT DISULFID 751 77 BY SIMILARITY.  
 FT DISULFID 123 168 BY SIMILARITY.  
 FT DISULFID 152 184 BY SIMILARITY.  
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 166 166 S -> T (IN REF. 2).  
 SQ SEQUENCE 275 AA; 30904 MW; 1101A2B5AC5A088 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 275;  
 Best Local Similarity 50.0%; Pred. No. 11;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQNRKAR 12  
 Db 261 CLTWQRWKKR 272

RESULT 10  
 FTSA\_HAEN STANDARD; PRT; 425 AA.  
 AC P45068;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cell division protein ftSa.  
 GN FTSA OR Hill42.  
 OS Haemophilus influenzae.

```

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glode A., Keiley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN ANOMALOUS FILAMENT
CC GROWTH (BY SIMILARITY). MAY BE A COMPONENT OF THE SEPTUM. IT
CC MAY INTERACT WITH FTSZ (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FTSZ/MREB FAMILY.
CC -----
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CC -----
CC EMBL; U32794; AAC22797.1; -
CC DR TIGR; H1142; -
CC DR InterPro; IPR003494; FtsA.
CC DR Pfam; PF02491; FtsA; 2.
CC DR TIGRFAMs; TIGR01174; ftsA; 1.
CC KW Cell division; Cell shape; Complete proteome.
CC SQ SEQUENCE 425 AA; 45836 MW; AF5C4B808D73CE9D CRC64;
CC -----
Query Match 52.8%; Score 37.5; DB 1; Length 425;
Best Local Similarity 58.3%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 1; Gaps 1;
QY 1 CFQ-WQRMKKA 11
DB 163 CHQDQNNLKKK 174
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RESULT 11
IL2A_HUMAN STANDARD; PRT; 272 AA.
AC P01589;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
DE subunit) (P55) (TAC antigen) (CD25 antigen).
GN IL2RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85012734; PubMed=6090949;
RA Nishida N., Shimizu A., Ishida N., Sabe H., Teshigawara K., Maeda M.,
RA Uchiyama T., Yodoi J., Honjo T.;
RT "Molecular cloning of cDNA encoding human interleukin-2 receptor.";
RL Nature 311:626-631(1984).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=85012733; PubMed=6090949;

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RA Leonard W.J., Depper J.M., Crabtree G.R., Rudikoff S., Pumphrey J.,
RA Robb R.J., Kroenke M., Svetlik P.B., Peffer N.J., Waldmann T.A.,
RA Greene W.C.;
RT "Molecular cloning and expression of cDNAs for the human
RT interleukin-2 receptor.";
RL Nature 311:626-631(1984).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=86067183; PubMed=2999698;
RA Ishida N., Kanamori H., Noma T., Nikaide T., Sabe H., Suzuki N.,
RA Shimizu A., Honjo T.;
RT "Molecular cloning and structure of the human interleukin 2 receptor
RT gene.";
RL Nucleic Acids Res. 13:7579-7589(1985).
[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=86018868; PubMed=2996141;
RA Leonard W.J., Depper J.M., Kanehisa M., Kroenke M., Peffer N.J.,
RA Svetlik P.B., Sullivan M., Greene W.C.;
RT "Structure of the human interleukin-2 receptor gene.";
RL Science 230:633-639(1985).
[5]
RN SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=87159546; PubMed=3030566;
RA Cross S.L., Feinberg M.B., Wolf J.B., Holbrook N.J., Wong-Stall F.,
RA Leonard W.J.;
RT "Regulation of the human interleukin-2 receptor alpha chain promoter:
RT activation of a nonfunctional promoter by the transactivator gene of
RT HTLV-I.";
RL Cell 49:47-56(1987).
[6]
RN 3D-STRUCTURE MODELING OF 23-83.
RX MEDLINE=95111955; PubMed=7529123;
RA Bamorough P., Hedgecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
RT modelling.";
RL Structure 2:839-851(1994).
CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC -!- DATABASE: NAME=PROM; NOTE=CD guide CD25 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd25.htm".
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CC -----
CC EMBL; X01057; CAA25525.1; -
CC DR EMBL; X03131; CAA26906.1; -
CC DR EMBL; X03132; CAA26906.1; JOINED.
CC DR EMBL; X03133; CAA26906.1; JOINED.
CC DR EMBL; X03134; CAA26906.1; JOINED.
CC DR EMBL; X03135; CAA26906.1; JOINED.
CC DR EMBL; X03136; CAA26906.1; JOINED.
CC DR EMBL; X03137; CAA26906.1; JOINED.
CC DR EMBL; X03138; CAA26906.1; JOINED.
CC DR EMBL; X03122; AAB59535.1; JOINED.
CC DR EMBL; M1066; AAA67527.1; -
CC DR EMBL; M10322; AAA67527.1; JOINED.
CC DR EMBL; M1060; AAA67527.1; JOINED.
CC DR EMBL; M1061; AAA67527.1; JOINED.
CC DR EMBL; M1062; AAA67527.1; JOINED.
CC DR EMBL; M1063; AAA67527.1; JOINED.
CC DR EMBL; M1064; AAA67527.1; JOINED.

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DR EMBL; M11065; AAA67527.1; JOINED.
DR EMBL; M15864; AAA59162.1; -.
DR PIR; A01856; UHHU2.
DR PIR; A24113; A24113.
DR PIR; A44186; A44186.
DR PDB; 1ILM; 26-JAN-95.
DR PDB; 1ILN; 26-JAN-95.
DR Genew; HGNC:6008; IL2RA.
DR MIM; 147730; -.
DR MIM; 606367; -.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 2.
DR SMART; SM00032; CCP; 2.
KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi;
KW 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 272
FT DOMAIN 22 240
FT TRANSMEM 241 259
FT DOMAIN 260 272
FT DOMAIN 23 81
FT DOMAIN 124 185
FT DISULFID 24 67
FT DISULFID 751 80
FT DISULFID 125 168
FT DISULFID 152 184
FT CARBOHYD 70 70
FT CARBOHYD 89 89
SQ SEQUENCE 272 AA; 83081 MW; 83D907C8B1D2C0E CRC64;

Query Match 52.1%; Score 37; DB 1; Length 272;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 WQRNMRKAR 12
DB 261 WQRQKRSR 269

RESULT 12
NLA DROME
ID NLA DROME STANDARD; PRT; 292 AA.
AC Q9XZL8; Q9V391;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 18-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
GN NLA OR CG6072.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RA McCormick A.V., Goldberg M.L.;
RT "Gene required for elongation of meiosis I spindle in Drosophila females."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbavani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
CC -!- SIMILARITY: BELONGS TO THE DSCRL FAMILY.
CC
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CC
DR EMBL; AF147700; AAD33987.1; -.
DR EMBL; AE003712; AAF5285.1; -.
DR FlyBase; FBGN0026629; nla.
SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 292;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 FQWQNRKAR 12
DB 150 FQWQNRKAR 160

RESULT 13
BUB2 YEAST
ID BUB2 YEAST STANDARD; PRT; 306 AA.
AC P28448;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitotic check point protein BUB2 (cell cycle arrest protein BUB2).
GN BUB2 OR YMR055C OR YMR996.08C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=51330299; PubMed=16511171;
RA Hoyt M.A., Totis L., Roberts B.T.;
RT "S. cerevisiae genes required for cell cycle arrest in response to
RT loss of microtubule function."

```

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RL Cell 66:507-517(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=828c / AB972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RN CHARACTERIZATION.
RP MEDLINE=21385309; PubMed=11493673;
RA Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.,
RA Johnston L.H.;
RT "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
RT regulates cytokinesis.";
RL J. Cell Sci. 114:2345-2354(2001).
CC -!- FUNCTION: Part of a checkpoint which monitors spindle integrity
CC and prevents premature exit from mitosis. This cell-cycle arrest
CC depends upon inhibition of the G-protein Tem1 by the BFA1/BUB2
CC complex.
CC -!- SUBUNIT: Interacts with BFA1.
CC -!- SUBCELLULAR LOCATION: Spindle poles.
CC -!- SIMILARITY: TO S.POMBE CDC16.
CC
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CC
CC EMBL; M64706; AAA16885.1; -.
CC DR EMBL; Z49703; CAA89785.1; -.
CC DR PIR; A39654; A39654.
CC DR SGD; S0004659; BUB2.
CC DR InterPro; IPR000195; RadCAP_TBC.
CC DR Pfam; PF00566; TBC; 1.
CC DR SMART; SM00164; TBC; 1.
CC KW Cell cycle; Mitosis.
CC SQ SEQUENCE 306 AA; 35027 MW; ALDDBFB549E81EA3 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 306;
Best Local Similarity 41.7%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQRNRK 12
   |||||
Db 108 CFANQQRQK 119

RESULT 14
ID YKYL_CABEL STANDARD; PRT; 455 AA.
AC Q19910;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein F30B5.4 in chromosome IV.
GN F30B5.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Ploloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N., Bradshaw H.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RN REVISIONS.
RA Waterston R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.
CC
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CC
CC EMBL; Z28622; CAA82262.1; -.
CC DR FlyBase; FBgn0004698; mus210.
CC DR InterPro; IPR004583; Rad4.
CC DR TIGRFAMs; TIGR00605; rad4; 1.
CC KW DNA repair; DNA-binding; Nuclear protein.
CC FT DOMAIN 33 40 POLY-ASP.
CC FT DOMAIN 632 637 POLY-SER.
CC FT DOMAIN 686 693 POLY-SER.
CC
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CC
CC EMBL; U42437; AAA93493.2; -.
CC DR WormPep; F30B5.4; CE28552.
CC KW Hypothetical protein.
CC SQ SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 455;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRNRK 10
   |||||
Db 102 CIQWLNRRR 111

RESULT 15
ID XPC_DROME STANDARD; PRT; 1293 AA.
AC Q24595;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-repair protein complementing XP-C cells homolog (Xeroderma
DE pigmentosum group C complementing protein homolog) (XPCDM) (Mutagen-
DE sensitive 209 protein).
GN MUS210 OR XPC OR XPC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=DP CN BW; TISSUE=Embryo;
MEDLINE=94173663; PubMed=8127661;
RA Henning K.A., Peterson C., Legerski R., Friedberg E.C.;
RT "Cloning the Drosophila homolog of the Xeroderma pigmentosum
RT complementation group C gene reveals homology between the predicted
RT human and Drosophila polypeptides and that encoded by the yeast RAD4
RT gene.";
RL Nucleic Acids Res. 22:257-261(1994).
CC -!- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA
CC DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO
CC ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES (BY SIMILARITY).
CC -!- FUNCTION: INVOLVED IN NUCLEOTIDE EXCISION REPAIR OF DNA DAMAGED
CC WITH UV LIGHT, BULKY ADDUCTS, OR CROSS-LINKING AGENTS.
CC -!- SUBUNIT: HETERODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: TO YEAST RAD4 AND MAMMALIAN XPC.
CC
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CC
CC EMBL; Z28622; CAA82262.1; -.
CC DR FlyBase; FBgn0004698; mus210.
CC DR InterPro; IPR004583; Rad4.
CC DR TIGRFAMs; TIGR00605; rad4; 1.
CC KW DNA repair; DNA-binding; Nuclear protein.
CC FT DOMAIN 33 40 POLY-ASP.
CC FT DOMAIN 632 637 POLY-SER.
CC FT DOMAIN 686 693 POLY-SER.

```

FT DOMAIN 922 938 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 1195 1211 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 1275 1291 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 SQ SEQUENCE 1293 AA; 144177 MW; 99DF671F9A4151CS CRC64;  
 Query Match 52.1%; Score 37; DB 1; Length 1293;  
 Best Local Similarity 50.0%; Pred. No. 84;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMRKAR 12.  
 Db 1016 CASWSTTVRKAR 1027

Search completed: February 21, 2003, 07:27:53  
 Job time : 5.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 20.8 Seconds  
(without alignments)  
118.873 Million cell updates/sec

Title: US-09-743-107b-78

Perfect score: 71

Sequence: 1 CFQWQNNRKR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	87.3	711	4 Q8TCD2	Q8tcd2 homo sapien
2	58	81.7	38	4 Q9UCV5	Q9ucv5 homo sapien
3	50	70.4	33	6 Q9TR80	Q9tr80 ovis aries
4	44	62.0	279	16 Q8XSE2	Q8xse2 ralestonia s
5	43	60.6	298	16 Q8YF77	Q8yfp77 anabaena sp
6	41	57.7	148	10 Q9XHP1	Q9xhp1 sesamum ind
7	41	57.7	222	16 P96876	P96876 mycobacteri
8	41	57.7	275	5 Q93780	Q93780 caenorhabdi
9	40	56.3	108	9 Q8SC55	Q8sc55 stx2 conver
10	40	56.3	373	16 Q9RJP2	Q9rjp2 streptomyce
11	40	56.3	469	9 Q38115	Q38115 bacterioph
12	40	56.3	584	17 Q9HPA3	Q9hpa3 halobacteri
13	40	56.3	647	3 Q93843	Q93843 emericella
14	40	56.3	2348	5 Q9V346	Q9v346 drosophila
15	39	54.9	105	10 Q9XFD5	Q9xdf5 oryza sativ
16	39	54.9	121	10 Q9LTD4	Q9ltd4 arabidopsis

17	39	54.9	306	4 Q8TAX2	Q8tax2 homo sapien
18	39	54.9	372	10 Q81653	Q81653 hemerocalli
19	39	54.9	466	4 Q9NUS2	Q9nus2 homo sapien
20	39	54.9	488	10 Q8S934	Q8s934 diospyros k
21	39	54.9	531	10 Q9LTD4	Q9ltd4 arabidopsis
22	39	54.9	742	5 Q18151	Q18151 caenorhabdi
23	39	54.9	1693	2 Q9F5F7	Q9f5f7 agrobacteri
24	39	54.9	1693	2 Q9R6L2	Q9r6l2 agrobacteri
25	39	54.9	1693	16 Q8U634	Q8u634 agrobacteri
26	38	53.5	191	15 Q77857	Q77857 human immun
27	38	53.5	165	7 Q78039	Q78039 triakis scy
28	38	53.5	205	8 Q98RR2	Q98rr2 guillardia
29	38	53.5	341	11 Q8R2A4	Q8r2a4 mus musculu
30	38	53.5	343	7 Q46819	Q46819 triakis scy
31	38	53.5	343	7 Q46838	Q46838 triakis scy
32	38	53.5	343	7 Q46886	Q46886 triakis scy
33	38	53.5	397	16 Q9XAX9	Q9xax9 streptomyce
34	38	53.5	464	16 Q8YF95	Q8yfp95 anabaena sp
35	38	53.5	511	16 Q8Z462	Q8z462 salmonella
36	38	53.5	515	10 Q22185	Q22185 arabidopsis
37	38	53.5	543	10 Q22188	Q22188 arabidopsis
38	38	53.5	2186	5 Q9N906	Q9n906 trypanosoma
39	37	52.1	169	4 Q9BWJ9	Q9bwj9 homo sapien
40	37	52.1	273	2 Q31090	Q31090 rhizobium l
41	37	52.1	274	4 Q9SM21	Q9sm21 homo sapien
42	37	52.1	331	10 Q9XEU4	Q9xeu4 oryza sativ
43	37	52.1	363	5 Q8SX19	Q8sxi9 drosophila
44	37	52.1	367	16 Q8UCR7	Q8ucr7 agrobacteri
45	37	52.1	393	10 Q9ZTP0	Q9ztp0 oryza sativ

## ALIGNMENTS

### RESULT 1

Q8TCD2	PRELIMINARY;	PRT;	711 AA.
ID Q8TCD2	DT 01-JUN-2002 (TREMREL. 21, Created)		
AC Q8TCD2	DT 01-JUN-2002 (TREMREL. 21, Last sequence update)		
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)	DE Lactotransferrin.		
OS Homo sapiens (Human).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OX NCBI_TaxID=9606;		
RN [1]	RP SEQUENCE FROM N.A.		
RC TISSUE=PROSTATE;	RA Strausberg R.;		
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.	DR EMBL; BC022347; AAH22347.1; -.		
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;			

Query Match 87.3%; Score 62; DB 4; Length 711;  
Best Local Similarity 100.0%; Pred. No. 0.0049;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 CFQWQNNRKR 10
DB	39 CFQWQNNRKR 48

### RESULT 2

Q9UCV5	PRELIMINARY;	PRT;	38 AA.
ID Q9UCV5	DT 01-MAY-2000 (TREMREL. 13, Created)		
AC Q9UCV5	DT 01-MAY-2000 (TREMREL. 13, Last sequence update)		
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)	DE Lactoferrin homolog (Fragment).		
OS Homo sapiens (Human).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96081613; PubMed=8551695;
RX Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
  seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
DR HSP; P02788; IBKA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDBE CRC64;

Query Match 81.7%; Score 58; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0011; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 2 FQWQNRKAR 12
   |||||
DB 21 FQWQNRKVR 31

RESULT 3
Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samou D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O77698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 70.4%; Score 50; DB 6; Length 33;
Best Local Similarity 70.0%; Pred. No. 0.028; 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1;

QY 1 CFQWQNRK 10
   |||||
DB 19 CYQWQNRK 28

RESULT 4
Q8XSE2 PRELIMINARY; PRT; 279 AA.
AC Q8XSE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ICC protein homolog.
GN ICC OR RSP0534 OR RS00414.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billaud A., Brottier P., Camus J.C., Cattolico L.,
RA Chandier M., Choisme N., Claudel-Renard C., Cumac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:457-502(2002)
DR EMBL; AL646079; CA017895.1; -;
DR InterPro; IPR004843; M-peptidase.
DR InterPro; IPR004844; S/T-phosphatase.
DR Pfam; PF00149; Metallophos; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 62.0%; Score 44; DB 16; Length 279;
Best Local Similarity 50.0%; Pred. No. 3.5; 3; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 3;

QY 1 CFQWQNRKAR 12
   |||||
DB 244 CFQWQNRKAR 255

RESULT 5
Q8YP77 PRELIMINARY; PRT; 298 AA.
AC Q8YP77;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr4323.
GN ALR4323.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
  cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003596; BAB76022.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 34513 MW; 64036B5B52299A9F CRC64;

Query Match 60.6%; Score 43; DB 16; Length 298;
Best Local Similarity 70.0%; Pred. No. 5.8; 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2;

QY 2 FQWQNRK 11
   |||||
DB 163 FHWQNRK 172

RESULT 6
Q9XHP1 PRELIMINARY; PRT; 148 AA.
AC Q9XHP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;

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RN  SEQUENCE FROM N.A.
RC  STRAIN=TAINAN 1;
RX  MEDLINE=20074970; PubMed=10606554;
RA  Tai S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT  "Molecular cloning of IIS globulin and 2S albumin, the two major seed
RT  storage proteins in sesame.";
RL  J. Agric. Food Chem. 47:4932-4938 (1999).
DR  EMBL; AF091841; AAD42943.1; -.
DR  InterPro; IPR003612; AAI.
DR  InterPro; IPR001768; Try/amy1_inhbr.
DR  Pfam; PF00234; tryp_alpha_amy1; 1.
DR  PRINTS; PR00496; NAPIIN.
DR  SMART; SM00499; AAI; 1.
SQ  SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match          57.7%; Score 41; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 6.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 CFQWQNNRMR 9
Db  54 CFQWQNNRMR 62

RESULT 7
ID  P96876          PRELIMINARY;      PRT; 222 AA.
AC  P96876;
DT  01-MAY-1997 (TrEMBLrel. 03, Created)
DT  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Hypothetical protein RV3271c.
GN  RV3271c OR MTCY71.11C OR MT3371.
OS  Mycobacterium tuberculosis.
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX  NCBI_TaxID=1773;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=H37RV;
RX  MEDLINE=98295987; PubMed=9634230;
RA  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA  Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekala F.,
RA  Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA  Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtrold S.,
RA  Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA  Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA  Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA  Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA  "Deciphering the biology of Mycobacterium tuberculosis from the
RT  complete genome sequence.";
RL  Nature 393:537-544 (1998).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CDC 1551 / OSHKOSH;
RX  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA  Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA  Kolonay J.F., Nelson W.C., Umayan L.A., Esmolaeva M.D., Salzberg S.L.,
RA  Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA  Bishai W.;
RT  "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT  laboratory strains.";
RL  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z92771; CAB07084.1; -.
DR  EMBL; AE007146; AAK47712.1; -.
DR  TIGR; MT3371; -.
DR  TubercuList; Rv3271c; -.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 222 AA; 23633 MW; B9714287801D44FB CRC64;

Query Match          57.7%; Score 41; DB 16; Length 222;

Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  3 QWQNNRMRKAR 12
Db  24 QWQNNRMRKAR 33

RESULT 8
ID  Q93780          PRELIMINARY;      PRT; 275 AA.
AC  Q93780;
DT  01-FEB-1997 (TrEMBLrel. 02, Created)
DT  01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  F53H4.4 protein.
GN  F53H4.4.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Dobson R.;
RL  Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99069613; PubMed=9851916;
RA  none;
RT  "Genome sequence of the nematode C.elegans: A platform for
RT  investigating biology.";
RL  Science 282:2012-2018 (1998).
DR  EMBL; Z81089; CAB03137.1; -.
SQ  SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match          57.7%; Score 41; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  2 FQWQNNRMRKAR 12
Db  262 FQWQNNRMRKTR 272

RESULT 9
ID  Q8SC55          PRELIMINARY;      PRT; 108 AA.
AC  Q8SC55;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Hypothetical 12.3 kDa protein.
OS  Stx2 converting bacteriophage I.
OC  Viruses.
OX  NCBI_TaxID=180816;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=STX2 PHAGE-I;
RA  Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
RA  Yamasaki S., Takeda Y.;
RT  "Genomic sequence of Shiga toxin 2-converting phage isolated from
RT  Escherichia coli O157:H7 Okayama strain and comparison with other
RT  Shiga toxin 2-converting phages.";
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF004402; BAB87947.1; -.
KW  Hypothetical protein.
SQ  SEQUENCE 108 AA; 12279 MW; 2FF2E76690C78BA7 CRC64;

Query Match          56.3%; Score 40; DB 9; Length 108;
Best Local Similarity 63.6%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  1 CFQWQNNRMRKA 11

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||||| : |||
Db 31 CFQWISDNKA 41

RESULT 10
Q9RJ2 PRELIMINARY; PRT; 373 AA.
AC Q9RJ2;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical protein SCO0602.
GN SCO0602 OR SCF55.26.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 MB Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; ALI32991; CAB61296.1; -
DR InterPro; IPR003447; Meth_resist.
DR Pfam; PF02388; FmA; 1.
DR Hypothetical protein.
SQ SEQUENCE 373 AA; 42190 MW; 313D32E959EAE8A58 CRC64;

Query Match 56.3%; Score 40; DB 16; Length 373;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CFQWISDNKA 11
||||| : |||
Db 196 QWRNRNKA 204

RESULT 11
Q38115 PRELIMINARY; PRT; 469 AA.
AC Q38115;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)

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DE ORE29.
OS Bacteriophage rit.
OC Viruses.
OX NCBI_TaxID=43685;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96332669; PubMed=8730874;
RA Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
RT "Inducible gene expression mediated by a repressor-operator system
RT isolated from Lactococcus lactis bacteriophage rit.";
RL Mol. Microbiol. 19:1331-1341(1996).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=96332669; PubMed=8730875;
RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.;
RA Venema G., Nauta A.;
RT "Sequence analysis and molecular characterization of the temperate
RT lactococcal bacteriophage rit.";
RL Mol. Microbiol. 19:1343-1355(1996).
DR EMBL; U38906; AAB18704.1; -
DR SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;

Query Match 56.3%; Score 40; DB 9; Length 469;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQNRK 10
||||| : |||
Db 39 CYPWQXNLLK 48

RESULT 12
Q9HPA3 PRELIMINARY; PRT; 584 AA.
AC Q9HPA3;
DT 01-MAR-2001 (TREMblrel. 15, Created)
DT 01-MAR-2001 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Vng1732c.
GN VNG1732C.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=2050483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.F., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Fohlischroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AB005078; AAG19967.1; -
DR InterPro; IPR001646; Speptide_repeat.
DR Pfam; PF001622; K-channel_pore.
DR Pfam; PF00805; Pentapeptide; 2.
DR Complete proteome.
SQ SEQUENCE 584 AA; 65151 MW; 21BF5D5F0486CC6 CRC64;

Query Match 56.3%; Score 40; DB 17; Length 584;
Best Local Similarity 41.7%; Pred. No. 42;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWQNRK 12
||||| : |||
Db 445 CFTWRKDMERK 456

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RESULT 13
O93843 ID O93843 PRELIMINARY; PRT; 647 AA.
AC DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE GI/S regulator.
GN NIMO.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutrotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R153;
RA James S.W., Prasauckas K.A., Scacheri P.C., Gyax S.E., Matura R.A.,
RA Bullock K.A.;
RT "nimo" gene of Aspergillus nidulans.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014812; AAD01519.1; -.
SQ SEQUENCE 647 AA; 72842 MW; A84A547CFB3D0EF1 CRC64;

Query Match 56.3%; Score 40; DB 3; Length 647;
Best Local Similarity 77.8%; Pred No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QWQRMKKA 11
Db 134 QWQRYHKA 142
|||: |||
|||: |||

RESULT 14
Q9V346 ID Q9V346 PRELIMINARY; PRT; 2348 AA.
AC Q9V346;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG8723 protein.
GN CG1198 OR CG8723.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houson K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Matteli B., McIntosh T.C., McLeod M.P., McPherson D.,

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusaker D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
CC -!- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AE003839; AAF59156.1; -.
DR HSSP; P24182; 1DVI.
DR Flybase; FBgn0033246; CG11198.
DR InterPro; IPR001882; Biotin attach.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR000901; CPSase.
DR Pfam; PF02785; Biotin-card_C; 1.
DR Pfam; PF03664; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Biotin.
SQ SEQUENCE 2348 AA; 263722 MW; ED7E6FB9976E1CD2 CRC64;

Query Match 56.3%; Score 40; DB 5; Length 2348;
Best Local Similarity 50.0%; Pred No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWQRMKRAK 12
Db 563 CFQWQRMKRAK 574
|||: |||
|||: |||

RESULT 15
Q9XFD5 ID Q9XFD5 PRELIMINARY; PRT; 105 AA.
AC Q9XFD5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANICLE;
RA Liu J., Yang J.;
RT "Suppression subtractive hybridization (SSH) identified candidate
genes that are differentially expressed at rice young panicle.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF140486; AAD29699.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;

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Query Match 54.9%; Score 39; DB 10; Length 105;  
Best Local Similarity 60.0%; Pred. No. 10;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWRNRK 10  
| | | | :  
Db 61 CFQWRLGKK 70

Search completed: February 21, 2003, 07:44:33  
Job time : 22.8 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:25:55 ; Search time 28.3 Seconds  
(without alignments)  
56.502 Million cell updates/sec

Title: US-09-743-107B-79  
Perfect score: 70  
Sequence: 1 CFQQRNMRKVA 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

* Result	No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AA1980	Human lactoferrin
2	66	94.3	12	21	AA1981	Human lactoferrin
3	66	94.3	12	21	AA1982	Human lactoferrin
4	66	94.3	12	21	AA1983	Human lactoferrin
5	66	94.3	13	21	AA1984	Human lactoferrin
6	66	94.3	13	21	AA1985	Human lactoferrin
7	66	94.3	13	21	AA1986	Human lactoferrin
8	66	94.3	13	21	AA1987	Human lactoferrin
9	66	94.3	14	21	AA1988	Human lactoferrin
10	66	94.3	14	21	AA1989	Human lactoferrin

11	66	94.3	15	17	AA198554	Peptide for anti-u
12	66	94.3	15	21	AA198030	Human lactoferrin
13	66	94.3	15	21	AA198035	Human lactoferrin
14	66	94.3	15	21	AA198062	Human lactoferrin
15	66	94.3	15	21	AA198063	Human lactoferrin
16	66	94.3	16	21	AA198031	Human lactoferrin
17	66	94.3	16	21	AA198064	Human lactoferrin
18	66	94.3	16	21	AA198065	Human lactoferrin
19	66	94.3	17	21	AA198034	Human lactoferrin
20	66	94.3	17	21	AA198066	Human lactoferrin
21	66	94.3	17	21	AA198067	Human lactoferrin
22	66	94.3	18	15	AA198352	Human lactoferrin
23	66	94.3	18	17	AA198397	Advanced glycosyla
24	66	94.3	18	21	AA198033	Human lactoferrin
25	66	94.3	19	21	AA198867	Amino acid sequenc
26	66	94.3	19	21	AA198486	Peptide used to tr
27	66	94.3	19	21	AA198032	Human lactoferrin
28	66	94.3	20	13	AA198180	Anti microbial pep
29	66	94.3	20	14	AA198481	Lactoferrin-relate
30	66	94.3	20	15	AA198530	Lactoferrin-derive
31	66	94.3	20	15	AA198531	Lactoferrin-derive
32	66	94.3	20	15	AA198746	Lactoferrin-derive
33	66	94.3	20	15	AA198746	Lactoferrin-derive
34	66	94.3	20	16	AA198498	Bovine lactoferrin
35	66	94.3	20	16	AA198499	Lactoferrin-derive
36	66	94.3	20	16	AA198026	Anti-parasitic lac
37	66	94.3	20	16	AA198026	Anti-parasitic lac
38	66	94.3	20	17	AA198553	Peptide for anti-u
39	66	94.3	20	17	AA198552	Lactoferrin-derive
40	66	94.3	20	17	AA198045	Lactoferrin-derive
41	66	94.3	20	17	AA198067	Lactoferrin-derive
42	66	94.3	20	17	AA198762	Lactoferrin-derive
43	66	94.3	20	17	AA198762	Lactoferrin-derive
44	66	94.3	20	18	AA198622	Lactoferrin-derive
45	66	94.3	20	18	AA198615	Anti-parasitic pep

#### ALIGNMENTS

RESULT 1  
AA198079  
ID AA198079 standard; Peptide; 12 AA.  
XX AA198079;  
-- XX  
DT 25-APR-2000 (first entry)  
XX Human lactoferrin derived peptide SEQ ID NO:79.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
XX urinary tract infection; colitis; Candida infection; fungicidal;  
XX bactericidal; preservative.

XX Homo sapiens.  
OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer I, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -  
 XX  
 XX Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 12 AA;

Query Match 100.0%; Score 70; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKVA 12  
 |||||  
 DB 1 CFQWQRMNRKVA 12

RESULT 2  
 AAY78038  
 ID AAY78038 standard; Peptide; 12 AA.  
 AC AAY78038;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:38.  
 DE  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-S01230.  
 PF  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.  
 PS  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRMNRKV 11  
 |||||  
 DB 1 CFQWQRMNRKV 11

RESULT 3  
 AAY78046  
 ID AAY78046 standard; Peptide; 12 AA.  
 XX  
 AC AAY78046;  
 XX  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:46.  
 DE  
 DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

OS Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 XX  
 XX 06-JUL-1999; 99WO-S01230.  
 PF  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.  
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.  
 PS  
 XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKV 11  
 |||||  
 DB 1 CFQWQRNMRKV 11

RESULT 4

AAV78047  
 ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;

DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SB01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 12 AA;

Query Match 94.3%; Score 66; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKV 11  
 |||||  
 DB 1 CFQWQRNMRKV 11

RESULT 5

AAV78037  
 ID AAY78037 standard; Peptide; 13 AA.

XX AC AAY78037;

DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SB01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food -

XX PS Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumours. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX SQ Sequence 13 AA;

Query Match 94.3%; Score 66; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOWQNRKRV 11  
 DB 2 CFOWQNRKRV 12

## RESULT 6

AAAY78048  
 ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

AC 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:48.

DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

PS Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

SQ Sequence 13 AA;

Query Match 94.3%; Score 66; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOWQNRKRV 11

DB 2 CFOWQNRKRV 12

## RESULT 7

AAAY78049

ID AAY78049 standard; Peptide; 13 AA.

XX AAY78049;

AC 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:49.

DE Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

PT inflammations and tumors and for use in infant formula food

PS Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

SQ Sequence 13 AA;

Query Match 94.3%; Score 66; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFOWQNRKRV 11

DB 2 CFOWQNRKRV 12

## RESULT 8

AAAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AAY78036;

AC 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:36.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 FN 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -  
 XX Claim 12; Page 69; 102pp; English.  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 94.3%; Score 66; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-05; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 0; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMRKV 11  
 Db 3 CFQWQRNMRKV 13  
 RESULT 9  
 ID AAY78050 standard; Peptide; 14 AA.  
 AC AAY78050;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:50.  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.

OS Synthetic.  
 XX WO200001730-A1.  
 PN 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 XX 06-JUL-1998; 98SE-0002441.  
 PR 17-JUL-1998; 98SE-0002562.  
 PR 29-DEC-1998; 98SE-0004614.  
 XX (ASCI-) A+ SCI INVEST AB.  
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
 PI WPI; 2000-147388/13.  
 DR New peptides used for treatment and prevention of infections,  
 XX inflammations and tumors and for use in infant formula food -  
 XX Claim 15; Page 75; 102pp; English.  
 CC AAY78001 to AAY78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations and/or tumors. The peptides can also be used  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.  
 XX Sequence 14 AA;  
 SQ Query Match 94.3%; Score 66; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-05; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 0; Indels 0; Gaps 0;  
 QY 1 CFQWQRNMRKV 11  
 Db 3 CFQWQRNMRKV 13  
 RESULT 10  
 ID AAY78051 standard; Peptide; 14 AA.  
 AC AAY78051;  
 XX 25-APR-2000 (first entry)  
 DT Human lactoferrin derived peptide SEQ ID NO:51.  
 XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200001730-A1.  
 FN 13-JAN-2000.  
 XX 06-JUL-1999; 99WO-SE01230.  
 PF

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XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX PI WPI; 2000-147388/13.
XX DR WPI; 2000-147388/13.
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food
XX PS Claim 18; Page 75; 102pp; English.
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumors. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.
XX SQ Sequence 14 AA;

Query Match 94.3%; Score 66; DB 21; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CFQWQNRKVK 11
Db 3 CFQWQNRKVK 13

RESULT 11
AAR98554
ID AAR98554 standard; Peptide; 15 AA.
XX AC AAR98554;
XX DT 12-NOV-1996 (first entry)
XX DE Peptide for anti-ulcer agent.
XX KW anti-ulcer agent; low toxicity; stable; heat-resistant.
XX OS Synthetic.
XX PN JP08143468-A.
XX PD 04-JUN-1996.
XX PF 17-NOV-1994; 94JP-0283869.
XX PR 17-NOV-1994; 94JP-0283869.
XX PA (MORG ) MORINAGA MILK IND CO LTD.
XX DR WPI; 1996-318857/32.
XX PT Anti-ulcer agent contg. peptide - has low toxicity, is
XX PT heat-resistant and water-soluble
XX PS Claim 1; Page 11; 11pp; Japanese.

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XX CC AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
XX CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
XX CC administered orally and be produced in large amounts.
XX SQ Sequence 15 AA;

Query Match 94.3%; Score 66; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CFQWQNRKVK 11
Db 2 CFQWQNRKVK 12

RESULT 12
AAY78030
ID AAY78030 standard; Peptide; 15 AA.
XX AC AAY78030;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:30.
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200001730-A1.
XX PD 13-JAN-2000.
XX PF 06-JUL-1999; 99WO-SE01230.
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX PI WPI; 2000-147388/13.
XX DR WPI; 2000-147388/13.
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -
XX PS Claim 11; Page 67; 102pp; English.
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumors. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.
XX SQ Sequence 15 AA;

```

Query Match 94.3%; Score 66; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQNRKRV 11  
 DB 5 CFQWQNRKRV 15

## RESULT 13

AAV78035  
 ID AAV78035 standard; Peptide; 15 AA.

XX AAV78035;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:35.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

FN WO200001730-A1.

XX 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food

XX Claim 12; Page 69; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations, colitis, and Candida infection on a mucosal  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 15 AA;

Query Match 94.3%; Score 66; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQNRKRV 11  
 DB 4 CFQWQNRKRV 14

## RESULT 14

AAV78062  
 ID AAV78062 standard; Peptide; 15 AA.

XX AAV78062;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:62.

XX Human; lactoferrin; modification; infection; inflammation; tumour;  
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
 KW urinary tract infection; colitis; Candida infection; fungicidal;  
 KW bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

PN WO200001730-A1.

XX 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR New peptides used for treatment and prevention of infections,  
 PT inflammations and tumors and for use in infant formula food

XX Claim 15; Page 81; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human  
 CC lactoferrin. The peptides are taken up in the intestine through  
 CC binding to specific lactoferrin receptors and are then transported  
 CC through the circulation. A medicinal product of the peptide or fragment  
 CC can be used for treating and/or prevention of infections (such as  
 CC urinary tract infections, colitis, and Candida infection on a mucosal  
 CC membrane), inflammations, colitis, and Candida infection on a mucosal  
 CC in food stuffs such as infant formula food. The peptides are also  
 CC fungicidal and bactericidal and may also be used as preservatives.  
 CC Even though native human lactoferrin have been shown to have desired  
 CC anti-inflammatory anti-infectious and anti-tumoural properties they  
 CC cannot be used clinically on a broad basis because of high production  
 CC costs. Therefore, provision of peptides based on lactoferrin would  
 CC enable them to be used for the same purposes as lactoferrin at lower  
 CC cost.

XX Sequence 15 AA;

Query Match 94.3%; Score 66; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWQNRKRV 11  
 DB 4 CFQWQNRKRV 14

## RESULT 15

AAV78063  
 ID AAV78063 standard; Peptide; 15 AA.

XX AAV78063;



XX 25-APR-2000 (first entry)  
DT Human lactoferrin derived peptide SEQ ID NO:63.  
DE  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001730-A1.  
XX  
PD 13-JAN-2000.  
XX  
XX 06-JUL-1999; 99WO-SE01230.  
PF  
XX 06-JUL-1998; 98SE-0002441.  
PR 17-JUL-1998; 98SE-0002562.  
PR 29-DEC-1998; 98SE-0004614.  
XX  
XX (ASCI-) A+ SCI INVEST AB.  
PA  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
PI WPI; 2000-147388/13.  
XX  
XX New peptides used for treatment and prevention of infections,  
PT inflammations and tumors and for use in infant formula food -  
XX  
XX Claim 18; Page 81; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
CC lactoferrin. The peptides are taken up in the intestine through  
CC binding to specific lactoferrin receptors and are then transported  
CC through the circulation. A medicinal product of the peptide or fragment  
CC can be used for treating and/or prevention of infections (such as  
CC urinary tract infections, colitis, and Candida infection on a mucosal  
CC membrane), inflammations and/or tumours. The peptides can also be used  
CC in food stuffs such as infant formula food. The peptides are also  
CC fungicidal and bactericidal and may also be used as preservatives.  
CC Even though native human lactoferrin have been shown to have desired  
CC anti-inflammatory anti-infectious and anti-tumoural properties they  
CC cannot be used clinically on a broad basis because of high production  
CC costs. Therefore, provision of peptides based on lactoferrin would  
CC enable them to be used for the same purposes as lactoferrin at lower  
CC cost.  
XX  
XX Sequence 15 AA;  
SQ

Query Match 94.3%; Score 66; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFWQRMNRKV 11  
| | | | |  
Db 4 CFWQRMNRKV 14

Search completed: February 21, 2003, 07:37:13  
Job time : 28.35 secs

